Subject: CBEP Global Bat Alliance meeting
Location: Hilton Alexandria Mark Center; exact location TBD

Start: Thursday, February 09, 2017 1:30 PM EST
End: Thursday, February 09, 2017 2:30 PM EST
Show Time As: Busy

Recurrence: None

Meeting Status: Not yet responded

Organizer: Flegler, Ayanna J CTR (US)
Required Attendees: Flegler, Ayanna J CTR (US) >; Stokes, Martha M CIV (US) l>; Lancaster, Mary J CIV (US) < Jon Epstein ecohealthalliance.org>; Gavin James Smith >; Ian Mendenhall @ecohealthalliance.org ecohealthalliance.org>; Kading,Rebekah >; vkapur ; jkmazet >; kityrob >; joram.buza >

CBEP would like to convene researchers from all CBEP-engaged regions to discuss formation of a Global Bat Alliance (GBA). The GBA will aim to build and leverage country and regional capabilities to generate an enhanced understanding of bats and their ecology within the context of pathogens of security concern. This meeting will serve to discuss future collaborative efforts of the Global Bat Alliance.

From: Megan Hudson
Sent: Thursday, June 14, 2018 2:31 PM EDT
To: nisreen.hmoud >; joram.buza >; c_demetria < >; Kading,Rebekah ; kityrob < >; tamar_kutateladze >; dreeder >; ksidamonidze >; l.urushadze ; spwa ; abelwade >; ecohealthalliance.org ian.mendenhall@ @ecohealthalliance.org ; vkapur >
CC: Katie Leahy >; Gano Cohen, Kelsey A CTR DTRA J3-7 (US) ; Stokes, Martha M CIV (US) ; Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) >
Subject: BOHRN Meeting Agenda and Materials 20 - 21 June
Attachment(s): "INSTRUCTIONSResearchQuadChart_BOHRN.pdf","Blank_ResearchQuadChart.docx","BOHRN Agenda v.5[6].pdf"

All,

The final agenda for our BOHRN 20 – 21 June meeting is attached. Our meeting will be held in the Garden South Meeting Room at the Hilton Garden Inn in Saskatoon (90 22 St. E, Saskatoon, SK S7K 3X6, Canada).

From our discussions in January we built in time to discuss your current research, as part of this event's agenda. In order to maintain time for BOHRN discussions, we are asking for you to fill out the attached quad chart. Quad charts are designed to give a quick overview of information. Therefore, please don't try to fit all of your research into the boxes, just important points or conclusions you would like to provide to the group. **Please review and fill in the quad chart prior to our meeting, and plan on presenting your chart in 5 minutes during the first day**.

We are requesting that you email your quad chart back **NLT Monday, 18 June**. Attached are instructions and a blank quad chart. Be advised that we will only project one slide, therefore all information must fit within the attached chart provided.

Let us know if you have any questions regarding any of the documents. **As a reminder we will need a completed quad chart from you NLT 18 June.** We look forward to seeing everyone next week in Canada.

Thank you,

Megan

Megan Hudson
Task Lead | Global Systems Engineering
6303 Little River Turnpike #208
Alexandria, VA 22312

http://globalsyseng.com

TECHNICAL DESCRIPTION AND OBJECTIVES

APPROACH

MILESTONES, SCHEDULE, AND STATUS

IMPACT

BOHRN STEERING COMMITTEE MEETING
20 -21 June 2018
Saskatoon, Canada

Hilton Garden Inn, Saskatoon Canada
Garden South Meeting room

Wednesday 20 June 2018 Day 1	
0900 – 1000	Executive Committee Meeting Only
1000 – 1045	Welcoming Remarks
1045 – 1100	House Keeping and Admin
1100 – 1130	BOHRN updates from January
1130 – 1145	Working Break
1145 – 1300	Current Research and Interest (quad chart presentations)
1300 – 1400	Working Lunch
1400 – 1600	Breakout Group Session
(1500 – 1530)	Working Break
1600 – 1630	Brief-out of Breakout Groups
1630 – 1645	Day 2 Agenda Review
Thursday 21 June 2018 Day 2	
0900 – 1000	Breakout Group – Review of Day 1
1000 – 1030	Large Group Discussion of next steps
1030 – 1045	Working Break
1045 – 1145	Network Analysis
1145 – 1215	BTCD Introduction
1215 – 1315	Working Lunch
1315 – 1345	Novel work at the Lugar Center – Tbilisi, Georgia
1345 – 1415	Large Group question and answer on BTCD
1415 – 1430	Working Break
1430 – 1500	Live edits of BTCD agenda
1500 – 1600	Next Steps

Quad Chart Instructions: Please fill out all four portions of the quad chart. The chart is read in a clockwise direction starting with the technical description. This activity is intended to provide a big picture overview and not an in-depth report of your research. Please limit the text to provide only the most important aspects of each quad. You will be given 5 minutes to present the information within this chart. Refer to the questions in each box for more guided assistance.

TECHNICAL DESCRIPTION AND OBJECTIVES

Briefly describe the research you are currently conducting and why. What questions are you trying to answer and what is the importance of this research to your field? What is currently known about your research? Consider the following:

1. **Underlying Challenges**

2. **Current State of Understanding**

APPROACH

What are the specific aims of your research, identify the challenges you will face, tools to overcome challenges, and approach to conducting the research. Consider the following:

1. **What can be done to address the challenges?**

2. **What are the key steps along the way**

3. **What tools and technologies are needed to address the challenges?**

MILESTONES, SCHEDULE, AND STATUS

Briefly explain the timeline of your research. When do you anticipate your research to be completed? Are there deliverables or steps along the way that will show substantial progress? Consider the following:

1. **Provide timeline for delivery**

2. **Quick overview on project status**

IMPACT

Describe the potential impact of your research. What will the impact be for the regional area? Globally? Will this lead to the need for future studies? Consider the following:

1. **Define the quantitative impact of project.**

2. **Define the regional and global impact.**

TECHNICAL DESCRIPTION AND OBJECTIVES

APPROACH

MILESTONES, SCHEDULE, AND STATUS

IMPACT

From: Megan Hudson
Sent: Thursday, March 22, 2018 1:46 PM EDT
To: nisreen.hmoud ; joram.buza <| ; cryanp ; c demetria ; ecohealthalliance.org >; Kading,Rebekah >; vkapur >; tigga.kingston kityrob ; tamar kutateladze >; ian.mendenhall@ ; @ecohealthalliance.org >; dreeder >; ksidamonidze ; gavin.smith ; l.urushadze spwa >; abelwade >
CC: Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) >; Gano Cohen, Kelsey A CTR DTRA J3-7 (US) >; Katie Leahy >; Stokes, Martha M CIV (US) ; Becker, Stephen M CTR DTRA J3-7 (US) >
Subject: BOHRN Steering Committee/One Health Congress Meeting

All,

You are receiving this email, as part of a save the date to attend our BOHRN Steering Committee meeting and the 5th International One Health Congress (OHC) in Saskatoon, Canada.

Our meeting will take place on 20-21 June (location TBD, though likely at the Hilton Garden Inn). The agenda and travel information for this two day event will follow shortly. The OHC will take place 22-25 June.

On behalf of Dr. Marty Stoke and Dr. Mary Lancaster, CBEP will provide funding your travel and registration to the OHC and BOHRN Planning Meeting. While the OHC is not required it would be a good opportunity for networking on behalf of BOHRN. CBEP will be paying for OHC attendance next week. **Therefore, we need you to confirm your attendance to the OHC NLT tomorrow 23 March.** However, please note if regulations for DoD travel are not met by the specified due date, funding for the conference and travel will not be provided.

Please respond with your availability to attend the meeting NLT 23 March.

v/r,

Megan

Megan Hudson
Task Lead | Global Systems Engineering
6303 Little River Turnpike #208
Alexandria, VA 22312

http://globalsyseng.com

From: Katie Leahy <
Sent: Tuesday, November 28, 2017 10:05 AM EST
To: cryanp >; ecohealthalliance.org ; Kading,Rebekah vkapur tigga.kingston >; ecohealthalliance.org >; dreeder

CC: Stokes, Martha M CIV (US) < Aleman, Nicki D CTR DTRA J3-7 (US) ; Megan Hudson >; Lancaster, Mary J CIV (US) >
Subject: BPERNet / PMAC Meeting January 2018
Attachment(s): "JKO SERE ATFP ISOPREP Instructions NOV 2016.doc","dd1351-2 pdf 1351-2 TRAVEL VOUCHER.pdf","ITO_Information.docx","BPERNet PMAC Meeting_Revision 1.docx","PMAC2018 Provisional Conference Program_as of Oct 27.pdf"

All,

You are receiving this email, as part of a formal invitation to attend our BPERNet Steering Committee meeting and the Prince Mahidol Award Conference (PMAC). This information is a couple weeks late, because we have been waiting to confirm our meeting as an official side meeting of PMAC and solicit invitations to PMAC or the entire team. You should be hearing officially from the PMAC planning committee with official letters of invitation. We understand you are very busy people, so please feel free to attend all or portions of the Conference. I am including the PMAC 2018 Provisional Conference Schedule; you should receive a more updated schedule along with your LOI from the PMAC planning committee.

Our meeting will take place on 30 January (location TBD, though likely at the Centara). The agenda is attached (document: BPERNet PMAC Meeting Revision 1). We had originally scheduled the meeting for 31 January; however, now the entire group will be invited to attend a field trip to a bat habitat at the Wat-Luang Phromawas Temple and interact with villagers who are playing a role in EID prevention and control.

On behalf of Dr. Marty Stoke and Dr. Mary Lancaster, CBEP will be funding your travel, lodging, and meals to the BPERNet Planning Meeting and PMAC via Invitational Travel Orders. Specific instructions may be found below my signature block. Please let us know what portions of the week you will be able to attend. I am creating the list for a hotel room block at the Renaissance Ratchaprasong Hotel, across the street from the PMAC venue.

We very much hope you will be able to attend our meeting and some or all of the conference thereafter. Again, please let me know your plans and begin communication with Nicki at your earliest convenience.

V/r,

Katie Leahy

Travel instructions:
Please fill out the attached document: "ITO_Information" and return it to Aleman, Nicki D NLT 7 December 2017. Some of you have inquired about multi-stops, as you are traveling on to other locations. This should be fine as long as it is within the DoD regulations. Nicki and the travel team will be able to work with you and answer any specific questions you may have.

Because you will be traveling on Department of Defense orders outside the United States, you will need to complete a couple training courses (attached – JKO SERE ATFP ISOPREP Instructions). We advise you to complete this NLT 7 December as well and follow the instructions within the form. Please contact me if you have any questions. Also attached a dd1351 Travel Voucher, which you will complete and submit when you return home.

Katie Leahy
Program Manager | Global Systems Engineering
6303 Little River Turnpike, Suite 208
Alexandria, VA 22305

http://globalsyseng.com

ITTEE MEETING AGENDA

gen and Ecology Research Network (BPERNet)

0 January – 3 February 2018

Date: Tuesday, 30 January 2018

BPERNet

Time	Session	Notes
0900 - 0915	Introduction and Meeting Objectives	Marty Stokes and Mary Lancaster will welcome all participants and provide a brief overview of the meeting objectives for the week
0915 - 0945	⊦ Review interim accomplishments since 27 June ⊦ Q&A on TORFTA changes ⊦ Call for votes to accept TORFTA	Executive Committee members will provide an overview of the TORFTA and mission areas; all participants will receive final version ahead of meeting
0945 - 1015	Working Group Focus Areas	Review WG focus areas that were outlined during the 27 June meeting
1015 - 1045	Break	
1045 - 1200	Breakout Group Session I	Breakout Group Session 1 Objectives: ⊦ Define WG research areas (sub-focus area definitions) ⊦ List and prioritize research questions and potential projects for each area ⊦ Identify internal and external research dependencies for each Working Group **Working Group 1: researching host / pathogen biology and interactions** (Dr. Deeann Reeder, Dr. Vivek Kapur, Dr. Joram Buza) **Working Group 2: researching pathogen surveillance, diagnostic capacity, and epidemiology** (Dr. Abel Wade, Dr. Jon Epstein, Dr. Catalino Demetria, Dr. Lela Urushadze, Dr. Supaporn Wacharapluesadee, Dr. Tamar Kutateladze)

		Working Group 3: researching ecology (bat, domesticated animal, and wildlife interface) (Dr. Paul Cryan, Dr. Tigga Kingston, Dr. Robert Kityo) **Working Group 4: researching human – bat interactions and risk characterization** (Dr. Kevin Olival, Dr. Ian Mendenhall)
1200 – 1330	Working lunch / Open discussion	Open discussion objectives Þ Discuss group marketing campaign Þ Members should be prepared to introduce other network affiliations, conferences, and meeting opportunities to market the network, globally Þ Discuss long-term process to collect and collate applications to the network
1330 – 1430	Breakout Group Session I Brief-out	Each group briefs out their discussions according to the objectives; brief-out 10 minutes / WG; Q&A 5 minutes / WG
1430 – 1515	Breakout Group Session II	Breakout Group Session 2 Objectives: Þ List out WG research coverage (who is researching what and where) Þ Identify research gaps and needs Þ Identify WG resource and coverage needs (e.g., target environmentalists in Europe); identify critical POCs for membership Þ Begin drafting short and long timelines and work plans
1515 – 1545	Tea Break	
1545 – 1645	Breakout Group Session II Brief-out	Each group briefs out their discussions according to the objectives; brief-out 10 minutes / WG; Q&A 5 minutes / WG
1645 – 1715	End of session	End of Session Objectives: Þ Review Action Items Þ Discuss date, level of participation, and location for next meeting (all participants should come prepared to briefly discuss their ideas for this topic)

ITTEE MEETING AGENDA

gen and Ecology Research Network (BPERNet)

0 January – 3 February 2018

ITTEE MEETING AGENDA

gen and Ecology Research Network (BPERNet)
0 January – 3 February 2018

Date: Wednesday, 31 January 2018

Site 4 Field Trip EID preparedness Linking Community-Based Approach and Research to National System

<table>
<tr><th>Time</th><th>Session</th><th>Notes</th></tr>
<tr><td>0630
-
0700</td><td>Check-In
Meeting point, ground floor Centara</td><td>Grand Hotel at Central World and get a group T-Shirt. *Please be advised that you have breakfast from the hotel of your stay before checking in for this trip.</td></tr>
<tr><td>0700</td><td>Depart</td><td>Depart from the Centara Grand Hotel to Wat-Luang Health Promoting Hospital</td></tr>
<tr><td>0700
-
0830</td><td>Activities on the Bus</td><td>Introductions and getting to know the group
Introducing the field trip agenda
Overview of the field trip program and Department of Disease Control (VCD)</td></tr>
<tr><td>0830
-
0840</td><td>Arrive at Wat-Luang Health Promoting Hospital</td><td>Welcome performance by Village Health Volunteers</td></tr>
<tr><td>0840
-
0850</td><td>Welcome</td><td>Welcome speech by Chonburi Governor</td></tr>
<tr><td>0850
-
0900</td><td>Introduction</td><td>Roles of Village Health Volunteers and community in disease prevention and control</td></tr>
<tr><td>0900
-
1000</td><td>Breakouts</td><td>Divide participants into three groups (20 minutes/group)
<table>
<tr><th>Group</th><th>0900-0920</th><th>0920-0940</th><th>0940-1000</th></tr>
<tr><td>A</td><td>Emerging Infectious Disease prevention and control system of Wat-Luang Health Promoting Hospital</td><td>Exhibition of bat lifestyle at Wat-Luang Promawas School</td><td>Roles of Village Health Volunteers in Emerging Infectious Disease prevention and control</td></tr>
</table></td></tr>
</table>

<table>
<tr><td></td><td></td><td>
<table>
<tr><td>B</td><td>Exhibition of bat lifestyle at Wat-Luang Promawas School</td><td>Roles of Village Health Volunteers in Emerging Infectious Disease prevention and control</td><td>Emerging Infectious Disease prevention and control system of Wat-Luang Health Promoting Hospital</td></tr>
<tr><td>C</td><td>Roles of Village Health Volunteers in Emerging Infectious Disease prevention and control</td><td>Emerging Infectious Disease prevention and control system of Wat-Luang Health Promoting Hospital</td><td>Exhibition of bat lifestyle at Wat-Luang Promawas School</td></tr>
</table>
</td></tr>
<tr><td>1000 - 1030</td><td>EIDs and bts</td><td colspan="2">Observe bat lifestyle at Wat-Luang Phromawas Temple by Kevin Olival</td></tr>
<tr><td>1030</td><td>Depart</td><td colspan="2">Depart to Phanat Nikhom Hospital</td></tr>
<tr><td>1045 - 1100</td><td>Refreshments</td><td colspan="2">Refreshments at Phanat Nikhom Hospital</td></tr>
<tr><td>1100 - 1200</td><td>Overview of Emerging Infectious Disease Prevention and Control Systems</td><td colspan="2">Þ Roles of Government Agencies
Þ Roles of Community
Þ Revisit Emerging Infectious Disease research</td></tr>
<tr><td>1200 - 1300</td><td>Lunch</td><td colspan="2">Lunch at Phanat Nikhom Hospital</td></tr>
<tr><td>1300 - 1400</td><td>Break out groups</td><td colspan="2">Divide Participants into two groups (30 minutes/group)
<table>
<tr><td>Group</td><td>1300-1330</td><td>1330-1400</td></tr>
<tr><td>A</td><td>Emerging Infectious Disease prevention and control systems of Phanat Nikhom Hospital</td><td>Infectious Unit and Thai Traditional Medicine</td></tr>
</table>
</td></tr>
</table>

		B	Infectious Unit and Thai Traditional Medicine	Emerging Infectious Disease prevention and control systems of Phanat Nikhom Hospital
1400 - 1500	Conclusion	Open discussion and conclusion		
1500 - 1515	Refreshments			
1515	Depart	Leave for Centara Grand Hotel		
1700	Arrive	Arrive at the Centara Grand Hotel		

Date: Thursday, 1 February 2018

Main Conference Program

Time	Session	Notes
0900 - 1030	Opening Session and Keynote Address	Opening Session by **Her Royal Highness Princess Maha Chakri Sirindhorn** Keynote Address Þ Prince Mahidol Award Laureate 2017 Þ Prince Mahidol Award Laureate 2017 Þ **TBC**
1030 - 1100	Break	
1100 - 1230	Plenary 0	Vision 2100: Re-Imagining the End Game for the End of the Pandemic Era
1230 - 1330	Lunch	

ITTEE MEETING AGENDA

gen and Ecology Research Network (BPERNet)
0 January – 3 February 2018

1330 - 1430	Plenary 1	Leadership Needed for Managing Emerging Infectious Diseases of the 21st Century
1430 - 1630	PMAC Sessions	PS1.1: Lessons Learned in Managing Emerging Infectious Diseases (EID) PS1.2: Strategic Information and the Evolution of Emerging Infectious Diseases: Lessons from the Past and New Opportunities PS1.3: Safeguarding Medicines in the Era of AMR: What Do We Know? What Works? PS1.4: Financing Pandemic Preparedness: Where is the Money? PS1.5: One Health on the Move: Nomadic Communities
1630 - 1700	Break	
1700 - 1800	Plenary 2	Futures of Partnerships for a Safer World

ITTEE MEETING AGENDA

gen and Ecology Research Network (BPERNet)

0 January – 3 February 2018

Date: Friday, 2 February 2018

Main Conference Program

Time	Session	Notes
0830 - 0930	Plenary 3	Managing Emerging Infectious Disease and AMR Risk across the Livestock Revolution
0930 - 1000	Break	
1000 - 1200	PMAC Sessions	PS2.1: Beyond MERS and Zika: Are we Prepared for the Next Big Epidemic? PS2.2: AMR: Addressing Excessive and Inappropriate Use of Antibiotics PS2.3: Dealing with an Inter-Connected World: Partnerships for Preparedness, Detection and Response during Mass Gatherings PS2.4: Changing Dynamics: Emerging Infectious Diseases and Antimicrobial Resistance in an Era of Expanding Global Human Population Growth and Movement PS2.5: Reducing the Gap: Addressing Neglected Disease; Neglected Populations
1200 - 1300	Lunch	
1300 - 1500	PMAC Sessions	PS3.1: PS3.2: Lessons Learned from a One Health Approach to AMRPS3.3: Climate Change and Emerging Diseases: The Importance of Resilient Societies PS3.4:

		PS3.5: Policy Coherence: Effective Partnerships for Global Health
1500 - 1530	Break	
1530 - 1730	PMAC Sessions	PS4.1: Moving Forward and Outward: Progress in Implementation of Global Frameworks and Initiatives PS4.2: Multi-sectoral Partnerships for Action on AMR PS4.3: Community Systems: The Bedrock of Responses to EID and AMR PS4.4: Finding the Win-Win Solutions for Better Health from Better Food Systems PS4.5: Bringing Solutions into Focus: Harnessing the Power of an Economic Lens
1800 - 2030	Welcome Dinner	Welcome Speech by Þ Minister, Ministry of Public Health, Thailand Þ President, Mahidol University, Thailand Þ Dinner Speech by Bill Gates, Bill and Melinda Gates Foundation, USA (TBC)

ITTEE MEETING AGENDA

gen and Ecology Research Network (BPERNet)

0 January – 3 February 2018

Date: Saturday, 3 February 2018

Main Conference Program

Time	Session	Notes
0900 - 0930	Closing Session	**Speech** by **Margaret Chan**, Former Director General, World Health Organization, Switzerland (TBC)
0930 - 1030	Synthesis	Summary, Conclusion, and Recommendations
1030 - 1100	Statement	
1100 - 1200	Closing Performance	
1200 - 1330	Lunch	
1400 - 1630	International Organizing Committee (IOC) Meeting	IOC Meeting for PMAC 2018/2019

TRAVEL VOUCHER OR SUBVOUCHER

Read Privacy Act Statement, Penalty Statement, and Instructions on back before completing form. Use typewriter, ink, or ball point pen. PRESS HARD. DO NOT use pencil. If more space is needed, continue in remarks.

1. PAYMENT
☐ Electronic Fund Transfer (EFT)
☐ Payment by Check

SPLIT DISBURSEMENT: The Paying Office will pay directly to the Government Travel Charge Card (GTCC) contractor the portion of your reimbursement representing travel charges for transportation, lodging, and rental car if you are a civilian employee, unless you elect a different amount. Military personnel are required to designate a payment that equals the total of their outstanding government travel card balance to the GTCC contractor.

☐ Pay the following amount of this reimbursement directly to the Government Travel Charge Card contractor: $ _____

2. NAME *(Last, First, Middle Initial) (Print or type)*	3. GRADE	4. SSN	5. TYPE OF PAYMENT *(X as applicable)*
			☐ TDY ☐ Member/Employee ☐ PCS ☐ Other ☐ Dependent(s) ☐ DLA

6. ADDRESS. a. NUMBER AND STREET	b. CITY	c. STATE	d. ZIP CODE

e. E-MAIL ADDRESS

10. FOR D.O. USE ONLY

7. DAYTIME TELEPHONE NUMBER & AREA CODE	8. TRAVEL ORDER/AUTHORIZATION NUMBER	9. PREVIOUS GOVERNMENT PAYMENTS/ ADVANCES

11. ORGANIZATION AND STATION

a. D.O. VOUCHER NUMBER

b. SUBVOUCHER NUMBER

12. DEPENDENT(S) *(X and complete as applicable)*
☐ ACCOMPANIED ☐ UNACCOMPANIED

a. NAME *(Last, First, Middle Initial)*	b. RELATIONSHIP	c. DATE OF BIRTH OR MARRIAGE

13. DEPENDENTS' ADDRESS ON RECEIPT OF ORDERS *(Include Zip Code)*

c. PAID BY

14. HAVE HOUSEHOLD GOODS BEEN SHIPPED? *(X one)*
☐ YES ☐ NO *(Explain in Remarks)*

d. COMPUTATIONS

15. ITINERARY

a. DATE		b. PLACE *(Home, Office, Base, Activity, City and State; City and Country, etc.)*	c. MEANS/ MODE OF TRAVEL	d. REASON FOR STOP	e. LODGING COST	f. POC MILES
	DEP					
	ARR					
	DEP					
	ARR					
	DEP					
	ARR					
	DEP					
	ARR					
	DEP					
	ARR					
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	DEP					
	ARR					

e. SUMMARY OF PAYMENT

(1) Per Diem	
(2) Actual Expense Allowance	
(3) Mileage	
(4) Dependent Travel	
(5) DLA	
(6) Reimbursable Expenses	
(7) Total	0.00
(8) Less Advance	
(9) Amount Owed	
(10) Amount Due	

16. POC TRAVEL *(X one)* ☐ OWN/OPERATE ☐ PASSENGER

17. DURATION OF TRAVEL
☐ 12 HOURS OR LESS
☐ MORE THAN 12 HOURS BUT 24 HOURS OR LESS
☐ MORE THAN 24 HOURS

18. REIMBURSABLE EXPENSES

a. DATE	b. NATURE OF EXPENSE	c. AMOUNT	d. ALLOWED

19. GOVERNMENT/DEDUCTIBLE MEALS

a. DATE	b. NO. OF MEALS	a. DATE	b. NO. OF MEALS

20.a. CLAIMANT SIGNATURE b. DATE

c. REVIEWER'S PRINTED NAME	d. REVIEWER SIGNATURE	e. TELEPHONE NUMBER	f. DATE

21.a. APPROVING OFFICIAL'S PRINTED NAME	b. SIGNATURE	c. TELEPHONE NUMBER	d. DATE

22. ACCOUNTING CLASSIFICATION

23. COLLECTION DATA

24. COMPUTED BY	25. AUDITED BY	26. TRAVEL ORDER/ AUTHORIZATION POSTED BY	27. RECEIVED *(Payee Signature and Date or Check No.)*	28. AMOUNT PAID

PRIVACY ACT STATEMENT

AUTHORITY: 5 U.S.C. Section 5701, 37 U.S.C. Sections 404 - 427, 5 U.S.C. Section 301, DoDFMR 7000.14-R, Vol. 9, and E.O. 9397.

PRINCIPAL PURPOSE(S): This record is used for reviewing, approving, accounting, and disbursing money for claims submitted by Department of Defense (DoD) travelers for official Government travel. The Social Security number (SSN) is used to maintain a numerical identification **filing system for filing and retrieving individual claims.**

ROUTINE USE(S): Disclosures are permitted under 5 U.S.C. 552a(b), Privacy Act of 1974, as amended. In addition, information may be disclosed to the Internal Revenue Service for travel allowances, which are subject to Federal income taxes, and for any DoD "Blanket Routine Use" as published in the Federal Register.

DISCLOSURE: Voluntary; however, failure to furnish the information requested may result in total or partial denial of the amount claimed.

PENALTY STATEMENT

There are severe criminal and civil penalties for knowingly submitting a false, fictitious, or fraudulent claim (U.S. Code, Title 18, Sections 287 and 1001 and Title 31, Section 3729).

INSTRUCTIONS

ITEM 1 - PAYMENT

Member must be on electronic funds (EFT) to participate in split disbursement. Split disbursement is a payment method by which you may elect to pay your official travel card bill and forward the remaining settlement dollars to your predesignated account. For example, $250.00 in the "Amount to Government Travel Charge Card" block means that $250.00 of your travel settlement will be electronically sent to the charge card company. Any dollars remaining on this settlement will automatically be sent to your predesignated account. Should you elect to send more dollars than you are entitled, "all" of the settlement will be forwarded to the charge card company. Notification: you will receive your regular monthly billing statement from the Government Travel Charge Card contractor; it will state: paid by Government, $250.00, 0 due. If you forwarded less dollars than you owe, the statement will read as: paid by Government, $250.00, $15.00 now due. Payment by check is made to travelers only when EFT payment is not directed.

REQUIRED ATTACHMENTS

1. Original and/or copies of all travel orders/authorizations and amendments, as applicable.
2. Two copies of dependent travel authorization if issued.
3. Copies of secretarial approval of travel if claim concerns parents who either did not reside in your household before their travel and/or will not reside in your household after travel.
4. Copy of GTR, MTA or ticket used.
5. Hotel/motel receipts and any item of expense claimed in an amount of $75.00 or more.
6. Other attachments will be as directed.

ITEM 15 - ITINERARY - SYMBOLS

15c. MEANS/MODE OF TRAVEL *(Use two letters)*

GTR/TKT or CBA *(See Note)*	- T	Automobile	- A
Government Transportation	- G	Motorcycle	- M
Commercial Transportation *(Own expense)*	- C	Bus	- B
		Plane	- P
Privately Owned Conveyance *(POC)*	- P	Rail	- R
		Vessel	- V

Note: Transportation tickets purchased with a CBA must not be claimed in Item 18 as a reimbursable expense.

15d. REASON FOR STOP

Authorized Delay	- AD	Leave En Route	- LV
Authorized Return	- AR	Mission Complete	- MC
Awaiting Transportation	- AT	Temporary Duty	- TD
Hospital Admittance	- HA	Voluntary Return	- VR
Hospital Discharge	- HD		

ITEM 15e. LODGING COST
Enter the total cost for lodging.

ITEM 19 - DEDUCTIBLE MEALS
Meals consumed by a member/employee when furnished with or without charge incident to an official assignment by sources other than a government mess *(see JFTR, par. U4125-A3g and JTR, par. C4554-B for definition of deductible meals)*. Meals furnished on commercial aircraft or by private individuals are not considered deductible meals.

29. REMARKS

a. INDICATE DATES ON WHICH LEAVE WAS TAKEN:

b. ALL UNUSED TICKETS *(including identification of unused "e-tickets")* MUST BE TURNED IN TO THE T/O OR CTO.

“Invitational Travel Orders”

Please make sure to password protect this file (send password in a separate email if possible) when emailing it back to due to the sensitivity of information on this form

The information required below is requested to support (fund) your travel via the Defense Travel System (DTS). The travel POC for ITO’s is: Mrs. Carron Leslie .
Carron will assist in coordinating your airfare via the system, our logistics contractor Tech Trans International (TTI) will reserve your hotel room separately. ***Please note:*** You will be “**self-pay”** for lodging (hotel) upon check in using your government issued Credit Card and or other card (for non-USG).

Once travel has been completed you are responsible for completing a DD1351 (Travel Voucher Form) for reimbursement of your expenses such as lodging, per-diem M&IE, ground transport if applicable, please note meals provided on travel by the event organizers will be deducted. The Travel Voucher form will need to be submitted to both contacts listed above after you have returned from your trip.

Reimbursement will be deposited at the designated account you list below. If you have any questions or concerns please contact: Nicki Aleman

Full Name**:**
Company/Organization:
Home Address:
Phone:
Email:
Bank account routing number
Account number:
SSN:
Date of Birth:
Airport of departure:

Additional travel notes/requests:

16 Nov 2016

JKO – SERE 100 – ATFP – ISOPREP Completion Instructions

- These instructions are for Civilians and Contractors without a Common Access Card (CAC).
- When emailing, use your Work Email address. - Training is not required by Foreign Nationals.

1. JKO Course # JS-US007: Level I Antiterrorism Awareness Training: Valid for 12 Months.
Training can be accessed via link below. You do not need a JKO account to access training.
Click link below. When site opens up, click OK to close DOD Security Banner after reading.
Click on Non-CAC users under JS-007 Level I Antiterrorism Awareness Training, and follow instructions.
https://jkodirect.jten.mil/Atlas2/faces/page/login/Login.seam

2. JKO Course J3TA-US1329, SERE 100.2 Level A SERE Education and Training in Support of the Code of Conduct (FOUO): Valid for 36 Months or AS REQUIRED BY THE FOREIGN CLEARANCE GUIDE. FREQUENCY SUBJECT TO CHANGE.
To complete SERE training follow these instructions. Click on the following link. http://jko.jten.mil/index.html on the page that opens up, click on enter JKO. Read the Security Banner then click OK to close. On the page you are viewing now, under **I DO NOT have a CaC, select Non-Government Personnel/Sponsored Account Registration.**
On the next page, fill out the requested information. In the Reason for Account, after you enter reason, add the CBEP Country Manager and Country you are supporting. Not providing this information will cause delays. Then click submit. My email is John.T.Patterson2.civ@mail.mil.
When you click submit it will send a notice to me. I will verify reason with Country manager and submit request. The JKO office will contact you with your logon information. Once you have obtained your log on information, return to https://jkodirect.jten.mil/Atlas2/faces/page/login/Login.seam to log into JKO. Once logged in, select the Catalog Tab at top of page and enter "SERE" in title/keyword box, and click search. SERE 100.2 Level A SERE Education and Training in Support of the Code of Conduct (FOUO) - (4 hrs) should be listed. Click enroll to access course.
If you get an out of office notice from me, you will have to resubmit your request using the CBEP Country Manager's email address that you are supporting, they can sponsor you. You may want to check before submitting request.

Contact JKO at JKOHelpDesk@jten.mil or 757-203-5654 for access issues.

DO NOT send form by email or regular mail. Once blocks 50-54 are completed the form is classified CONFIDENTIAL. And must be sent using shipping instructions on page 2

3. DD Form 1833 Isolated Personnel Report (ISOPREP): Valid 12 Months or AS REQUIRED BY THE FOREIGN CLEARANCE GUIDE. FREQUENCY SUBJECT TO CHANGE.

If you have a DOD CAC, click on link below and follow instructions to complete your **initial ISOPREP**. You must be on a .mil or .gov domain computer system.
https://prmsglobal.prms.af.mil/prmsconv/Profile/Survey/start.aspx

If you need to update or want to verify your ISOPREP, contact one of individuals listed below.

If you are in the local area, you may contact John.T.Patterson2.civ@mail.mil / 703-767-5938 to arrange completion of your ISOPREP at the CTR office. If you receive an out of office response, you may contact theodore.w.carlson.civ@mail.mil / 703-767-6382 for assistance. Use these same contacts for updates.

If you do not have a DOD CAC, and are not in the local area, fill out DD Form 1833. This can be found by searching online. Instructions are included in form. Finger prints are not required. Section 9 blocks 50-54 should be typed on separate piece of paper and included with the form. Once completed, form is classified as Confidential and must be sent following instructions on page 2. Your SSN is needed. You Blood type is needed. Your DOB is needed. Make sure to follow the instructions for the 4 Statements and the Authentication Number.

Submit two photos, a front view and right side profile view, from the shoulders up. Photos may be sent with the form or the preferred method is to email the photos only to John.T.Patterson2.civ@mail.mil

DO NOT send form by email or regular mail. Once blocks 50-54 are completed the form is classified CONFIDENTIAL. Send using instructions below

Mailing Instructions

Seal package with type of tape to retain postal stamp impressions. Prepare, package, and securely seal classified material in ways to MAXIMIZE evidence of tampering and MINIMIZE undetected deliberate compromise, or risk of accidental exposure. To minimize the risk of exposure of classified information, package documents so that classified material is not in direct contact with the inner envelope or container (e.g., fold so classified material faces together).
Double wrap classified information in two opaque, sealed envelopes, wrappings, or containers, durable enough to properly protect the material from accidental exposure and facilitate detection of tampering.
Do not place classification marking or any other unusual marks on the outer package that might invite special attention to the fact that the contents are classified

After completing form, fold so classified information faces together. Place folded form, disk or photos if you did not email them inside fully addressed and marked package as instructed and shown below.

Form	Inner Package	Outer Package
CONF IDEN TIAL	Full Name CONFIDENTIAL Full Address (Mark Front and Back) ATTN: J3CTB/John Patterson and CTR	Office Name Only Office Address See proper address

Inner Package:

Mark inner package as shown above. Be sure to replace the CTR CBEP Country Managers' name shown with the actual name you are supporting.

- Complete recipients and sender address
- Mark top/bottom and front/ back with CONFIDENTIAL markings.
- Seal package as stated at top of this page.

Place this package inside of another package (outer package).

Outer Package:

Mark outer package as shown above.

- Use only office name and office address. Do not use individual names.
- Do not use markings of any kind indicating classification or that the package contains classified material.
- Seal package as stated at top of this page.
- Send package via USPS, FEDEX, UPS, DHL, etc. Make sure you have a tracking # for Package.
- After sending package notify John.T.Patterson2.civ@mail.mil, and applicable CTR CBEP Country Manager so we are aware to be watching for package.

Use correct address below depending on shipper. Make sure you have a tracking number for your package.

For Registered / Express mail via the US Postal Service	**For Express mail via Federal Express, DHL, UPS**
DEFENSE THREAT REDUCTION AGENCY 8725 JOHN J KINGMAN RD STOP 6201	DEFENSE THREAT REDUCTION AGENCY 6200 MEADE ROAD

FORT BELVOIR VA 22060-6201	FORT BELVOIR VA 22060-526

PRINCE MAHIDOL AWARD CONFERENCE 2018

Making the World Safe from the Threats of Emerging Infectious Diseases

Background

The Prince Mahidol Award Conference (PMAC) is an annual international conference focusing on policy-related health issues. The Prince Mahidol Award Conference 2018 is co-hosted by the Prince Mahidol Award Foundation, the Thai Ministry of Public Health, Mahidol University, the World Health Organization, The World Bank, U.S Agency for International Development, Japan International Cooperation Agency, The Rockefeller Foundation, with support from other key related partners. The Conference will be held in Bangkok, Thailand, from 29 January – 3 February 2018. The theme for PMAC 2018 is "Making the World Safe from the Threats of Emerging Infectious Diseases".

We live in an era when the emergence of novel infectious disease agents is posing an increasing threat to global health and security. The threat from novel infectious diseases is accelerating at a pace and with an intensity unprecedented in human history, driven by increasing human populations, climate change and surging global travel. The possibility that a single lethal microbe could suddenly emerge and sweep through every household, through every community without regard to national borders or social and economic standing is a shared fear across the globe. Just the fear can cost billions, as illustrated by recent Ebola and Zika virus panics in little-affected countries. But the reality of the threat is all too clear, proven by the decades of response to the HIV-AIDS pandemic. Yet the world is not prepared to either mitigate the impact of an emergent disease threat or prevent its emergence.

Zoonotic and AMR related diseases account for more than 95% of all emerging infectious diseases reported during the second half of the 20th century[1]. In this century the emergence of SARS, pandemic influenza, MERS, and the spread of Ebola and Zika reflect the world's increasing vulnerability to novel zoonotic threats. The simultaneous emergence of pathogens resistant to antibiotic therapies raises the prospect of a "post antibiotic" world. While the drivers underlying the emergence of zoonotic and antibiotic resistant diseases are complex, human behaviours and their impact on animal populations and the environment are understood to be central to the emergence of both disease threats. The role of increasing animal-human contact in the emergence of zoonotic diseases has been well documented and been increasingly the focus of One Health initiatives across the globe. The contribution made by the inappropriate use of antibiotics in animal husbandry to AMR is less well documented but in recent years has been increasingly understood to be a core driver behind the emergence and global spread of antibiotic resistant organisms, along with inappropriate "prescriber-user" practices associated with antibiotic use in clinical care. Changing environmental and climatic conditions have also been closely linked to the emergence of novel infectious diseases. That infectious disease emergence is closely associated with practices and

[1] K. E. Jones *et al.*, Global trends in emerging infectious diseases. *Nature* **451**, 990-993 (2008).

behaviours at the animal-human-environment interface speak to the importance of an expanded multi-sectoral alliance across the animal, human and environmental sectors to address the threats posed by both zoonosis and AMR. The Global Health Security Agenda and related One Health movement provide important frameworks for mobilizing international action.

The Rising Threat of Zoonotic Diseases

Since the Influenza Pandemic of 1918 when between 50-100 million died (5-10% of the human population) we have been fully aware of how vulnerable our place on this planet is.

Even in the absence of significant global mortality, epidemics and pandemics can cost tens of billions of dollars, reversing development gains and pushing communities and households into poverty. The SARS outbreak in 2003 cost the economies of East Asia between $30-50 billion and estimates of the global economic cost of an influenza pandemic range from $374 billion, for a mild pandemic, to $7.3 trillion, for a severe pandemic - with a 12.6% loss of gross domestic product.

Strategically, policies to address a potential pandemic threat are constrained by an unresolved debate over the use of adaptive measures - that aim through the use of technological measures to reduce the impact of diseases after they have emerged vs mitigation measures - that focus on the underlying causes of disease emergence. The adaptive tools we traditionally rely on to protect us from the world of infectious diseases – vaccine and therapeutics – too often are shown ineffective against a novel threat; and, the timely development and deployment of new and effective biomedical countermeasures is undercut by the speed at which the threat spreads.

Similarly, our ability to mitigate the emergence of new threats is undermined by a lack of knowledge about the viral ecology and the drivers, including human behaviors, which propel the emergence of a new threat. It is at these moments we realize just how few our adaptive and mitigation options are – and how vulnerable the global community is. After each episode the world admonishes itself for being ill prepared to deal with a global threat – but after decades of largely reacting adaptively to each event, with only a tangential focus on mitigation, we are only marginally better able to deal with the next one.

A “Post Antibiotic World”

The development and commercialization of antimicrobials stands as a defining achievement of 20th century medical practice. Antimicrobials heralded an era of expanded life expectancy, paved the way for advanced medical and surgical treatments, improved animal health and welfare, and made possible curative therapy for once fatal infections. Decades of superfluous and inattentive use of antimicrobials across the human and animal health sectors now threaten these advancements. The pace of reported treatment failures and antimicrobial resistance (AMR) in common pathogens is increasing, with multi-drug resistant pathogens creating the prospect of a ‘post antibiotic’ world. In the absence of interventions, AMR-associated human mortality is projected to soar from a current rate of 700 000 to over 10 million annually by 2050—as readily treatable infections become life threatening, and routine procedures are rendered unsafe.[2] Asia is expected to account for half of this projected global mortality. The impact of AMR on morbidity and mortality is matched by a substantial economic burden, with resistance linked to aggregate losses anticipated to exceed USD 100 trillion by 2050.

[2] O’Neill, J. Review on Antimicrobial Resistance. Tackling a Global Health Crisis: Initial Steps. 2015

Antimicrobial resistance is exacerbated by the unregulated use of antimicrobials across both the human health and animal health sectors. A particular concern is the shared use of same classes of antibiotics in humans and in animals, potentially exacerbating the selection pressures on pathogen populations in animals and humans that encourage the development of resistance and exchange of resistance genes. By example, in the United States the livestock production industry accounts for 80% of the total use of antibiotics used for treatment of human infections.

Antimicrobial resistance is one of the three flagship topics for the tripartite (FAO, OIE and WHO) collaboration. At the Sixty-eight World Health Assembly in May 2015, the World Health Assembly endorsed the Global Action Plan (GAP)[3] on AMR and requested to strengthen the tripartite collaboration between FAO, OIE and WHO for combating antimicrobial resistance in the spirit of the "One Health" approach. The Global Action Plan, which ensured a One Health approach and consistency with Codex Alimentarius and OIE inter-governmental standards and guidelines, aims to ensure continuity of successful treatment and prevention of infectious diseases with effective and safe medicines that are quality-assured, used in a responsible way, and accessible to all who need them. Guided by this global action plan, the Member States, the Secretariat, and their international and national partners aim to: (1) improve awareness and understanding of antimicrobial resistance; (2) strengthen knowledge through surveillance and research; (3) reduce the incidence of infection; (4) optimize the use of antimicrobial agents; and (5) develop the economic case for sustainable investment that takes account of the needs of all countries, and increase investment in new medicines, diagnostic tools, vaccines and other interventions.

A high level meeting on anti-microbial resistance was held in September 2016 at the United Nations General Assembly, generating a statement of global commitment to address AMR through a multi-disciplinary approach.[4]

PMAC 2018 Will Be Action Focused. Protecting the world from the threat of zoonotic diseases and ensuring effective stewardship of antibiotics requires a common and well-coordinated multi-sectoral effort. While there has been significant progress in building multi-sectoral One Health action against zoonotic diseases, AMR efforts remain highly siloed with an unequal focus on the respective contributions made by the inappropriate use of antibiotics in clinical care and animal production, as well as limited opportunities for bringing human, animal and environmental health sectors together to forge a common strategy. There is an urgent need to bring a comprehensive One Health risk mitigation approach to address zoonotic and AMR related diseases that addresses the direct consequences of animal-human interactions and contributory pressures related to environmental and climate changes.

PMAC 2018 will provide an important setting for fostering policy and strategic action by engaging multi-sectoral experts in zoonosis and AMR, as well as climate change and related environmental fields from across the public and private sectors, international organizations, foundations, academics and non-governmental organizations, as well as critical players in Global Health Security Agenda (GHSA). Importantly, a PMAC sponsored "Making the World Safe from the Threats of Emerging Infectious Diseases" would build on PMAC 13's highly successful conference on One Health and lead to real change.

PMAC 2018 Will Build On Past PMAC Themes. Since 2007, the Prince Mahidol Award Conference has been organized as an annual international conference focusing on policy-related public health issues of global significance – including, Universal Health Coverage, Health Equity, Meeting the

[3] Global Action Plan on Antimicrobial Resistance, http://www.who.int/drugresistance/global_action_plan/en/
[4] http://www.un.org/pga/71/2016/09/21/press-release-hl-meeting-on-antimicrobial-resistance/

Needs of Vulnerable Populations, and addressing the threats posed by infectious diseases. Each of these meeting has brought together leading public health leaders and stakeholders from around the world to propose concrete solutions and recommendations. PMAC 2018 will explicitly look to build on the successes of past PMACs and to identify opportunities to further contribute to the systems and capacities required to address the comprehensive health needs of the world's populations

Objectives

1. To accelerate progress in the adoption of multi-sectoral approaches for addressing zoonotic diseases and antimicrobial resistance
2. To advocate for evidence-based priority setting and policy decisions for zoonotic diseases and antimicrobial resistance
3. To share knowledge and experience in addressing the challenges posed by zoonotic diseases and antimicrobial resistance
4. To promote a greater understanding of the range and nature of the "drivers" underlying the emergence of new disease threats and options for their mitigation
5. To highlight emerging demographic, climatic and travel trends to better understand how disease emergence will evolve over the course of this century
6. To underscore the collateral socio-economic and development benefits associated with a One Health Agenda

Sub-themes

Sub-theme 1: Learning from the Past: Towards Effective and Sustainable Policies, Practices and Capacities for "Prevention, Detection and Response" to Emerging Zoonosis and Antimicrobial Resistance

This sub-theme is focused on presenting evidence for how efforts across the globe over the past two decades to address zoonotic and AMR related threats are contributing to more effective policies, practices and capacities for "prevention, detection and response" to EIDs. Given the inherent multi-sectoral aspects of disease emergence this is an opportunity to learn from recent experience with efforts such as the Global Health Security Agenda (GHSA), International Health Regulations, the One Health movement, and other platforms illustrating challenges and solutions for building effective partnerships for addressing zoonosis and AMR.

Issues to be discussed under this sub-theme are:

1. Evidence for optimal policies, regulations and systems for addressing EIDs
    - What we have learned from country, regional and global level experiences in addressing EIDs
        - Case studies illustrating successes and failures; how well do we manage and mitigate present threats (e.g. MERS CoV, Nipah virus, Zika virus, Zoonotic Influenza, Ebola virus, AMR, and others)
        - Organizational options for building sustainable national-level partnerships across multi-ministerial groups, including Health, Agriculture, Environment, Finance and Education
            - What are the policy requirements
            - What are the human resource requirements
            - What are the organization requirements

        - What are resource requirements
    - How are these experiences translated to the sub-national level
        - What are the equivalent requirements for provincial/county level operations

2. Evidence for optimal global and regional level structures for addressing EIDs

- What are the lessons learned on building global and regional level partnerships, including the GHSA, One Health and Planetary Health, to address EIDs
    - How effective have global and regional partnerships been in building multi-sectoral alliances to enable country level actions
        - What are the policy requirements
        - What are the human resource requirements
        - What are the organization requirements
        - What are resource requirements

- What is the evidence for proactive, flexible structures that enhance capacities and preparedness across the prevention-detection-response continuum?
    - What have we learned from the pandemic vaccine development banks; consortia for conservation of antimicrobials?
    - What can we learn from parallel efforts, such as those addressing global climate change and carbon emissions?
    - What examples demonstrate the ability to bridge the apparent dichotomy between capacity building and a research agenda concerning emerging zoonoses and AMR?

3. Evidence of novel, upstream approaches to earlier detection and trends monitoring, including but not limited to:

- Novel surveillance postures and strategies,
- digital diseases detection,
- crowdsourcing big data,
- predictive analytics on disease distribution

4. Evidence for more sustainable approaches for “prevention, detection and response”

- What are examples of sustainable financing structures? What have we learned from:
    - The World Bank Pandemic Emergency Financing Facility?
    - Evolving schemes for engaging insurance companies to “share” pandemic risk?
    - Efforts to quantify cost attributable to zoonotic disease and AMR burden, project pandemic influenza economic impact, and make a credible investment case for prevention and risk mitigation?
- What are examples of “preparedness” activities that address long-term sustainability?
    - What have we learned from the World Bank and WHO’s joint effort to develop strategies for both pandemic and “all hazards” preparedness and related long-term financing schemes?
- Which financing models have proven utility in employing an evidence driven approach to discouraging high risk practices and incentivizing risk mitigation in approaching pandemic prevention as a global public good?

Sub-theme 2: Harnessing the Power of Public-Private-Community (PPC) Partnerships for "Preventing, Detecting, and Responding" to Zoonosis and AMR

This sub-theme is focused on examining the evidence for building effective partnerships that bring together community, private sector and public sector resources for sustainably addressing the threats posed by zoonosis and AMR. As with the previous sub-theme, the inherently multi-sectoral nature of zoonosis and AMR requires active engagement across multiple stakeholders. In addition to the Public sector, Private sector actors who may be directly engaged in activities that inadvertently contribute to "drivers" for EIDs will need to be actively involved in any efforts to better mitigate the consequences of their activities. Similarly, communities are key stakeholders, both as consumers and potential contributors to some of the drivers that underlie disease emergence (e.g. inappropriate use of antibiotics in rearing of livestock and aquaculture)

Issues to be discussed under this sub-theme are:

1. Evidence for strong PPC partnerships that have contributed to "prevention, detection and response" to Zoonosis and AMR

- What are the lessons from PPC partnerships in addressing EIDs
    - Country, regional or global examples of how PPC partnerships have been able to harness across each of the constituencies to address EIDs in ways that greatly enhanced the overall impact
        - What were the incentives for PPC partnerships
        - What were the roles and responsibilities of each group
        - What were the metrics for valuing the PPC partnerships
        - What were the operational factors for sustainability of PPC parntership

2. Evidence of successful outreach and community empowerment
    - What are examples of how risk communications have successfully affected community and/or individual level practices and behaviors on a scale significant enough to reduce the risk from zoonotic threats and/or AMR

3. Evidence for an active and sustainable engagement of the private sector
    - What are examples of how private sector partners have been actively and sustainably engaged in efforts to address zoonotic threats and/or AMR
    - What can be learned from partnerships with biomedical industry in developing and marketing vaccines and medical countermeasures? Employing novel diagnostic platforms enabling rapid detection and response to emerging threats?
    - What are examples of partnerships with industry in the use of non-medical countermeasures within communities to help mitigate, prevent, and control infectious disease threats? Employing new technologies and platforms for health communication and the application of non-pharmaceutical interventions.

4. Evidence for how consumer advocacy can contribute to change policies and practices

5. Evidence of economic benefits from PPC

Sub-theme 3: Understanding the Selection Pressures Underlying Emergence of Zoonotic Diseases and Antimicrobial Resistance and the Broad Benefits Realized From Promoting Healthy Animals and Healthy People

This sub-theme is focused on both:

a) exploring the contributions made by climate change, population growth, global travel, habitat change, expanding settlements, resource extraction, increased livestock and crop production and other underlying drivers that contribute to the emergence of new zoonotic and anti-microbial disease threats, and
b) examining the broad benefits that are accrued from promoting practices across multiple sectors that aim at reducing these drivers and the risk of zoonotic diseases and antimicrobial resistance.

There has been a general recognition that the adoption of a core set of best practices that are designed to directly target the drivers associated with zoonosis and AMR are likely to simultaneously contribute to positive outcomes across a range of "other" domains and the achievement of the United Nations Sustainable Development Goals, such as food security, household wealth and economic growth, as well as healthier environments and sustainable communities.

a) Issues to be discussed under this sub-theme will allow a presentation of the evidence for the drivers of EID emergence:

1. Evidence for Climate Change in Increasing Infectious Disease threats and models projecting future impact

- How does climate change contribute to spread of infectious disease threats
    - Topics to be considered could include: impact on vector ecology, animal migration, altered range and distribution of reservoir host species;
    - variance in freshwater availability, sanitation, and waterborne disease

2. Evidence for demographic and population change on increasing Infectious Disease threats, including how settlement patterns (peri-urbanization), population movement (increased air travel, trade etc), habitat change (impact on animal bio-diversity) contribute to disease emergence and spread

3. Evidence for how increased economic activity impacts on increased Infectious Disease risk, including how expanded incursions of extractive industry operations and agricultural intensification into wildlife domains increase risk for "spillover" and spread of novel diseases

- Options for how "risk" can be mitigated at the site of industry operations or in planning/selecting where industry operations occur

4. Evidence for how increased livestock production and marketing in geographic "hot spots" for disease emergence may increase risk of pathogen "spillover" and spread

- How projected increases in livestock production in Africa and shifting production contexts in Asia over the 21st century will impact on the risk of disease emergence, including zoonosis and AMR
    - Models for likely changes in terrestrial and aquatic animal production and marketing patterns over the coming century
    - Models for potential increased environmental impact that could elevate risk
    - Options for minimizing risks associated with increased livestock production and marketing

- Considering the impact of a global supply chain of agricultural commodities and production inputs (e.g. animal feed), and trans-continental risk management strategies

b) Issues to be discussed under this sub-theme also will allow a presentation of the evidence to broad collateral benefits accrued from targeting the drivers of EID emergence:

5. Evidence that adoption of practices to reduce zoonotic and AMR risks associated with livestock production would also contribute to more efficient and more profitable operations.

- How do improved biosecurity and husbandry practices that strengthen control of pathogenic zoonotic viruses improve the overall health of livestock and the environment
  - Reduced animal diseases
  - Improved animal health can lead to increased livestock productivity and reduced input costs for production
  - Enhanced productivity and yield per animal production unit
  - Reduction in prophylactic antibiotic use

- How does proper management of antimicrobials in livestock production and aquaculture improve economic returns
  - Improved hygienic conditions, nutrition, and vaccination in animal husbandry associated with reduced use of antibiotics and corresponding returns on investment
  - What can be learned from the experience of countries that have phased out and enacted regulatory controls on use of antimicrobials in animal production
  - AMR reduces potency of veterinary drugs and negatively affects animal health
  - Consumer demand for antimicrobial residue free animal source foods
  - Market based incentives and penalties for reduced antimicrobial use and enhanced adherence to drug withholding periods, minimizing residues in products entering the food chain
  - Best practices in strengthening antimicrobial usage regulatory and enforcement structures in animal production

6. Evidence that reduction in habitat fragmentation has led to the control of zoonosis

- How does habitat fragmentation impact on both vector-borne and non vector-borne diseases
  - Evidence that changes in habitat leads to changes (increase/decrease) the transmission dynamics of infectious diseases (e.g. chikungunya, malaria)

7. Evidence that that the real and/or projected economic impact from emerging zoonoses and AMR has informed resource allocation policies and an investment case for prevention

- What practices and approaches have shown promise in fostering decision making informed by economic analyses
- What novel structures have proven utility in transcending the challenge of inequitable sectoral cost and benefit distribution
  - Evidence for one or more sectors bearing the cost for benefits accruing to different sectors/stakeholders (e.g. H7N9 control in China: costs borne by producers and markets, but benefits accrue to health sector; or resource extraction and disease emergence: costs borne by health sector, but benefits accrue to industry and land planning/mining/forestry entities)

Venue and Dates of the Conference

Centara Grand at Central World Hotel, Bangkok

Monday 29 – Tuesday 30 January 2018	Side Meetings
Wednesday 31 January 2018	Field Trip
Thursday 1 – Saturday 3 February 2018	Main Conference

Structure of the Conference

This is a closed, invitation only conference host by the Prince Mahidol Award Foundation, and the Royal Thai Government, together with other international co-hosts. The conference consists of:

1. **Pre-conference**
    a. Side meetings
    b. Field trip

2. **Main conference**
    a. Keynote speeches
    b. Plenary sessions
    c. Parallel sessions
    d. Synthesis: Summary and recommendations
    e. Poster display

Pre-Conference Program

Monday 29 January 2018

09:00-17:30	Side Meetings

Tuesday 30 January 2018

09:00-17:30	Side Meetings

Wednesday 31 January 2018

06:30–18:00	Field Trip

Main Conference Program

Thursday 1 February 2018

09:00-10:30	**Opening Session & Keynote Address** Opening Session by **Her Royal Highness Princess Maha Chakri Sirindhorn** Keynote Address • Prince Mahidol Award Laureate 2017 • Prince Mahidol Award Laureate 2017 • **TBC**
10:30-11:00	Break
11:00-12:30	**Plenary 0: Vision 2100: Re-Imagining the End Game for the End of the Pandemic Era**
12:30-13:30	Lunch
13:30-14:30	**Plenary 1: Leadership Needed for Managing Emerging Infectious Diseases of the 21st Century**
14:30-16:30	**PS1.1: Lessons Learned in Managing Emerging Infectious Diseases (EID)** **PS1.2: Strategic Information and the Evolution of Emerging Infectious Diseases: Lessons from the Past and New Opportunities** **PS1.3: Safeguarding Medicines in the Era of AMR: What Do We Know? What Works?** **PS1.4: Financing Pandemic Preparedness: Where is the Money?** **PS1.5: One Health on the Move: Nomadic Communities**
16:30-17:00	Break
17:00-18:00	**Plenary 2: Futures of Partnerships for a Safer World**

Friday 2 February 2018

08:30-09:30	**Plenary 3: Managing Emerging Infectious Disease and AMR Risk across the Livestock Revolution**
09:30-10:00	Break
10:00-12:00	**PS2.1: Beyond MERS and Zika: Are we Prepared for the Next Big Epidemic?** **PS2.2: AMR: Addressing Excessive and Inappropriate Use of Antibiotics** **PS2.3: Dealing with an Inter-Connected World: Partnerships for Preparedness, Detection and Response during Mass Gatherings** **PS2.4: Changing Dynamics: Emerging Infectious Diseases and Antimicrobial Resistance in an Era of Expanding Global Human Population Growth and Movement** **PS2.5: Reducing the Gap: Addressing Neglected Disease; Neglected Populations**
12:00-13:00	Lunch
13:00-15:00	**PS3.1:** **PS3.2: Lessons Learned from a One Health Approach to AMR** **PS3.3: Climate Change and Emerging Diseases: The Importance of Resilient Societies** **PS3.4:**

	PS3.5: Policy Coherence: Effective Partnerships for Global Health
15:00-15:30	Break
15:30-17:30	**PS4.1: Moving Forward and Outward: Progress in Implementation of Global Frameworks and Initiatives** **PS4.2: Multi-sectoral Partnerships for Action on AMR** **PS4.3: Community Systems: the Bedrock of Responses to EID and AMR** **PS4.4: Finding the Win-Win Solutions for Better Health from Better Food Systems** **PS4.5: Bringing Solutions into Focus: Harnessing the Power of an Economic Lens**
18:00-20:30	**Welcome Dinner** • **Welcome Speech** by - Minister, Ministry of Public Health, Thailand - President, Mahidol University, Thailand • **Dinner Speech** by **Bill Gates**, Bill and Melinda Gates Foundation, USA (TBC)

Saturday 3 February 2018

09.00-09.30	**Closing Session** • **Speech** by **Margaret Chan**, Former Director General, World Health Organization, Switzerland (TBC)
09.30-10.30	**Synthesis: Summary, Conclusion & Recommendations**
10.30-11.00	**Statement**
11.00-12.00	**Closing Performance**
12.00-13.30	Lunch
14:00-16:30	**International Organizing Committee (IOC) Meeting for PMAC 2018/2019**

OPENING SESSION AND KEYNOTE ADDRESS

Opening Session

by Her Royal Highness Princess Maha Chakri Sirindhorn

Keynote Address

- Prince Mahidol Award Laureate 2017
- Prince Mahidol Award Laureate 2017
- **TBC**

Note: All speakers to be confirmed

PLENARY 0 (PL0)

Vision 2100: Re-Imagining the End Game for the End of the Pandemic Era

Background

We live in an era when the emergence of novel infectious disease agents is posing an increasing threat to global health and security. The threat from novel infectious diseases is accelerating at a pace and with an intensity unprecedented in human history, driven by increasing human populations, climate change and surging global travel. The possibility that a single lethal microbe could suddenly emerge and sweep through every household, through every community without regard to national borders or social and economic standing is a shared fear across the globe. Just the fear can cost billions, as illustrated by recent Ebola and Zika virus panics in little-affected countries. But the reality of the threat is all too clear, proven by the decades of response to the HIV-AIDS pandemic.

Zoonotic and AMR related diseases account for more than 95% of all emerging infectious diseases reported during the second half of the 20th century[5]. In this century the emergence of SARS, pandemic influenza, MERS, and the spread of Ebola and Zika reflect the world's increasing vulnerability to novel zoonotic threats. The simultaneous emergence of pathogens resistant to antibiotic therapies raises the prospect of a "post antibiotic" world. While the drivers underlying the emergence of zoonotic and antibiotic resistant diseases are complex, human behaviours and their impact on animal populations and the environment are understood to be central to the emergence of both disease threats. The role of increasing animal-human contact in the emergence of zoonotic diseases has been well documented and been increasingly the focus of One Health initiatives across the globe. The contribution made by the inappropriate use of antibiotics in animal husbandry to AMR is less well documented but in recent years has been increasingly understood to be a core driver behind the emergence and global spread of antibiotic resistant organisms, along with inappropriate "prescriber-user" practices associated with antibiotic use in clinical care. Changing environmental and climatic conditions have also been closely linked to the emergence of novel infectious diseases. That infectious disease emergence is closely associated with practices and behaviours at the animal-human-environment interface speak to the importance of an expanded multi-sectoral alliance across the animal, human and environmental sectors to address the threats posed by both zoonosis and AMR.

As we look forward towards the end of this century, the predictable escalation in the interactions between humans and animals speaks to a world of increasing global risk. The consequences of these trends, however, are avoidable. Success in "making the world safe from the threats of emerging infectious diseases" requires we think and act differently; to not continue with the half-measures that have made the world ill prepared to address these threats.

Rapid advances in science and a corresponding revolution in technologies allow us, for the first time, to imagine a world where these "threats" can be minimized. What is required is bold action; that embraces an aggressive time horizon; and, that is global in scope. Such action can build systems and

[5] K. E. Jones *et al.*, Global trends in emerging infectious diseases. *Nature* **451**, 990-993 (2008).

capacities able to mitigate the emergence of future threats and to control them when they do. With this knowledge comes the power to end panic and move to prevention.

This Plenary will present and discuss examples of new, innovative and bold global ventures which are now laying the groundwork for the "beginning of the end of the Pandemic Era".

Objectives

- Explore novel and transformative approaches that address the underlying drivers of zoonotic disease and AMR
- Harness methodologies, technologies, and thinking across a range of disciplines to promote a vision for a proactive approach to emerging zoonoses and AMR
- Enable a conversation that transcends current impediments and envisions possible pathways and enabling factors to realize the end of the "pandemic era"

Moderator

- **Dennis Carroll**, USAID

Keynote Speaker

- **Harvey Feinberg,** President, The Gordon and Betty Moore Foundation

Panelists

- **Richard Hatchett**, CEO, Coalition for Epidemic Preparedness Innovations (CEPI)
- **George Gao**, Director, China Center for Disease Control and Prevention
- **Margaret Hamburg**, President, American Association for the Advancement of Science (AAAS)
- **Larry Brilliant**, Chairman, Skoll Global Threats Fund

Note: All speakers to be confirmed

PLENARY 1 (PL1)

Leadership Needed for Managing Emerging Infectious Diseases of the 21st Century

Background

We now live in a world where any local infectious disease outbreak event has the potential to become an epidemic or pandemic. While preparedness of local agencies is key to quickly identify and contain outbreaks, global partnerships and international collaboration across all sectors must be effective to support and manage events. These partnerships have the potential to proactively alter the global architecture in order to quickly detect, prevent and respond to infectious disease threats as they emerge.

The plenary session will address the *Leadership Needed for Managing Emerging Infectious Diseases of the 21st Century*. It will set the scene of the global health architecture and how the international community is organizing to address effectively EIDs. It will also address leadership needed at country level for managing emerging infectious diseases.

The session will feature speakers from organizations with recent experience of preparing for, and responding to global health crises in the 21st century and consider how, as risks, environment and global architecture change, funding varies, how organizations change and adapt to tackle the contemporary challenges, and how are the lessons learned from recent challenges being incorporated into plans for future events. Speakers from countries and civil societies will bring a national and community level perspective on how to respond to global health crises.

Objectives

The objective is to identify what kind of leadership, at all levels, is needed to address the increased risk and the complexity of EID and AMR and bring together different partners and groups acknowledging the various organizational and sectoral cultures.

Moderator

- **Sylvie Briand**, WHO, Director Infectious Hazard Management

Panelists

- **Peter Salama**, EXD, WHO's Health Emergencies Programme – WHO perspective-
- **Elhadj As Sy**, Secretary General of the IFRC – civil society and community perspective
- **Francoise Barré-Sinoussi**, Nobel Prize Awardee for HIV discovery, Institute Pasteur – perspective on HIV pandemic management
- **Oly Ilunga Kalenga**, DRC MOH – country perspective

Note: All speakers to be confirmed

PLENARY 2 (PL2)

Futures of Partnerships for a Safer World

Background

This plenary is an interactive session that will introduce four core questions, based on the Futures approach, to shape the discourse of partnerships for greater biosecurity in the world. It will begin with an introduction of Futures thinking by Dr. Sohail Inayatullah, UNESCO Chair of Futures Studies and Professor at Tamkang University, Taiwan. Then, the plenary will involve a short discussion on the current state of partnerships or lack of in certain thematic areas, and challenges in forging effective partnerships. It will delve into exploring various futures for partnerships and what effective and inclusive partnerships can achieve to make the world a safer place for all. Attempting to jointly uncover the "unknown unknowns" within a Futures methodology will lead to an innovative approach in organizing an interactive plenary that would hopefully lead to new directions and interesting discussions within the parallel sessions.

Objectives

- To jointly envision possible scenarios for the future of partnerships in EID and AMR.
- To generate excitement in creating effective partnerships for a safer world by imagining alternate futures based on Futures techniques. It is envisioned that the novelty of the technique will add to the richness of PMAC and to bring in cross-disciplinary approaches into a Public Health conference.
- To get participants to think creatively in an out-of-the-box manner on working collaboratively together to build greater biosecurity for all.

Moderator

- **Sohail Inayatullah**, who is experienced in working on Biosecurity issues as well as other Development challenges

Panelists

- **Diah Saminarsih**, Special Advisor to Minister, Ministry of Health Indonesia, Indonesia
- **Sania Nishtar**, President, Heartfile, Pakistan
- **Ken Banks**, Founder, FrontlineSMS, United Kingdom

Note: All speakers to be confirmed

PLENARY 3 (PL3)

Managing Emerging Infectious Disease and AMR Risk across the Livestock Revolution

Background

Widespread demand for animal protein nutrition over the last half century has fueled an explosive growth in global livestock production systems. Between 2000 and 2030, demand for beef and dairy is expected to nearly double, and poultry to nearly triple. In select high growth regions, such as South Asia, demand for poultry is expected to soar to 725%.[6] Keeping pace with this demand, the production, marketing, and distribution of terrestrial and aquatic animal production has undergone transformational change. While rural livelihoods globally remain largely dependent upon grain, tubercle, and legume-based nutrition, an overall consolidation and commercialization of the production and marketing chains is shifting the disease emergence risk profile.

Increasingly, global animal product supply chains impact disease risk variably, through secondary and tertiary order effects that may be geographically separated. Within the context of zoonotic disease emergence risk, what are the linkages across geographically distinct areas where demand for animal protein is growing, the production of that protein, and the production of inputs such as animal feed? Can a total "emergence risk footprint" be developed to quantify this risk and prioritize reduced impact production scenarios? And what incentives and structures are needed to expedite a global shift toward such lower impact production systems?

The collective capacity to mitigate emerging zoonotic disease and AMR risks associated with increasingly complex global animal production chains will be dependent upon a robust understanding of the disease transmission drivers within these global systems. This session will enable a detailed evaluation of the role of animal production in potentiating zoonotic disease emergence and AMR, and will identify commonalities across regions, production contexts, and sectors that can inform applied risk mitigation approaches. While the session will focus on animal production systems, a balance with the role of anti-microbial use in crops, animal feed, and human health will need to be included.

Objectives

- Evaluation of terrestrial and aquatic animal production systems within the context of emerging zoonotic disease and AMR risk
- Understand how projected increases in livestock production in Africa and shifting production contexts in Asia over the 21st century will impact the future of farming systems and the risk of emerging zoonoses and AMR
- Identify common risk threads across regions, production contexts, and sectors that can inform applied risk mitigation approaches
    - Exploration of what is known about the quality and integrity of veterinary medicines - and their supply chains - used in animal production and their contribution to AMR risk.

[6] FAO. 2011. *Mapping supply and demand for animal-source foods to 2030,* T.P. Robinson & F. Pozzi. Animal Production and Health Working Paper. No. 2. Rome

- Review practical options for minimizing risks associated with increased animal production and marketing

Moderator

- **Dennis Carroll**, USAID

Panelists

- **Simplice Nouala**, African Union Interafrican Bureau of Animal Resources
- **Ugo Picaciamarra**, FAO
- **Peter Daszak**, EcoHealth Alliance
- **Dan Schar**, USAID

Note: All speakers to be confirmed

PARALLEL SESSION 1.1 (PS1.1)

Lessons Learned in Managing Emerging Infectious Diseases (EID)

Background

Several outbreaks since 2000 have shaped the way in which we prepare for and respond to infectious diseases outbreaks. The emergence of SARS CoV in the first years of this century was a wakeup call to the global health community followed by H5N1 avian influenza outbreaks and the first influenza pandemic in the 21st century. The renewed IHR (2005) marked a major change in the approach to global health security, going beyond specific diseases to apply to all health risks, irrespective of their origin or source.

Objectives

To present and discuss the management of a selection of recent crisis in different settings and draw lessons for the future. The session will tackle what works, what doesn't work from the political, public health, social and economic perspectives.

The following events will be discussed:

- **Ebola** : management of local and extended outbreaks: comparison of local outbreaks (DRC Uganda) and the epidemic in West Africa (2014-2015) with a particular emphasis on :
  - Community engagement and the socio-cultural aspects of outbreak response;
  - Cross-border collaboration between neighboring countries (surveillance, contact tracing, case management);
  - The role of international assistance;
  - Clinical management and vaccine.
- **MERS**: limiting spread example of Kingdome of Saudi Arabia, Republic of Korea and Thailand, managing the regional and global aspects of MERS-CoV, with a particular emphasis on:
  - Monitoring the health of international travelers and migrant workers;
  - Hospital preparedness
- **Zika and yellow fever** : managing vector borne outbreaks and emerging infectious diseases in Brazil / Angola (Yellow fever) and mitigating the risk of international spread (example of Portugal), with a particular emphasis on:
  - Controlling vectors and other environmental factors;
  - Vaccination and other preventive measures;
  - Effective communication to address public fear and potential panic.
- *Also **potentially discussed** : From SARS to influenza A(H7N9); lessons learned in China, with a particular emphasis on:*
  - *Addressing the human-animal interface and cross-sectoral collaboration;*
  - *Resolving conflicting interests between the commercial and public health sectors*
  - *Strengthening preparedness based on experience of past outbreaks*

Keywords: Ebola, Zika, MERS, Influenza, contact tracing, clinical management, migrations.

Moderator

- **Ron St John**, Public Health Agency of Canada

Panelists

- **Bruce Aylward**, WHO, Special Representative for Ebola Response – Ebola response
- **Adullah Assiri**, KSA MOH – MERS (country of origin)
- Director General, Department of Disease Control, Ministry of Health, Thailand
- **João Paulo Toledo**, Director, surveillance department, Ministry of Health, Brazil
- **Francisco George**, Portugal MOH – yellow fever: stockpiling and preventing importation and spread of infectious viruses

Note: All speakers to be confirmed

PARALLEL SESSION 1.2 (PS1.2)

Strategic Information and the Evolution of Emerging Infectious Diseases: Lessons from the Past and New Opportunities

Background

The last century has witnessed an increase in the frequency of emerging infectious diseases (EID) and antimicrobial resistance (AMR). Climate change, environmental pressure, population movement, population growth and increasing overlaps between human and animal livelihoods have contributed to an acceleration of novel infectious diseases. In addition, the increasing pace of human and animal pathogens resistant to antibiotic therapies raises serious concerns about treatable infections becoming life threatening, raising the death toll and the economic cost to potentially unsustainable level within decades.

In this context, early warning systems and strategic information play a key role in preventing, detecting and responding adequately to emerging zoonosis and antimicrobial resistance. More surveillance systems are needed. New technologies, electronic health records, internet and social media have the potential to provide timely information on emerging infectious diseases and antimicrobial resistance that can supplement traditional surveillance systems. With these new tools, individuals and their communities can play a new role in participatory syndromic surveillance. Nevertheless, there are important caveats that need to be addressed, such as ensuring data privacy, underrepresentation of some categories such as infants, the elderly, or people lacking access to these new technologies.

Objectives

This session will look at the recent changes in strategic information and how can they contribute to current surveillance systems in order to identify appropriate actions and interventions for preparedness and response to emerging infectious diseases and antimicrobial resistance.

Moderator

- TBD

Panelists

- Shweta Bansal, Department of Biology, Georgetown University, Washington, USA
- Laurel Sprague, Executive Director GNP+, The Hague, The Netherlands
- Marcel Salathé, Centre for Infectious Disease Dynamics, Penn State University, Pennsylvania, USA or Caroline Guerrisi Sorbonne University, INSERM
- Margaret D. Straton, Tufts University Initiative for Forecasting and Modelling of Infectious Diseases (InForMID), Medford, Massachusetts, USA or Sarah Del Valle, Los Alamos National Laboratory New Mexico, USA
- Osama Ahmed Hassan, Umea University, Sweden, Public Health Institute, Khartoum, Sudan
- Amy Wesolowski, Centre for Communicable Disease Dynamics, Harvard TH Chan School of Public Health

Note: All speakers to be confirmed

PARALLEL SESSION 1.3 (PS1.3)

Safeguarding Medicines in the Era of AMR: What Do We Know? What Works?

Background

The prevention, detection and mitigation of emerging and re-emerging infectious diseases involve both applying preventive controls in animal production as well as ensuring the safety, efficacy, quality, and appropriate use of vaccines, diagnostics and medicines through secure supply chains and health delivery systems.

Complex and fragmented supply chains, especially in countries and regions with limited regulatory and quality oversight, increase the likelihood of substandard, fraudulent or adulterated medicines entering the market. Poor quality medicines ensure microbial replication in the presence of drug pressure. Substandard and falsified medicines also contribute to lack of efficacy and adverse events, undermining trust in the health system. Inappropriate use of anti-microbials is another driver of AMR. Both poor quality medicines and inappropriate use are preventable and can be addressed through the development of robust regulatory and quality assurance systems, treatment guidelines and enforcement.

While there are major limitations in evidence and best practice in the human health sector, even less is known in the veterinary sector, both with respect to use and quality of antibiotics in animals, and effective controls. Further, environmental factors are beginning to come to light.

Objectives

- Review evidence of what is known about the links between medicines quality and AMR.
- Highlight successful efforts in, and benefits from, strengthening systems that monitor and strive to improve medicines quality.
- Address environmental impacts of antibiotic manufacturing on AMR.
- Relate frameworks for addressing medicines quality and appropriate use in the human sector to the animal sector and discern what lessons and approaches from other initiatives could be mobilized to address these drivers of infectious disease risk and AMR.

Moderator

- **Katherine Bond** – overview of issue/session and introduction

Panelists

- Panelist 1 – Overview of evidence linking medicines quality and use to AMR; directions for more attention and link to current response (Proposed: **Michael Deats**, WHO)
- Panelist 2 – Reflections on effective strategies, approaches and benefits to strengthen medicines quality monitoring and quality assurance systems (Proposed: **Margareth Ndomondo-Sigonda**, Tanzania)

- Panelist 3 – Reflections on veterinary sector; insights into how approaches on drug quality and use in human health sector could be applied in the veterinary health sector (Proposed: **Angkana Sommanustwichai**, London School of Hygiene and Tropical Medicine/IHPP Thailand
- Panelist 4 – **Sasi Jaroenpoj**, Head of Veterinary Medicinal Product, Department of Livestock Development, Ministry of Agriculture, Thailand
- Panelist 5 – Environmental impacts of antibiotic production: Proposed: **Dan Andersson**, Department of Biochemistry and Microbiology, Uppsala University, Sweden
- Panelist/Discussant – Broad overview and reflections on how medicines quality and practices contribute to ID and AMR risk from; experience in outbreaks; and links to current initiatives/broad perspectives (Proposed: **Margaret Hamburg**, National Academies of Medicine)

Note: All speakers to be confirmed

PARALLEL SESSION 1.4 (PS1.4)

Financing Pandemic Preparedness: Where is the Money?

Background

Recent experiences with the Ebola, Zika, and SARS outbreaks, among others, have underscored the need for countries to invest in pandemic preparedness, and to do so not only from a health perspective but also from an economic perspective: the socio-economic cost of outbreaks is often proportionally much larger than the corresponding impact on mortality and morbidity.

The International Working Group on Financing Preparedness (IWG) has recently made several recommendations to integrate pandemic preparedness into international macro-economic and market assessments that determine the availability of concessionary and other international financing eligible lower and middle income countries.

To date, however, what has largely been missing in global and country-level discussions is a systematic understanding about adequacy and modality of *current* financing arrangements for health security. Part of pandemic preparedness is embedded in health financing and service delivery. Part also deals with animal health which is the responsibility of livestock/agriculture sector. In addition to its multisectoral nature, there are contingency financing arrangements for pandemic preparedness that may or may not be linked to how countries manage other natural or man-made disasters. There is also risk that health security and pandemic preparedness may get lost in health financing transition that focuses more on financial protection and access to individual services than public goods.

Given the complexity of pandemic preparedness, better understanding of the current financing landscape would enable an informed dialogue on financing gaps and how best they could be filled given domestic and international fiscal constraints. The nature of health security implies that some of the objectives and functions that may be applicable to a generic health financing system would need to be amended to consider some of the unique characteristics of the specific sub-set of activities that constitute health security.

Objectives

The objective of this session is to discuss issues on financing health security within the broader context of trends in health and public financing more generally. Specifically, the session will:

- Provide an overview of how to conceptualize and estimate financing for health security, including preparedness, response and recovery;
- Present and discuss some preliminary findings on health security financing analysis from select countries, including a 10-year evaluation of OIE PVS Pathway and gap analysis to strengthen/finance veterinary services;
- Examine key domestic policies and interventions to ensure sustainable financing for pandemic preparedness and opportunities for mobilizing domestic and international financing for rapid response.

Moderator

- **Timothy Grant Evans**, Senior Director, Health, Nutrition and Population Global Practice. World Bank Group

Panelists

- **Netsanet Workie**, Senior Health Economist, World Bank Group. *Experiences from Health Security Financing Assessment Tool (HSFAT)*
- **Ronella Abila**, OIE sub-regional representative Southeast Asia. *10 years of experience with OIE PVS Pathway*
- **Eduardo Banzon**, Principal Health Specialist, Asian Development Bank. *Financing Health Security in the Mekong Region*
- **Tran Dac Phu**, General Director, General Department of Preventive Medicine, Vietnam. *Country Experience*
- **Julian Naidoo**, Chief of Party, Wits Health Consortium, South Africa. *Country Experience*
- **Benjamin Rolfe**, CEO, Asia Pacific Leaders Malaria Alliance. *Civil Society perspective*

Note: All speakers to be confirmed

PARALLEL SESSION 1.5 (PS1.5)

One Health on the Move: Nomadic Communities

Background

Fully dependent on their animals for their livelihood and income, pastoralists employ mobility as a key strategy to ensure the availability of pasture and water for their herds, thus increasing their resilience. While their movement allows them to overcome the vagaries of nature prevalent in the harsh environments they inhabit, their remoteness and often trans-boundary livelihoods have made it challenging to access services and engage in decision-making. Pastoralist are at the forefront of the human, livestock and wildlife interface. They are especially vulnerable to zoonotic diseases, because they live in close contact with their animals and often consume raw milk and meat. Furthermore changing environmental conditions also affect the availability of pasture for their animals, and in-turn affect their nutrition status.

The animal-human-environment sectors are interconnected and associated with the emergence of infectious diseases as Middle East Respiratory Syndrome (MERS). Multisectoral approaches such as One Health can help address the challenges at this interface by providing adapted vaccinations campaigns and veterinary services to pastoralists.

Objectives

- To foster a deeper understanding of the health risks faced by mobile pastoral communities, and the challenges they encounter in accessing animal and human healthcare
- To share examples of interventions and policies that tackle pastoralists' health issues at the animal-human-environment interface
- To promote the participation of pastoral communities in health policy decisions and sanitation campaigns

Moderator

- **Gregorio Velasco Gil**, Food and Agricultural Organization of the United Nations

Panelists

- **Asiimwe Benon**, Associate Professor. Makerere University
- **Maty Ba Diao**, Regional Coordinator of the Support Pastoralism in Sahelian Countries project- CILSS.
- **Marite Alvarez**, Pastoral representative. Argentina. Pastoamericas.
- **Taghi Farvar**, Pastoral representative. Iran. Cenesta.

Note: All speakers to be confirmed

PARALLEL SESSION 2.1 (PS2.1)

Beyond MERS and Zika: Are we Prepared for the Next Big Epidemic?

Background

Over the past decade, Ebola, MERS, highly pathogenic avian influenza and, more recently, the Zika virus outbreaks have demonstrated the ability of epidemics to devastate communities through both extraordinary losses of life and severe morbidity as well as adverse social and economic impacts that jeopardize global health security. These recent disease outbreaks have not only made evident countries' lack of preparedness to adequately prevent, detect and respond to epidemics, but also the extent to which measures must cut across governance levels and all sectors of society in order to truly be effective. Furthermore, only one third of countries have met their commitments under the International Health Regulations (IHR). And although several tools and frameworks have been developed (by WHO, USAID, CDC, OIE, etc.) to provide guidance for countries to develop country epidemic preparedness and response plans, these are generally disease specific, have not been updated or tested through routine exercises, remain largely underfunded and are, therefore, not fully operational. As a result, many countries remain unprepared to prevent, detect, mitigate risks and respond to health threats and disease epidemics before they cause devastating consequences in the livelihoods of communities and the economies of countries.

Objectives

- To present country experiences on strengthening IHR core capacities, including efforts for effective coordination, partnership models and financing mechanisms to strengthen health security.
- To identify critical elements needed for sustainable, inclusive, and effective preparedness at country level and propose solutions for more effective epidemic preparedness guidance.
- To discuss gaps in the current guidance and frameworks that need to be filled to develop country epidemic preparedness and response plans.

Moderator

- **John Nkengasong**, Director, Africa CDC

Panelists

- **Isabella Ayagah**, IHR Focal Point, Ministry of Health, Kenya. *Strengthening Pandemic Preparedness across Sectors in Kenya: Lessons Learned & the Way Forward*
- **Ronello Abila**, OIE sub-regional representative Southeast Asia. *Lessons Learned from 10yrs of Implementing the OIE PVS Pathway*
- **Tran Dac Phu**, General Director, General Department of Preventive Medicine, Ministry of Health, Vietnam
- **Casey Barton Behravesh**, Director, One Health Office, U.S. CDC

Note: All speakers to be confirmed

PARALLEL SESSION 2.2 (PS2.2)

AMR: Addressing Excessive and Inappropriate Use of Antibiotics

Background

The tripartite, Food and Agricultural Organization, World Health Organization and World Organization for Animal Health and other relevant organizations had declared Antimicrobial resistance (AMR) a serious and growing global public health threat. The loss of effective antibiotics is reducing an ability to protect people from infectious diseases, with profound impacts on healthcare systems, global trade, agriculture, environment and health sectors. Based on World Bank Group projections of the world economy in 2017-2050, if AMR problems continue at the current pace, the annual global GDP would fall by 1.1-3.8% by 2050 and the global healthcare cost would range from US$ 300 billion to more than US$ 1 trillion.

Though AMR is a natural mechanism of pathogen survival; the excessive and inappropriate use of antibiotics are key drivers of the emergence of antimicrobial resistance. Decision to prescribe antibiotics by health professionals still occurs in the absence of adequate information about the nature of the infection or before the results of diagnostic and sensitivity tests become available. Moreover, the regulation of antimicrobial use is poorly enforced in some areas, such as over-the-counter, unregulated use of antibiotic in agriculture, substandard medicines for both human and animal antibiotics.

Several attempts to optimize use of antibiotics in human and animal sectors have shown in the last decade at global, regional and national levels. To fulfill key action proposed by the Global Action Plan, countries need to strengthen the evidence base through surveillances of AMR and the consumption of antimicrobials, and strengthen regulation of the distribution and use of antibiotics in human and animals. The information on AMR and antibiotic consumption will guide the treatment of patients and inform local and national actions. Thus, antibiotic, as a global public good requires regulation on distribution and use.

It is imperative that PMAC audiences recognize the drivers contributing to excessive and inappropriate use of antibiotics; but more importantly, learn and share practical and successful solutions.

Objectives

The panelists in this session will address the following questions

On problem streams

1. Why there are excessive and inappropriate use of antibiotics in humans, animals and crops (i.e. in citrus for treatment of greening disease), such as self-medication of antibiotic from over-the-counter purchases, inefficiently regulated the use of antibiotic. Stakeholder analysis are helpful to unpack the complexity. Key actors involved in the use of antibiotics:
   a) Demand for antibiotics: patients and farmers,
   b) Supply of antibiotics: pharmaceutical industry, professionals: veterinarians, physicians and pharmacists,

On solution streams

2. What are the good practices and lessons for countries or regional organization such as ECDC and networks such as ESAC and ESVAC, to develop and maintain an effective system for surveillance of AMR, antimicrobial consumption and Point prevalence survey in human, and animal?
3. How evidences of surveillance of antimicrobial consumption are used:
    a. To guide antibiotic prescribing decisions of health professionals
    b. To formulate, support and monitor policies which curb down antimicrobial consumption and promote rational use of antibiotics
4. What are the challenges of use of antibiotics in crops? Is there any monitoring system on impacts of antibiotic use in crops, such as antibiotic resistance in food crops and environment, and antibiotic residue in environment and food crops?
5. How does the regulatory system support the control of antibiotic use?

On recommendations

6. What are the policy interventions on "demand" and "supply" sides, which address the excessive and inappropriate use of antibiotics in developing countries?

Moderator

- **Klara Tisocki**, WHO SEARO

Panelists

- **Otto Cars**, Senior Professor, Founder and senior adviser, ReAct-Action on Antibiotic Resistance, Uppsala University, Sweden
- **Jonathan Rushton**, Professor of Animal Health and Food Systems Economics Epidemiology and Population Health, University of Liverpool
- **Lilit Ghazaryan**, Scientific Center of Drug and Medical Technology Expertise, MoH, Armenia
- **Angkana Sommanustweechai**, Doctoral student at LSHTM on AMR, IHPP Thailand

Note: All speakers to be confirmed

PARALLEL SESSION 2.3 (PS2.3)

Dealing with an Inter-Connected World: Partnerships for Preparedness, Detection and Response during Mass Gatherings

Background

Mass gatherings are recognised to have the potential to enhance spread of infectious diseases as well as being potential targets for deliberate events. Although both these risks are unlikely, the rise of Zika infection in the run up to the Rio 2016 Olympic and Paralympic Games and Middle East Respiratory Syndrome (MERS) in Saudi Arabia highlighted how these events can create a perceived, if not actual, global health threat and a political as well as health challenge.

The inspiration of this session derives from the next three Olympiads (Winter 2018, Summer 2020 and Winter 2022) being in the western pacific region (S Korea, Japan and China respectively). This session will be based on previous sporting mass gatherings such as the Rio Olympics, the London Olympics, and the World Cup, religious gatherings such as the Hajj, and large state events such as the King's funeral in Thailand. The session aims to share learning and best practices from a biosecurity and terrorism perspective and to explore how such mass gathering events can best be planned to minimise any health risks. Many mass gatherings, especially international sporting events, are organised by what are effectively private sector companies and the relationship between the private and public sector partners is vitally important.

Objectives

- To share learning and experience from previous events
- To explore effective risk mitigation strategies
- To examine the health and political interface of mass gatherings, including private sector partners
- To explore how mass gatherings can be used to improve global health security capacity

Moderator

- **Brian McCloskey**, Senior Consulting Fellow, Chatham House; Consultant in Global Health Security, Public Health England; & Professor, Faculty Epidemiology and Population Health, London School of Hygiene and Tropical Medicine

Panelists

- **Tina Endericks**, Director, WHO Collaborating Centre on Mass Gatherings and Global Health Security, Public Health England, London
- **Maurizio Barbeschi**, Mass Gathering Unit, WHO, Geneva
- **Lucille Bloomberg**, National Institute Infectious Diseases, South Africa
- **Badriah Alotaibi**, Global Centre for Mass Gathering Medicine, Riyadh, Saudi Arabia
- Speaker (to be identified) from Thailand Ministry of Health
- **Koji Wada**, National Centre for Global Medicine, Tokyo

Note: All speakers to be confirmed

PARALLEL SESSION 2.4 (PS2.4)

Changing Dynamics: Emerging Infectious Diseases and Antimicrobial Resistance in an Era of Expanding Global Human Population Growth and Movement

Background

The global human population is projected to peak at over 11 billion this century. Accelerated human population growth and corresponding changes in demography, along with associated food and companion animal population increases, are altering disease dynamics and will continue to drive emerging infections and transmission over the course of the next century. This session will explore the connections among infectious disease emergence, antimicrobial resistance (AMR), and changing human and animal population dynamics. We will explore the state-of-the-art in emerging disease and AMR detection and forecasting and answer the question, "How can we minimize emerging disease and AMR risks linked to changing demography."

Objectives

This session aims to explore and address the impacts of growing human and animal populations and unplanned mega-cities and peri-urban settlements on disease emergence, amplification, and global distribution. Accordingly, presenters will also tackle the risks associated with surging global trade and travel and illustrate how forecasting can inform risk mitigation.

Specific Objectives:

- Explore projected demographic trends over the 21st century and their impact on expected zoonotic disease emergence and AMR
- Enhance understanding of how trends in demography will differ regionally; how differences in agricultural productivity and marketing practices will impact emerging disease risk, including spread of AMR; and how purchasing power and animal protein demand will have global supply chain impacts and associated emerging disease risk
- Highlight practical, evidence-driven approaches to defining, forecasting, and mitigating human demographic-driven emerging disease risk

Moderator

- **Jonna A.K. Mazet**, University of California, Davis

Speakers

- **Martin (Marty) Cetron**, Division of Global Migration & Quarantine, US CDC
- **Saber Yezil**, WHO/MoH, Saudi Arabia
- **Thuy Bich Hoang**, Viet Nam, Wildlife Conservation Society
- **Christine Kreuder Johnson**, University of California, USA Davis/Nepal context
- **Evelyn Wesangula**, Global Antibiotic Resistance Partnership-Kenya
- **Kamran Khan**, Associate Professor, Department of Medicine, Division of Infectious Diseases, University of Toronto, Canada
- **Olaniran Alabi**, Nigeria Chief Veterinary Officer

Note: All speakers to be confirmed

PARALLEL SESSION 2.5 (PS2.5)

Reducing the Gap: Addressing Neglected Disease; Neglected Populations

Background

Preventable, endemic diseases are rarely prioritized for surveillance as they do not pose a risk of epidemic or pandemic outbreak. This is a failing on two levels: (1) the presence of preventable diseases acts an indicator of the overall state of the health system; and (2) the knowledge of 'usual' allows for detection of the unusual. Strengthening surveillance and other systems for endemic diseases, infectious or otherwise, provides necessary infrastructure to combat the existing and target the emerging. In addition, most of these subsisting populations live in close proximity with their animals and experience a double burden, disease in their animals and disease in their families and communities. A pro-poor initiative on a massive scale, control of NTDs has much to offer in terms of what can be adapted, innovated and built in low-resource settings most burdened by NTDs in an agenda that makes poverty alleviation its overarching objective and aims to leave no one behind.

The success celebrated for some of the NTDs shows that it is possible to build private-public partnerships that lead to concrete results, such as the Global Partners' Meeting on NTDs based on the theme "Collaborate. Accelerate. Eliminate". This encapsulates an exemplary informal collaboration that marks a 'turning point' in global efforts to control and eliminate poverty-related diseases.

The discussion will center on forging cross-sectoral partnerships to tackle NTDs and "diseases of poverty", and will include a range of elements crucial to an effective collaboration across sectors such as financing, research and development, production and delivery of vaccinations and treatment, disease surveillance, role of local communities and other actors on the field. It will elucidate the incentives of building effective cross-sectoral and public-private partnerships by using the case of NTDs. Lessons may be derived from the NTD experience to other areas requiring cross-sectoral partnerships in health where a population-based intervention is appropriate.

Objectives

Marginalized and neglected populations bear the epidemic risk of infectious diseases especially neglected tropical diseases. They are more exposed to disease vectors as well as have less access to effective and timely health care. Without addressing prevention, detection and response among this segment of the population, the world cannot be safe from infectious disease. This session aims to discuss successful examples of cross-sectoral partnerships across human and animal health sectors to tackle "diseases of poverty" including financing, vaccine development, and distribution as well as delivery. It will also address how to target this neglected segment of the population against the threat of infectious diseases. Intervention based approaches through specific diseases can be discussed as well as tackling access and inclusion into the health system through a social determinants approach. Tackling NTDs is addressing the causes of poverty and the pathways to reach the poorest and most vulnerable in society those that will have slower access to universal health coverage and would be a pathway to strengthen health systems, human, animal and environmental.

Moderator

- Dan Normandeau (TBC)

Panelists

- Mark Bradley, Director Global De-worming , Global Health Programs, GSK
  Or, Klaus Brill, Vice President Corporate Commercial Relations, Bayer Pharmaceuticals
  Or, Alasdair King, Director, Intergovernmental Veterinary Health Merck Animal Health
- Dr Nwankwo Uzoma, Senior Medical Officer and Health Economist, Ministry of Health, Nigeria
- Dr Amila Gunesekera, MD, Medical Officer in charge Rabies treatment National Hospital of Sri Lanka
- Harena Rasamoelina, Veterinary epidemiologist, Indian Ocean Commission
- Representative from local NGO involved in distribution and delivery of vaccines/treatment (TBC)
- Representative from WHO or UN system (TBC)
- Representative from CEPI co-founders or Board (TBC)

Note: All speakers to be confirmed

PARALLEL SESSION 3.1 (PS3.1)

To be updated

Note: All speakers to be confirmed

PARALLEL SESSION 3.2 (PS3.2)

Lessons Learned from a One Health Approach to AMR

Background

Antimicrobial resistance (AMR) is a major threat to global health, the world economy, food safety and food security, and therefore poses a unique challenge to humanity. All countries – regardless of their economic situation, the strength of their health systems or their level of antibiotic consumption – will face disastrous consequences if the spread of AMR is not contained. Global and community solutions are needed to prevent overuse of antibiotics, including development of new vaccines, improved diagnostic tests and, above all, universal access to antibiotics which are affordable and effective against drug-resistant diseases. Antimicrobials also play a significant role in both plant and animal health, and therefore, in global food production. While the important goal of reducing antibiotic usage for growth promotion in animals is increasingly implemented, antibiotics will be needed in maintaining the health of food-producing animals, and the safety of their products.

AMR occurs when disease-causing pathogens (including bacteria, fungi, parasites, or viruses) develop defense mechanisms against the drugs designed to treat them, making these resistant pathogens difficult or even impossible to treat. This resistance is the inevitable result of antimicrobial use and an example of natural selection in practice. The more antimicrobials are used, the less effective they become. Rising levels of AMR are a sign that natural selection is taking place more rapidly than innovation in developing new antimicrobials. If this process is to be reversed, the world must innovate more, but also slow natural selection – by eliminating excess use of all antimicrobials; only using second- and third-level treatments when absolutely necessary; and ensuring appropriate access to treatments.

The importance for countries to develop and implement one health focused national action plans

In line with the Global Action Plan on Antimicrobial Resistance, developed by WHO with participation and endorsement by the OIE and FAO, the development of countries' own National Action Plans (NAPs) on AMR is an essential first step towards establishment of an effective response to combat AMR. At the Sixty-eighth WHA in 2015, Member States committed to have NAPs in place by May 2017. Also in 2015, the OIE World Assembly of Delegates adopted Resolution No 26, committing to development of NAPs in the spirit of "One Health", taking into account the use of antimicrobial in animals and ensuring collaboration with public health officials. In February 2016, WHO, in collaboration with FAO and OIE, developed a manual for developing NAPs on AMR and a set of accompanying tools. The three organizations have been working closely with stakeholders to provide technical support to countries for the effective development of their NAPs.

Sharing Expertise for a Coordinated AMR Response

Ensuring political commitment, engagement and support has been a challenge as understanding of AMR, multisectoral collaboration and the importance of developing and implementing NAPs is still somewhat limited. The identification of best practices in human, animal and plant health continues to play an important role as the world is still learning what works best in particular contexts. WHO is sharing expertise regarding human health and developing communities of practice to support countries with ongoing efforts. Inter-sectoral action, and the complexity of coordination within and across sectors, continues to be a challenge, particularly as countries shift towards NAP implementation.

Global Action Plan for Antimicrobial Resistance

At the Sixty-Eighth World Health Assembly in May 2015, WHO Member States endorsed a global action plan through resolution WHA68.7 to tackle antimicrobial resistance, including antibiotic resistance, the most urgent drug resistance trend.
The AMR global action plan contains five major strategic objectives:

1. to improve awareness and understanding of antimicrobial resistance;
2. to strengthen knowledge through surveillance and research;
3. to reduce the incidence of infection;
4. to optimize the use of antimicrobial agents; and
5. to develop the economic case for sustainable investment that takes account of the needs of all countries, and increase investment in new medicines, diagnostic tools, vaccines and other interventions.

The global action plan, which takes into account the commitment, perspectives and roles of all relevant stakeholders is a plan in which everyone has clear and shared ownership and responsibilities. The endorsement of the plan reflects a global consensus that AMR poses a profound threat to human health.

One Health Approach
Addressing the rising threat of AMR requires a holistic and multisectoral ("One Health") approach because antimicrobials used to treat various infectious diseases in animals may be the same as or similar to those used in humans. Resistant bacteria arising in humans, animals, plants or the environment may spread from one to the other, and from one country to another. One Health recognizes that the health of humans, animals and ecosystems are interconnected. It involves applying a coordinated, collaborative, multidisciplinary and cross-sectoral approach.

The WHO, FAO and OIE speak with one voice and take collective action to minimize the emergence and spread of AMR. The aim is to:

- Ensure that antimicrobial agents continue to be effective and useful to cure diseases in humans and animals;
- Promote prudent and responsible use of antimicrobial agents;
- Ensure global access to medicines of good quality.

Objectives

- To gain a better understanding of how the world can learn from the past 2.5 years of AMR response since the Global Action Plan as we shift from development of AMR strategies towards implementation
- To identify main challenges and successes in implementing national action plans and determine ways to productively more forward

Moderator

- **Martha Gyansa-Lutterodt**, Chief Pharmacist of Ghana, IACG Member

Panelists

- WHO
  - **Marc Sprenger**, Director of AMR Secretariat, WHO
- FAO
  - **Juan Lubroth**, Chief Veterinary Officer, FAO
- OIE
  - **Matthew Stone**, Deputy Director General, OIE
- Professional association – health

  - **Judith Shamian,** President, International Council of Nurses
- Professional association – agriculture
  - **Marco Marzano de Marnis**, Secretary General, World Farmers Association

Note: All speakers to be confirmed

PARALLEL SESSION 3.3 (PS3.3)

Climate Change and Emerging Diseases: The Importance of Resilient Societies

Background

During the long processes of human cultural evolution, population dispersal, and subsequent inter-population contact and conflict, several distinct transitions in human ecology and inter-population interactions have changed profoundly the patterns of infectious disease in human populations. As we move further into the 21st century, the spread and increased lability of infectious diseases, new and old, reflects the impacts of demographic, environmental, technological and other rapid changes in human ecology. Climate change, one of the global environmental changes under way, is anticipated to have a wide range of increased impacts upon the occurrence of infectious diseases affecting human, animal, and plant populations.

Climate and weather patterns affect the distribution and risk of many infectious diseases, including vector-borne diseases such as malaria, Rift Valley fever, plague, encephalitis and dengue fever. Weather patterns also affect the distribution of food- and water-borne diseases and emerging infectious diseases such as West Nile virus, Hantavirus, and Ebola hemorrhagic fever and the sporulation of diseases such as anthrax and other clostridia.

The effect of climate variability on infectious diseases is determined largely by the unique transmission cycle of each pathogen. Transmission cycles that require a vector or non-human host are more susceptible to external environmental influences than those diseases which include only the pathogen and human. Important environmental factors include temperature, altitude, precipitation and humidity. Several possible transmission components include pathogen nature (viral, bacterial, etc.), vector (mosquito, snail, etc.), abiotic physical vehicle (water, soil, etc.), non-human reservoir (mice, deer, etc.), and human host.

Humans are more than passive recipients of climate change-induced health effects. We can play a significant and active role through proactive adaptation and mitigation measures in order to control and alleviate the negative health impacts of climate change. The magnitude of changes in climate variables varies across the globe, posing more challenges and stresses for some groups, societies and populations than others. Given the same magnitude of climate change, some population groups and areas are more vulnerable to the elevated risks due to their lack of the ability and resources to effectively respond to the stresses and challenges, including nutrition, immune status, and access to goods, services, and clean water. Inadequate public policies may be perpetuating the marginalization that increases vulnerability to adverse events or change processes. Given that infectious diseases do not confine themselves within a vulnerable population group, these diseases pose a shared global risk and require a coordinated global effort to reduce their vulnerability to climate change-induced health risks. Importantly, human vulnerability to the changing risks for infectious diseases driven by climate change may be altered through proper adaptation measures. Examples include the continuous evolution of public health programmes, the cyclical re-allocation of financial and health care resources and the pre-emptive alteration of policies following scientific projection of spatial–temporal changes in health risk for human infectious diseases. Early warning systems based on such projections have been proven effective in helping societies take proactive measures to prevent or alleviate the possible health impacts.

Objectives

- Explore projected trends in climate change over the 21st century, and their expected impact on infectious disease emergence/re-emergence and AMR
- Highlight practical, evidence-driven policy and approaches to defining and mitigating human-driven emerging disease risk

Moderator

- **Pradeep Kurukulasuriya**, GEF/GCF, UNDP Bangkok

Panelists

- **Sander Koenraadt**, Wageningen University, Netherlands. Climate change and vector-borne diseases; climate change effects on highland malaria, arboviruses.
- Two panelists from government /NGO partners involved in GEF projects on Strengthening national capacities for health and climate change adaptation. Selected speakers to represent case studies from Nepal **Meghnath Dhimal** (Consultant on leave from MOH) and Bangladesh **Iqbal Kabir** (MOH)
- **Montira J. Pongsiri** PhD, MPH, Senior Research Associate, Planetary Health Science Policy, Cornell University, College of Veterinary Medicine, Dept. of Population Medicine and Diagnostic Sciences
- **Kristie Ebi**, Professor, visiting at Department of Public Health and Clinical Medicine Occupational Medicine, Umea University.

Note: All speakers to be confirmed

PARALLEL SESSION 3.4 (PS3.4)

To be updated

Note: All speakers to be confirmed

PARALLEL SESSION 3.5 (PS3.5)

Policy Coherence: Effective Partnerships for Global Health

Background

The 2030 Agenda for Sustainable Development set ambitious health-related targets to "ensure healthy lives and promote well-being for all at all ages" and "strengthen the means of implementation and revitalise the Global Partnerships for Sustainable Development". To this end, for example, the epidemics of AIDS, tuberculosis, malaria and neglected tropical diseases, as well as effectively addressing the threat of emerging infectious zoonotic diseases will require substantial policy coherence and investments. These are critical for the needed health innovations, as well as the development of systems-wide capacities within countries for the necessary measures of "prevention, detection and response".

While many global efforts have focused on increasing research and development for new health innovations, it is also now clear that there must be a corresponding emphasis on strengthening systems and capacities to deliver the range of needed health services and products. The Ebola outbreak in West Africa was an important reminder of the importance of effective, and continuing, core government functions, within and beyond the health sector. As the global community contemplates responses to address epidemics and infectious diseases, the imperatives for ensuring an integrated approach are clear: effective partnerships are required between the public, private and the community sectors.

This signals a clear need for increased policy coherence, which demands coordination between a broad range of actors; not just between government agencies, private sector and community actors at the national and local levels, but also between those working at the global level, including on innovation, R&D, financing, governance and management. Addressing interconnected elements, and encouraging effective synergies of efforts of stakeholders in the public, private and community sectors, will be critical, not only in effectively addressing infectious and new emerging diseases, but also in helping low- and middle-income countries (LMICs) achieve universal health coverage (UHC) and other health-related targets.

Objectives

In this context, the session aims to stimulate a dialogue between key stakeholders with the aim of identifying how public-private-community partnerships (PPCs) can address the needs of LMICs for effective "prevention, detection and response" to the threat of infectious diseases. The aim is to generate recommendations and proposals that can promote effective policy coherence and public-private-community partnerships at all levels. It is proposed that the discussions focus on three key, inter-related elements, as follows:

Policy coherence

- How can cross sectoral, multidisciplinary approaches at the national, regional and global levels be effected and prioritised?
- Which are key factors in facilitating policy, operational delivery environment and effectiveness for such approaches?
- What are relevant experiences and lessons learnt from existing projects and initiatives?
- What are the means to promote adoption of evidenced-based best practices and transferable lessons learned for policy coherence, including South-South approaches and strategies?

Effective partnerships

- What can we learn from existing PPC partnerships in terms of their contribution to the prevention, detection and response to infectious diseases?
- Are there experiences outside the health arena that are transferable?
- How can such partnerships be further strengthened?
- What are the right incentives for collaboration at different levels?
- What are the key considerations for ensuring the sustainability of PPC partnerships?

Evaluation and measuring success

- How can evaluation of PPC partnerships be undertaken?
- How do we measure success; e.g., what should be the matrix of success and effectiveness?
- Can there be evidence-based assessments of investments in innovation and R&D? And their eventual delivery in countries, including best practice, data and knowledge sharing?

Moderator

- **Tenu Avafia**, Team Leader, HIV, Health and Development Team, UNDP

Speakers

- **Mandeep Dhaliwal**, Director of HIV, Health and Development Team, UNDP
- **Hayato Urabe**, Director of Investment Strategy & Management, Global Health Innovative Technology (GHIT) Fund
- **Chalermsak Kittitrakul**, AIDS Access Thailand

Panelists

- **Yodi Mahendradhata**, Director, Center for Health Policy and Management, Universitas Gadjah Mada, Indonesia
- **Mwele Ntuli Malecela**, Director, WHO Regional Office for Africa
- **Richard Kock**, Professor of Wildlife Health and Emerging Diseases at the Royal Veterinary College, University of London, UK
- **Osman Dar**, Project Director, One Health Project, Centre on Global Health Security, London

Note: All speakers to be confirmed

PARALLEL SESSION 4.1 (PS4.1)

Moving Forward and Outward: Progress in Implementation of Global Frameworks and Initiatives

Background

Historically, international organizations, academia and others have provided regulations, standards or guidance to the global community (e.g., International Health Regulations, OIE Terrestrial Animal Health Code, and Codex Alimentarius). However, the challenge at all levels (i.e., globally, regionally, nationally and locally) has been in the actual implementation of these regulations, standards or guidance with the available resources and existing infrastructures. In response to requests from national authorities and as a result of breakdowns or delays in global, regional, national and local responses to emergent diseases, the global community has moved forward to develop frameworks and advance initiatives that further support national and local authorities in their efforts to prevent, detect and respond to human, animal and environmental health concerns. Critical to the utility and effectiveness of these frameworks and initiatives is the ability to build synergy among multiple stakeholder efforts and to address the needs of individual countries and communities.

Objectives

- To present a selection of global frameworks and initiatives, discuss the challenges and successes in their implementation and draw lessons to build sustainable, inclusive and effective preparedness and response systems.
- To discuss how these different global frameworks may (or may not) build upon each other or provide opportunities for synergies in supporting national and local capacity building efforts.

Moderator

- **Julie R. Sinclair**, CDC One Health Liaison to the OIE
- **Ronello C. Abila**, OIE SubRegional Representative for Southeast Asia

Panelists

- Development and implementation of the WHO's Joint External Evaluation (JEE) and role in implementation of the International Health Regulations and building national capacity (Mozambique as case study) – **Ali Ahmed Yahaya**, WHO
- OIE Performance of Veterinary Services (PVS) Missions and future course – **John Stratton**, OIE
- WHO Research and Development Blueprint – **Young-Mee YEE**, member of Advisory Group National of Health, Korea Centers for Disease Control and Prevention
- Global Rabies Initiative business plan – **Bernadette Abela-Ridder**, WHO

Note: All speakers to be confirmed

PARALLEL SESSION 4.2 (PS4.2)

Multi-sectoral Partnerships for Action on AMR

Background

Antimicrobial Resistance (AMR) respects no borders and has become an increasing threat to all countries - developed and developing alike. Common infections become untreatable, devastating infectious diseases become much more difficult to contain and standard medical procedures become a challenge. Thus, AMR has a major negative impact on growth and global economic stability. Given the breadth of impact from AMR, the only effective means to address AMR sustainably is through multisectoral action and partnership; however, challenges have been identified as to how stakeholders from different sectors can meaningfully come together to produce action and change. Innovative new approaches are needed to truly harness the potential of all people and perspectives, particularly those most vulnerable.

The UN Sustainable Development Goals (SDGs) recognize the importance of AMR (paragraph 26 of the Declaration). The attainment of many of them will depend on the availability of and access to affordable and effective antimicrobial medicines and other technologies such as diagnostic tests. AMR seriously threatens the health and lives of vulnerable populations, such as newborns, children, and women, as well as sustainable food and agriculture production and a healthy environment. AMR is reducing our ability to protect the health of animals and therefore is threatening safe and sustainable food and agriculture.

In a tripartite approach, WHO, the Food and Agriculture Organization (FAO) and the World Organization for Animal Health (OIE) recognize that addressing health risks at the human–animal-plant-ecosystems interfaces requires strong partnerships among entities that may have different perspectives and much work is currently ongoing.

On 21 September 2016, the President of the UN General Assembly convened a one-day high-level meeting at the UN Headquarters on AMR with the participation of Member States, non-governmental organizations, representatives of civil society, the private sector and academic institutions. The primary objective of the meeting was to summon and maintain strong national, regional and international political commitment in addressing AMR and the meeting emphasized the important role and responsibilities of governments, as well as the roles of non-State actors, the private sector and relevant inter-governmental organizations, particularly the WHO, FAO and OIE in establishing, implementing and sustaining a cooperative global, multi-sectoral and cross-sectoral approach.

Objectives

- How can the world come together to meaningfully and effectively address AMR in a sustainable way and in particular, engage non-traditional partners?
- Multisectoral partnerships have been identified as essential for addressing AMR – how can the world now move from planning to action at both the international and local levels?
- How does addressing AMR contribute to the attainment of the SDG's? How to effectively engage all relevant sectors: environment, food, employment, poverty reduction, agriculture, development partners, academia, private sector, etc.?
- How can the voice of all people be heard, particularly those marginalized and most vulnerable?
- What are the issues and opportunities around ensuring linkage between global and community/country-level partnerships? How can partnerships focus on possibilities for

meaningful collaboration, action on the ground and specific problems affecting communities rather than focusing only on the broader policy levels?

- What are some good practices and lessons learned from past multisectoral collaborations that could be applied to collaborations on AMR?

Moderator

- **Matthew Stone**, Deputy Director General, OIE

Panelists

- Civil society representative
  Arturo Quizhpe Peralta, Head, ReAct Latin America and Dean of the Faculty of Medical Science at University of Cuenca, Ecuador
  Stefano Nobile, Focal Point for Health, Caritas International, Vatican City
- Stakeholder perspective
  Maria Lettini, Director, FAIRR
- Country representative
  Ana Marie Garfin, National TB Control Program Manager, Department of Health, Phillippines
- WHO
  Marc Sprenger, Director of AMR Secretariat, WHO
- Representative from the interagency coordination group
  Jaana Husu-Kallio, Member of IACG, Permanent Secretary, Ministry of Agriculture and Forestry, Finland

Note: All speakers to be confirmed

PARALLEL SESSION 4.3 (PS4.3)

Community Systems: the Bedrock of Responses to EID and AMR

Background

Community preparedness and response to emerging infectious diseases (EID) and antimicrobial Resistance (AMR) is critical to the health outcomes of individuals. In HIV, people both living with and affected by HIV have been at the forefront of providing treatment preparedness to promote health-seeking behavior, improve adherence and other health outcomes, whilst advocating for increased availability, accessibility and uptake of key viral load diagnostics as well as 2nd and 3rd line antiretroviral therapy. In Malaria, civil societies work with other stakeholders to address artemisinin resistance in Southeast Asia via educating communities about the hazards of substandard drugs and organizing public awareness campaigns to complete a 3-day treatment course and on measures to prevent further spread of resistant pathogen strains. Similarly in tuberculosis, community-based outpatient treatment of MDR-TB in resource poor settings yield higher cure rates and facilitated better referrals to other health services required by TB affected communities. Furthermore, lessons learned from the early response to Ebola in West Africa have recognised the problem of sidelining community engagement as a key factor contributing to failure of the early emergency health programs to meet the needs and realities confronting affected populations in the region.

Today, prevention, detection and response to EID relies significantly on an effective surveillance system which starts at the community level with effective mechanisms in place to ensure linkage into national level health systems reporting. The Ebola crisis highlights the importance of integrated community case management (iCCM) and the roles of the network of community health workers and community leaders in early and better case reporting, contact tracing and bringing people into care, whilst reducing stigma and discrimination associated with the virus. Community-based control and preventive behaviours for vector control is recognized as a key pillar in disease response and preparedness for Zika and other mosquito-borne diseases. The use of innovative technologies in the response to EID by communities and community health workers contributed to the prompt control of the outbreak by providing a valuable platform for early warning and guiding early actions.

Objectives

The session aims to explore community roles in preparedness and response to EID and AMR, concentrating on lessons and approaches deployed in disease-specific programs, such as HIV, TB, Malaria, Ebola and Zika, whilst underscoring the importance of focusing on people, i.e. ensuring that systems for health involve the affected community and promotes community action as part of the overall health system critical for identifying, reporting and responding to emergency health threats.

The session is designed to generate discussions on commonalties and contexts of community action, and to reflect on emerging challenges that still persist in response to EID and AMR from the community perspectives, as well as to identify practical solutions drawing the lessons learned from community responses to the epidemics of HIV, TB, Malaria and to the most recent outbreaks of Ebola and Zika across the globe.

Moderator

- **RD Marte**, Asia Pacific Coalition of AIDS Service Organizations or Alessandra Nilo of GESTOS

Panelists

- **Othman Mellouk**, International Treatment Preparedness Coalition, HIV treatment advocate and educator, Morocco
- **Lina Kharn**, ARC Cambodia, Malaria Consortia, Cambodia
- **Anton Basenko**, Eastern Europe and Central Asia Network of People who Inject Drugs (ENPUD), Ukraine
- **Bhargavi Rao**, MSF-Holland, U.K
- **Alessandra Nilo**, GESTOS, Brazil
- **Abdulai Sesay**, Civil Society Movement Against Tuberculosis, Sierra Leone
- **Kannikar Kijtiwatchakul**, NHS Board member, Thailand

Note: All speakers to be confirmed

PARALLEL SESSION 4.4 (PS4.4)

Finding the Win-Win Solutions for Better Health from Better Food Systems

Background

The surging global demand for animal source foods and rapid growth rates in livestock and aquaculture production are being met with a range of approaches including both aggressive consolidations of production and marketing chains into intensive, large-scale commercial operations, as well as expansion of extensive, small- and medium-scale production systems. Most current approaches contain inherent vulnerabilities. How can the present food systems be reconfigured to feed the growing human population without leading to unintended health consequences for people, animals and the ecosystem? All the stakeholders in these food systems from production, marketing and consumption need to be actively involved in developing coherent and comprehensive approaches where almost everyone can benefit—i.e. collaborative win-win solutions.

Objectives

- Build upon the existing evidence base for the broad collateral benefits realized when longer term investments in shifting production toward reduced impact practices is achieved
- Review cases from the field of how these production shifts were achieved, the methodologies used in measuring the impact realized, and how the impacts were translated into advocacy efforts influencing policy and decision making
- Identify strategies for scaling up these approaches involving the critical stakeholders in a broad range of food systems based on animal production contexts

Moderator

- **Peter Black**, United Nations Food and Agriculture Organization

Speakers

- Farming organization representative representing small/medium size producers: **Andrey Susanto**, Indonesia
- Large producer: **Randal Giroux**, Cargill
- Consumer organization representative: **Niyada Kiatying-Angsulee**, Thailand
- Pharmaceutical industry representative: Elanco, **Kerry Keffaber**, Chief Veterinarian, Scientific Affairs and Policy.
- Knowledgeable Food Systems expert: **Robyn Alders**, University of Sydney, Australia.

Note: All speakers to be confirmed

PARALLEL SESSION 4.5 (PS4.5)

Bringing Solutions into Focus: Harnessing the Power of an Economic Lens

Background

Beyond the tragic loss of human life, the economic impact attributable to epidemics and pandemics can be catastrophic. SARS, $30 billion; Pandemic H1N1: $40 billion; Ebola: $2.8 billion in the three West African economies alone. Recent estimates place the inclusive costs from a moderately severe influenza pandemic at $570 billion annually, within the range projected for the annual cost associated with global climate change.[7] And, without intervention, the cumulative economic impact from anti-microbial resistance (AMR) through 2050 is projected to exceed $100 trillion (two-thirds of which is in low- and middle-income countries), substantially more than current annual global economic output.[8]

Despite a repeated pattern of costly response, the economic case for investing in proactive, preventive measures targeting a reduction in the pressures that facilitate disease emergence has not been widely adopted. A yearly investment of $1.9-3.4 billion to strengthen animal and human public health systems would yield a global public benefit estimated at over $30 billion annually through avoided economic damages associated with pandemics.[9] High return on investment is expected even if only a portion of pandemics are prevented, and strengthened One Health capacity in countries may confer additional benefits via improved prevention and control of endemic disease and AMR. However, challenges in mobilizing capital; an anemic evidence base and difficulty in translating evidence into policy advocacy with budget decision-makers; competing priorities for scarce health systems funding; and inequitable distribution of costs and benefits across sectors and stakeholders are all amongst the impediments to adopting the economic case for investing in preventive approaches.

Recent efforts designed to address these challenges have employed a range of approaches. Structures prioritizing risk avoidance and transference are being developed (e.g. multi-sectoral health security planning and capacity investments; epidemic/pandemic insurance structures). Also underway are new models capturing the economic impact of disease emergence as a function of land use, which will enable the disease regulatory role of ecosystems to be fairly valued and incorporated into payment for environmental services frameworks. And global financing structures promoting targeted, multi-sectoral systems strengthening and incentivizing investments in preparedness are being established.

[7] http://www.nber.org/papers/w22137

[8] O'Neill. Antimicrobial Resistance: Tackling a crisis for the health and wealth of nations. Review on Anti-Microbial Resistance. February 2015

[9] World Bank. People, Pathogens and Our Planet: Economics of One Health. 2012.

Objectives

- Highlight successful practices and approaches that have demonstrated promise in fostering decision making informed by economic analyses;
- Profile structures with proven utility in transcending the identified challenges, including resource prioritization and inequitable sectoral cost and benefit distribution;
- Discuss approaches that strengthen the economic evidence base for investments in proactive, preventive disease mitigation approaches; and
- Review policy and regulatory options, such as tax and incentive structures, that can contribute to a favorable investment environment for more wide scale adoption of risk mitigation approaches

Moderator

- **Dan Schar**, Regional Emerging Infectious Disease Advisor, USAID Regional Office

Panelists

- **Gavin Yamey**, Duke University Global Health Institute
  Introduction/overview; making the investment case for a preventive, One Health approach; challenges and opportunities in financing preparedness
- **Ramanan Laxminarayan**, The Center for Disease Dynamics, Economics, & Policy
  Global consumption of antimicrobials in animal production, costing antimicrobial growth promoter phase out, and catalyzing fit-for-purpose, enforceable AMU policies
- **Carlos Zambrana-Torrelio**, EcoHealth Alliance (A328)
  Analyzing the economics of disease emergence from deforestation to support better practices in the extractive industries and reduce pandemic risk
- **Nita Madhav**, Metabiota
  Catastrophe modeling and pandemic insurance: approaches to managing risk and incentivizing mitigation postures
- **Victoria Fan**, University of Hawai‘i at Mānoa.
  Expected economic losses from potentially vaccine preventable epidemics and pandemics

Note: All speakers to be confirmed

From: Katie Leahy >
Sent: Wednesday, November 01, 2017 4:53 PM EDT
To: Robert Kityo >; Ian Mendenhall >; Joram Buza ; Vivek Kapur >; ecohealthalliance.org>; Jon Epstein Kading,Rebekah >; Lela Urushadaze >; Lela Urushadaze <| ; Tamar Kutateladze >; Supaporn Wacharapluesadee >; Abel Wade >; Catalino Demetria >; Tigga Kingston >; Paul Cryan ; DeeAnn Reeder ; Gavin Smith ; Nisreen Alhmoud <
CC: Stokes, Martha M CIV (US) ; Lancaster, Mary J CIV (US) >; Flegler, Ayanna J CTR (US)
Subject: BPERNet Update and Meeting Date
Attachment(s): "PMAC2018 Provisional Conference Program_as of Oct 27.pdf"

Dear BPERNet Steering Committee Members,

After careful consideration of the size and scope of PENAPH and increased travel and schedule concerns from BPERNet members, CBEP has decided to move the date of our second meeting to coordinate with the Prince Mahidol Award Conference (PMAC) 2018 in Bangkok, Thailand. We will hold our meeting on Wednesday, 31 January. We have yet to set a time or location, but anticipate that travel planning should support a full day meeting.

Most of PMAC's objectives are focused on zoonoses and some complement BPERNet's ecological focus, this will assist members of the group who plan to attend the conference and use it as an opportunity to advertise our network. I am attaching PMAC information for everyone's situational awareness.
Please consider this email an official a save the date on behalf of CBEP, with more information to follow, which will include travel, agenda, time, and location information. At your earliest convenience, please let me know if you can support attending this meeting.

Thanks!

V/r,

Katie Leahy

PRINCE MAHIDOL AWARD CONFERENCE 2018

Making the World Safe from the Threats of Emerging Infectious Diseases

Background

The Prince Mahidol Award Conference (PMAC) is an annual international conference focusing on policy-related health issues. The Prince Mahidol Award Conference 2018 is co-hosted by the Prince Mahidol Award Foundation, the Thai Ministry of Public Health, Mahidol University, the World Health Organization, The World Bank, U.S Agency for International Development, Japan International Cooperation Agency, The Rockefeller Foundation, with support from other key related partners. The Conference will be held in Bangkok, Thailand, from 29 January – 3 February 2018. The theme for PMAC 2018 is "Making the World Safe from the Threats of Emerging Infectious Diseases".

We live in an era when the emergence of novel infectious disease agents is posing an increasing threat to global health and security. The threat from novel infectious diseases is accelerating at a pace and with an intensity unprecedented in human history, driven by increasing human populations, climate change and surging global travel. The possibility that a single lethal microbe could suddenly emerge and sweep through every household, through every community without regard to national borders or social and economic standing is a shared fear across the globe. Just the fear can cost billions, as illustrated by recent Ebola and Zika virus panics in little-affected countries. But the reality of the threat is all too clear, proven by the decades of response to the HIV-AIDS pandemic. Yet the world is not prepared to either mitigate the impact of an emergent disease threat or prevent its emergence.

Zoonotic and AMR related diseases account for more than 95% of all emerging infectious diseases reported during the second half of the 20th century[1]. In this century the emergence of SARS, pandemic influenza, MERS, and the spread of Ebola and Zika reflect the world's increasing vulnerability to novel zoonotic threats. The simultaneous emergence of pathogens resistant to antibiotic therapies raises the prospect of a "post antibiotic" world. While the drivers underlying the emergence of zoonotic and antibiotic resistant diseases are complex, human behaviours and their impact on animal populations and the environment are understood to be central to the emergence of both disease threats. The role of increasing animal-human contact in the emergence of zoonotic diseases has been well documented and been increasingly the focus of One Health initiatives across the globe. The contribution made by the inappropriate use of antibiotics in animal husbandry to AMR is less well documented but in recent years has been increasingly understood to be a core driver behind the emergence and global spread of antibiotic resistant organisms, along with inappropriate "prescriber-user" practices associated with antibiotic use in clinical care. Changing environmental and climatic conditions have also been closely linked to the emergence of novel infectious diseases. That infectious disease emergence is closely associated with practices and

[1] K. E. Jones *et al.*, Global trends in emerging infectious diseases. *Nature* **451**, 990-993 (2008).

behaviours at the animal-human-environment interface speak to the importance of an expanded multi-sectoral alliance across the animal, human and environmental sectors to address the threats posed by both zoonosis and AMR. The Global Health Security Agenda and related One Health movement provide important frameworks for mobilizing international action.

The Rising Threat of Zoonotic Diseases

Since the Influenza Pandemic of 1918 when between 50-100 million died (5-10% of the human population) we have been fully aware of how vulnerable our place on this planet is.

Even in the absence of significant global mortality, epidemics and pandemics can cost tens of billions of dollars, reversing development gains and pushing communities and households into poverty. The SARS outbreak in 2003 cost the economies of East Asia between $30-50 billion and estimates of the global economic cost of an influenza pandemic range from $374 billion, for a mild pandemic, to $7.3 trillion, for a severe pandemic - with a 12.6% loss of gross domestic product.

Strategically, policies to address a potential pandemic threat are constrained by an unresolved debate over the use of adaptive measures - that aim through the use of technological measures to reduce the impact of diseases after they have emerged vs mitigation measures - that focus on the underlying causes of disease emergence. The adaptive tools we traditionally rely on to protect us from the world of infectious diseases – vaccine and therapeutics – too often are shown ineffective against a novel threat; and, the timely development and deployment of new and effective biomedical countermeasures is undercut by the speed at which the threat spreads.

Similarly, our ability to mitigate the emergence of new threats is undermined by a lack of knowledge about the viral ecology and the drivers, including human behaviors, which propel the emergence of a new threat. It is at these moments we realize just how few our adaptive and mitigation options are – and how vulnerable the global community is. After each episode the world admonishes itself for being ill prepared to deal with a global threat – but after decades of largely reacting adaptively to each event, with only a tangential focus on mitigation, we are only marginally better able to deal with the next one.

A “Post Antibiotic World”

The development and commercialization of antimicrobials stands as a defining achievement of 20th century medical practice. Antimicrobials heralded an era of expanded life expectancy, paved the way for advanced medical and surgical treatments, improved animal health and welfare, and made possible curative therapy for once fatal infections. Decades of superfluous and inattentive use of antimicrobials across the human and animal health sectors now threaten these advancements. The pace of reported treatment failures and antimicrobial resistance (AMR) in common pathogens is increasing, with multi-drug resistant pathogens creating the prospect of a ‘post antibiotic’ world. In the absence of interventions, AMR-associated human mortality is projected to soar from a current rate of 700 000 to over 10 million annually by 2050—as readily treatable infections become life threatening, and routine procedures are rendered unsafe.[2] Asia is expected to account for half of this projected global mortality. The impact of AMR on morbidity and mortality is matched by a substantial economic burden, with resistance linked to aggregate losses anticipated to exceed USD 100 trillion by 2050.

[2] O’Neill, J. Review on Antimicrobial Resistance. Tackling a Global Health Crisis: Initial Steps. 2015

Antimicrobial resistance is exacerbated by the unregulated use of antimicrobials across both the human health and animal health sectors. A particular concern is the shared use of same classes of antibiotics in humans and in animals, potentially exacerbating the selection pressures on pathogen populations in animals and humans that encourage the development of resistance and exchange of resistance genes. By example, in the United States the livestock production industry accounts for 80% of the total use of antibiotics used for treatment of human infections.

Antimicrobial resistance is one of the three flagship topics for the tripartite (FAO, OIE and WHO) collaboration. At the Sixty-eight World Health Assembly in May 2015, the World Health Assembly endorsed the Global Action Plan (GAP)[3] on AMR and requested to strengthen the tripartite collaboration between FAO, OIE and WHO for combating antimicrobial resistance in the spirit of the "One Health" approach. The Global Action Plan, which ensured a One Health approach and consistency with Codex Alimentarius and OIE inter-governmental standards and guidelines, aims to ensure continuity of successful treatment and prevention of infectious diseases with effective and safe medicines that are quality-assured, used in a responsible way, and accessible to all who need them. Guided by this global action plan, the Member States, the Secretariat, and their international and national partners aim to: (1) improve awareness and understanding of antimicrobial resistance; (2) strengthen knowledge through surveillance and research; (3) reduce the incidence of infection; (4) optimize the use of antimicrobial agents; and (5) develop the economic case for sustainable investment that takes account of the needs of all countries, and increase investment in new medicines, diagnostic tools, vaccines and other interventions.

A high level meeting on anti-microbial resistance was held in September 2016 at the United Nations General Assembly, generating a statement of global commitment to address AMR through a multi-disciplinary approach.[4]

PMAC 2018 Will Be Action Focused. Protecting the world from the threat of zoonotic diseases and ensuring effective stewardship of antibiotics requires a common and well-coordinated multi-sectoral effort. While there has been significant progress in building multi-sectoral One Health action against zoonotic diseases, AMR efforts remain highly siloed with an unequal focus on the respective contributions made by the inappropriate use of antibiotics in clinical care and animal production, as well as limited opportunities for bringing human, animal and environmental health sectors together to forge a common strategy. There is an urgent need to bring a comprehensive One Health risk mitigation approach to address zoonotic and AMR related diseases that addresses the direct consequences of animal-human interactions and contributory pressures related to environmental and climate changes.

PMAC 2018 will provide an important setting for fostering policy and strategic action by engaging multi-sectoral experts in zoonosis and AMR, as well as climate change and related environmental fields from across the public and private sectors, international organizations, foundations, academics and non-governmental organizations, as well as critical players in Global Health Security Agenda (GHSA). Importantly, a PMAC sponsored "Making the World Safe from the Threats of Emerging Infectious Diseases" would build on PMAC 13's highly successful conference on One Health and lead to real change.

PMAC 2018 Will Build On Past PMAC Themes. Since 2007, the Prince Mahidol Award Conference has been organized as an annual international conference focusing on policy-related public health issues of global significance – including, Universal Health Coverage, Health Equity, Meeting the

[3] Global Action Plan on Antimicrobial Resistance, http://www.who.int/drugresistance/global_action_plan/en/
[4] http://www.un.org/pga/71/2016/09/21/press-release-hl-meeting-on-antimicrobial-resistance/

Needs of Vulnerable Populations, and addressing the threats posed by infectious diseases. Each of these meeting has brought together leading public health leaders and stakeholders from around the world to propose concrete solutions and recommendations. PMAC 2018 will explicitly look to build on the successes of past PMACs and to identify opportunities to further contribute to the systems and capacities required to address the comprehensive health needs of the world's populations

Objectives

1. To accelerate progress in the adoption of multi-sectoral approaches for addressing zoonotic diseases and antimicrobial resistance
2. To advocate for evidence-based priority setting and policy decisions for zoonotic diseases and antimicrobial resistance
3. To share knowledge and experience in addressing the challenges posed by zoonotic diseases and antimicrobial resistance
4. To promote a greater understanding of the range and nature of the "drivers" underlying the emergence of new disease threats and options for their mitigation
5. To highlight emerging demographic, climatic and travel trends to better understand how disease emergence will evolve over the course of this century
6. To underscore the collateral socio-economic and development benefits associated with a One Health Agenda

Sub-themes

Sub-theme 1: Learning from the Past: Towards Effective and Sustainable Policies, Practices and Capacities for "Prevention, Detection and Response" to Emerging Zoonosis and Antimicrobial Resistance

This sub-theme is focused on presenting evidence for how efforts across the globe over the past two decades to address zoonotic and AMR related threats are contributing to more effective policies, practices and capacities for "prevention, detection and response" to EIDs. Given the inherent multi-sectoral aspects of disease emergence this is an opportunity to learn from recent experience with efforts such as the Global Health Security Agenda (GHSA), International Health Regulations, the One Health movement, and other platforms illustrating challenges and solutions for building effective partnerships for addressing zoonosis and AMR.

Issues to be discussed under this sub-theme are:

1. Evidence for optimal policies, regulations and systems for addressing EIDs
    - What we have learned from country, regional and global level experiences in addressing EIDs
        - Case studies illustrating successes and failures; how well do we manage and mitigate present threats (e.g. MERS CoV, Nipah virus, Zika virus, Zoonotic Influenza, Ebola virus, AMR, and others)
        - Organizational options for building sustainable national-level partnerships across multi-ministerial groups, including Health, Agriculture, Environment, Finance and Education
            - What are the policy requirements
            - What are the human resource requirements
            - What are the organization requirements

        - What are resource requirements
    - How are these experiences translated to the sub-national level
        - What are the equivalent requirements for provincial/county level operations

2. Evidence for optimal global and regional level structures for addressing EIDs

- What are the lessons learned on building global and regional level partnerships, including the GHSA, One Health and Planetary Health, to address EIDs
    - How effective have global and regional partnerships been in building multi-sectoral alliances to enable country level actions
        - What are the policy requirements
        - What are the human resource requirements
        - What are the organization requirements
        - What are resource requirements

- What is the evidence for proactive, flexible structures that enhance capacities and preparedness across the prevention-detection-response continuum?
    - What have we learned from the pandemic vaccine development banks; consortia for conservation of antimicrobials?
    - What can we learn from parallel efforts, such as those addressing global climate change and carbon emissions?
    - What examples demonstrate the ability to bridge the apparent dichotomy between capacity building and a research agenda concerning emerging zoonoses and AMR?

3. Evidence of novel, upstream approaches to earlier detection and trends monitoring, including but not limited to:

- Novel surveillance postures and strategies,
- digital diseases detection,
- crowdsourcing big data,
- predictive analytics on disease distribution

4. Evidence for more sustainable approaches for “prevention, detection and response”

- What are examples of sustainable financing structures? What have we learned from:
    - The World Bank Pandemic Emergency Financing Facility?
    - Evolving schemes for engaging insurance companies to “share” pandemic risk?
    - Efforts to quantify cost attributable to zoonotic disease and AMR burden, project pandemic influenza economic impact, and make a credible investment case for prevention and risk mitigation?
- What are examples of “preparedness” activities that address long-term sustainability?
    - What have we learned from the World Bank and WHO’s joint effort to develop strategies for both pandemic and “all hazards” preparedness and related long-term financing schemes?
- Which financing models have proven utility in employing an evidence driven approach to discouraging high risk practices and incentivizing risk mitigation in approaching pandemic prevention as a global public good?

Sub-theme 2: Harnessing the Power of Public-Private-Community (PPC) Partnerships for "Preventing, Detecting, and Responding" to Zoonosis and AMR

This sub-theme is focused on examining the evidence for building effective partnerships that bring together community, private sector and public sector resources for sustainably addressing the threats posed by zoonosis and AMR. As with the previous sub-theme, the inherently multi-sectoral nature of zoonosis and AMR requires active engagement across multiple stakeholders. In addition to the Public sector, Private sector actors who may be directly engaged in activities that inadvertently contribute to "drivers" for EIDs will need to be actively involved in any efforts to better mitigate the consequences of their activities. Similarly, communities are key stakeholders, both as consumers and potential contributors to some of the drivers that underlie disease emergence (e.g. inappropriate use of antibiotics in rearing of livestock and aquaculture)

Issues to be discussed under this sub-theme are:

1. Evidence for strong PPC partnerships that have contributed to "prevention, detection and response" to Zoonosis and AMR

- What are the lessons from PPC partnerships in addressing EIDs
    - Country, regional or global examples of how PPC partnerships have been able to harness across each of the constituencies to address EIDs in ways that greatly enhanced the overall impact
        - What were the incentives for PPC partnerships
        - What were the roles and responsibilities of each group
        - What were the metrics for valuing the PPC partnerships
        - What were the operational factors for sustainability of PPC parntership

2. Evidence of successful outreach and community empowerment
    - What are examples of how risk communications have successfully affected community and/or individual level practices and behaviors on a scale significant enough to reduce the risk from zoonotic threats and/or AMR

3. Evidence for an active and sustainable engagement of the private sector
    - What are examples of how private sector partners have been actively and sustainably engaged in efforts to address zoonotic threats and/or AMR
    - What can be learned from partnerships with biomedical industry in developing and marketing vaccines and medical countermeasures? Employing novel diagnostic platforms enabling rapid detection and response to emerging threats?
    - What are examples of partnerships with industry in the use of non-medical countermeasures within communities to help mitigate, prevent, and control infectious disease threats? Employing new technologies and platforms for health communication and the application of non-pharmaceutical interventions.

4. Evidence for how consumer advocacy can contribute to change policies and practices

5. Evidence of economic benefits from PPC

Sub-theme 3: Understanding the Selection Pressures Underlying Emergence of Zoonotic Diseases and Antimicrobial Resistance and the Broad Benefits Realized From Promoting Healthy Animals and Healthy People

This sub-theme is focused on both:

a) exploring the contributions made by climate change, population growth, global travel, habitat change, expanding settlements, resource extraction, increased livestock and crop production and other underlying drivers that contribute to the emergence of new zoonotic and anti-microbial disease threats, and
b) examining the broad benefits that are accrued from promoting practices across multiple sectors that aim at reducing these drivers and the risk of zoonotic diseases and antimicrobial resistance.

There has been a general recognition that the adoption of a core set of best practices that are designed to directly target the drivers associated with zoonosis and AMR are likely to simultaneously contribute to positive outcomes across a range of "other" domains and the achievement of the United Nations Sustainable Development Goals, such as food security, household wealth and economic growth, as well as healthier environments and sustainable communities.

a) Issues to be discussed under this sub-theme will allow a presentation of the evidence for the drivers of EID emergence:

1. Evidence for Climate Change in Increasing Infectious Disease threats and models projecting future impact

- How does climate change contribute to spread of infectious disease threats
    - Topics to be considered could include: impact on vector ecology, animal migration, altered range and distribution of reservoir host species;
    - variance in freshwater availability, sanitation, and waterborne disease

2. Evidence for demographic and population change on increasing Infectious Disease threats, including how settlement patterns (peri-urbanization), population movement (increased air travel, trade etc), habitat change (impact on animal bio-diversity) contribute to disease emergence and spread

3. Evidence for how increased economic activity impacts on increased Infectious Disease risk, including how expanded incursions of extractive industry operations and agricultural intensification into wildlife domains increase risk for "spillover" and spread of novel diseases

- Options for how "risk" can be mitigated at the site of industry operations or in planning/selecting where industry operations occur

4. Evidence for how increased livestock production and marketing in geographic "hot spots" for disease emergence may increase risk of pathogen "spillover" and spread

- How projected increases in livestock production in Africa and shifting production contexts in Asia over the 21st century will impact on the risk of disease emergence, including zoonosis and AMR
    - Models for likely changes in terrestrial and aquatic animal production and marketing patterns over the coming century
    - Models for potential increased environmental impact that could elevate risk
    - Options for minimizing risks associated with increased livestock production and marketing

- Considering the impact of a global supply chain of agricultural commodities and production inputs (e.g. animal feed), and trans-continental risk management strategies

b) Issues to be discussed under this sub-theme also will allow a presentation of the evidence to broad collateral benefits accrued from targeting the drivers of EID emergence:

5. Evidence that adoption of practices to reduce zoonotic and AMR risks associated with livestock production would also contribute to more efficient and more profitable operations.

- How do improved biosecurity and husbandry practices that strengthen control of pathogenic zoonotic viruses improve the overall health of livestock and the environment
  - Reduced animal diseases
  - Improved animal health can lead to increased livestock productivity and reduced input costs for production
  - Enhanced productivity and yield per animal production unit
  - Reduction in prophylactic antibiotic use

- How does proper management of antimicrobials in livestock production and aquaculture improve economic returns
  - Improved hygienic conditions, nutrition, and vaccination in animal husbandry associated with reduced use of antibiotics and corresponding returns on investment
  - What can be learned from the experience of countries that have phased out and enacted regulatory controls on use of antimicrobials in animal production
  - AMR reduces potency of veterinary drugs and negatively affects animal health
  - Consumer demand for antimicrobial residue free animal source foods
  - Market based incentives and penalties for reduced antimicrobial use and enhanced adherence to drug withholding periods, minimizing residues in products entering the food chain
  - Best practices in strengthening antimicrobial usage regulatory and enforcement structures in animal production

6. Evidence that reduction in habitat fragmentation has led to the control of zoonosis

- How does habitat fragmentation impact on both vector-borne and non vector-borne diseases
  - Evidence that changes in habitat leads to changes (increase/decrease) the transmission dynamics of infectious diseases (e.g. chikungunya, malaria)

7. Evidence that that the real and/or projected economic impact from emerging zoonoses and AMR has informed resource allocation policies and an investment case for prevention

- What practices and approaches have shown promise in fostering decision making informed by economic analyses
- What novel structures have proven utility in transcending the challenge of inequitable sectoral cost and benefit distribution
  - Evidence for one or more sectors bearing the cost for benefits accruing to different sectors/stakeholders (e.g. H7N9 control in China: costs borne by producers and markets, but benefits accrue to health sector; or resource extraction and disease emergence: costs borne by health sector, but benefits accrue to industry and land planning/mining/forestry entities)

Venue and Dates of the Conference

Centara Grand at Central World Hotel, Bangkok

Monday 29 – Tuesday 30 January 2018	Side Meetings
Wednesday 31 January 2018	Field Trip
Thursday 1 – Saturday 3 February 2018	Main Conference

Structure of the Conference

This is a closed, invitation only conference host by the Prince Mahidol Award Foundation, and the Royal Thai Government, together with other international co-hosts. The conference consists of:

1. **Pre-conference**
    a. Side meetings
    b. Field trip

2. **Main conference**
    a. Keynote speeches
    b. Plenary sessions
    c. Parallel sessions
    d. Synthesis: Summary and recommendations
    e. Poster display

Pre-Conference Program

Monday 29 January 2018

09:00-17:30	Side Meetings

Tuesday 30 January 2018

09:00-17:30	Side Meetings

Wednesday 31 January 2018

06:30–18:00	Field Trip

Main Conference Program

Thursday 1 February 2018

09:00-10:30	**Opening Session & Keynote Address** Opening Session by **Her Royal Highness Princess Maha Chakri Sirindhorn** Keynote Address • Prince Mahidol Award Laureate 2017 • Prince Mahidol Award Laureate 2017 • **TBC**
10:30-11:00	Break
11:00-12:30	**Plenary 0: Vision 2100: Re-Imagining the End Game for the End of the Pandemic Era**
12:30-13:30	Lunch
13:30-14:30	**Plenary 1: Leadership Needed for Managing Emerging Infectious Diseases of the 21st Century**
14:30-16:30	**PS1.1: Lessons Learned in Managing Emerging Infectious Diseases (EID)** **PS1.2: Strategic Information and the Evolution of Emerging Infectious Diseases: Lessons from the Past and New Opportunities** **PS1.3: Safeguarding Medicines in the Era of AMR: What Do We Know? What Works?** **PS1.4: Financing Pandemic Preparedness: Where is the Money?** **PS1.5: One Health on the Move: Nomadic Communities**
16:30-17:00	Break
17:00-18:00	**Plenary 2: Futures of Partnerships for a Safer World**

Friday 2 February 2018

08:30-09:30	**Plenary 3: Managing Emerging Infectious Disease and AMR Risk across the Livestock Revolution**
09:30-10:00	Break
10:00-12:00	**PS2.1: Beyond MERS and Zika: Are we Prepared for the Next Big Epidemic?** **PS2.2: AMR: Addressing Excessive and Inappropriate Use of Antibiotics** **PS2.3: Dealing with an Inter-Connected World: Partnerships for Preparedness, Detection and Response during Mass Gatherings** **PS2.4: Changing Dynamics: Emerging Infectious Diseases and Antimicrobial Resistance in an Era of Expanding Global Human Population Growth and Movement** **PS2.5: Reducing the Gap: Addressing Neglected Disease; Neglected Populations**
12:00-13:00	Lunch
13:00-15:00	**PS3.1:** **PS3.2: Lessons Learned from a One Health Approach to AMR** **PS3.3: Climate Change and Emerging Diseases: The Importance of Resilient Societies** **PS3.4:**

	PS3.5: Policy Coherence: Effective Partnerships for Global Health
15:00-15:30	Break
15:30-17:30	**PS4.1: Moving Forward and Outward: Progress in Implementation of Global Frameworks and Initiatives** **PS4.2: Multi-sectoral Partnerships for Action on AMR** **PS4.3: Community Systems: the Bedrock of Responses to EID and AMR** **PS4.4: Finding the Win-Win Solutions for Better Health from Better Food Systems** **PS4.5: Bringing Solutions into Focus: Harnessing the Power of an Economic Lens**
18:00-20:30	**Welcome Dinner** • **Welcome Speech** by - Minister, Ministry of Public Health, Thailand - President, Mahidol University, Thailand • **Dinner Speech** by **Bill Gates**, Bill and Melinda Gates Foundation, USA (TBC)

Saturday 3 February 2018

09.00-09.30	**Closing Session** • **Speech** by **Margaret Chan**, Former Director General, World Health Organization, Switzerland (TBC)
09.30-10.30	**Synthesis: Summary, Conclusion & Recommendations**
10.30-11.00	**Statement**
11.00-12.00	**Closing Performance**
12.00-13.30	Lunch
14:00-16:30	**International Organizing Committee (IOC) Meeting for PMAC 2018/2019**

OPENING SESSION AND KEYNOTE ADDRESS

Opening Session

by Her Royal Highness Princess Maha Chakri Sirindhorn

Keynote Address

- Prince Mahidol Award Laureate 2017
- Prince Mahidol Award Laureate 2017
- **TBC**

Note: All speakers to be confirmed

PLENARY 0 (PL0)

Vision 2100: Re-Imagining the End Game for the End of the Pandemic Era

Background

We live in an era when the emergence of novel infectious disease agents is posing an increasing threat to global health and security. The threat from novel infectious diseases is accelerating at a pace and with an intensity unprecedented in human history, driven by increasing human populations, climate change and surging global travel. The possibility that a single lethal microbe could suddenly emerge and sweep through every household, through every community without regard to national borders or social and economic standing is a shared fear across the globe. Just the fear can cost billions, as illustrated by recent Ebola and Zika virus panics in little-affected countries. But the reality of the threat is all too clear, proven by the decades of response to the HIV-AIDS pandemic.

Zoonotic and AMR related diseases account for more than 95% of all emerging infectious diseases reported during the second half of the 20th century[5]. In this century the emergence of SARS, pandemic influenza, MERS, and the spread of Ebola and Zika reflect the world's increasing vulnerability to novel zoonotic threats. The simultaneous emergence of pathogens resistant to antibiotic therapies raises the prospect of a "post antibiotic" world. While the drivers underlying the emergence of zoonotic and antibiotic resistant diseases are complex, human behaviours and their impact on animal populations and the environment are understood to be central to the emergence of both disease threats. The role of increasing animal-human contact in the emergence of zoonotic diseases has been well documented and been increasingly the focus of One Health initiatives across the globe. The contribution made by the inappropriate use of antibiotics in animal husbandry to AMR is less well documented but in recent years has been increasingly understood to be a core driver behind the emergence and global spread of antibiotic resistant organisms, along with inappropriate "prescriber-user" practices associated with antibiotic use in clinical care. Changing environmental and climatic conditions have also been closely linked to the emergence of novel infectious diseases. That infectious disease emergence is closely associated with practices and behaviours at the animal-human-environment interface speak to the importance of an expanded multi-sectoral alliance across the animal, human and environmental sectors to address the threats posed by both zoonosis and AMR.

As we look forward towards the end of this century, the predictable escalation in the interactions between humans and animals speaks to a world of increasing global risk. The consequences of these trends, however, are avoidable. Success in "making the world safe from the threats of emerging infectious diseases" requires we think and act differently; to not continue with the half-measures that have made the world ill prepared to address these threats.

Rapid advances in science and a corresponding revolution in technologies allow us, for the first time, to imagine a world where these "threats" can be minimized. What is required is bold action; that embraces an aggressive time horizon; and, that is global in scope. Such action can build systems and

[5] K. E. Jones *et al.*, Global trends in emerging infectious diseases. *Nature* **451**, 990-993 (2008).

capacities able to mitigate the emergence of future threats and to control them when they do. With this knowledge comes the power to end panic and move to prevention.

This Plenary will present and discuss examples of new, innovative and bold global ventures which are now laying the groundwork for the "beginning of the end of the Pandemic Era".

Objectives

- Explore novel and transformative approaches that address the underlying drivers of zoonotic disease and AMR
- Harness methodologies, technologies, and thinking across a range of disciplines to promote a vision for a proactive approach to emerging zoonoses and AMR
- Enable a conversation that transcends current impediments and envisions possible pathways and enabling factors to realize the end of the "pandemic era"

Moderator

- **Dennis Carroll**, USAID

Keynote Speaker

- **Harvey Feinberg,** President, The Gordon and Betty Moore Foundation

Panelists

- **Richard Hatchett**, CEO, Coalition for Epidemic Preparedness Innovations (CEPI)
- **George Gao**, Director, China Center for Disease Control and Prevention
- **Margaret Hamburg**, President, American Association for the Advancement of Science (AAAS)
- **Larry Brilliant**, Chairman, Skoll Global Threats Fund

Note: All speakers to be confirmed

PLENARY 1 (PL1)

Leadership Needed for Managing Emerging Infectious Diseases of the 21st Century

Background

We now live in a world where any local infectious disease outbreak event has the potential to become an epidemic or pandemic. While preparedness of local agencies is key to quickly identify and contain outbreaks, global partnerships and international collaboration across all sectors must be effective to support and manage events. These partnerships have the potential to proactively alter the global architecture in order to quickly detect, prevent and respond to infectious disease threats as they emerge.

The plenary session will address the *Leadership Needed for Managing Emerging Infectious Diseases of the 21st Century*. It will set the scene of the global health architecture and how the international community is organizing to address effectively EIDs. It will also address leadership needed at country level for managing emerging infectious diseases.

The session will feature speakers from organizations with recent experience of preparing for, and responding to global health crises in the 21st century and consider how, as risks, environment and global architecture change, funding varies, how organizations change and adapt to tackle the contemporary challenges, and how are the lessons learned from recent challenges being incorporated into plans for future events. Speakers from countries and civil societies will bring a national and community level perspective on how to respond to global health crises.

Objectives

The objective is to identify what kind of leadership, at all levels, is needed to address the increased risk and the complexity of EID and AMR and bring together different partners and groups acknowledging the various organizational and sectoral cultures.

Moderator

- **Sylvie Briand**, WHO, Director Infectious Hazard Management

Panelists

- **Peter Salama**, EXD, WHO's Health Emergencies Programme – WHO perspective-
- **Elhadj As Sy**, Secretary General of the IFRC – civil society and community perspective
- **Francoise Barré-Sinoussi**, Nobel Prize Awardee for HIV discovery, Institute Pasteur – perspective on HIV pandemic management
- **Oly Ilunga Kalenga**, DRC MOH – country perspective

Note: All speakers to be confirmed

PLENARY 2 (PL2)

Futures of Partnerships for a Safer World

Background

This plenary is an interactive session that will introduce four core questions, based on the Futures approach, to shape the discourse of partnerships for greater biosecurity in the world. It will begin with an introduction of Futures thinking by Dr. Sohail Inayatullah, UNESCO Chair of Futures Studies and Professor at Tamkang University, Taiwan. Then, the plenary will involve a short discussion on the current state of partnerships or lack of in certain thematic areas, and challenges in forging effective partnerships. It will delve into exploring various futures for partnerships and what effective and inclusive partnerships can achieve to make the world a safer place for all. Attempting to jointly uncover the "unknown unknowns" within a Futures methodology will lead to an innovative approach in organizing an interactive plenary that would hopefully lead to new directions and interesting discussions within the parallel sessions.

Objectives

- To jointly envision possible scenarios for the future of partnerships in EID and AMR.
- To generate excitement in creating effective partnerships for a safer world by imagining alternate futures based on Futures techniques. It is envisioned that the novelty of the technique will add to the richness of PMAC and to bring in cross-disciplinary approaches into a Public Health conference.
- To get participants to think creatively in an out-of-the-box manner on working collaboratively together to build greater biosecurity for all.

Moderator

- **Sohail Inayatullah**, who is experienced in working on Biosecurity issues as well as other Development challenges

Panelists

- **Diah Saminarsih**, Special Advisor to Minister, Ministry of Health Indonesia, Indonesia
- **Sania Nishtar**, President, Heartfile, Pakistan
- **Ken Banks**, Founder, FrontlineSMS, United Kingdom

Note: All speakers to be confirmed

PLENARY 3 (PL3)

Managing Emerging Infectious Disease and AMR Risk across the Livestock Revolution

Background

Widespread demand for animal protein nutrition over the last half century has fueled an explosive growth in global livestock production systems. Between 2000 and 2030, demand for beef and dairy is expected to nearly double, and poultry to nearly triple. In select high growth regions, such as South Asia, demand for poultry is expected to soar to 725%.[6] Keeping pace with this demand, the production, marketing, and distribution of terrestrial and aquatic animal production has undergone transformational change. While rural livelihoods globally remain largely dependent upon grain, tubercle, and legume-based nutrition, an overall consolidation and commercialization of the production and marketing chains is shifting the disease emergence risk profile.

Increasingly, global animal product supply chains impact disease risk variably, through secondary and tertiary order effects that may be geographically separated. Within the context of zoonotic disease emergence risk, what are the linkages across geographically distinct areas where demand for animal protein is growing, the production of that protein, and the production of inputs such as animal feed? Can a total "emergence risk footprint" be developed to quantify this risk and prioritize reduced impact production scenarios? And what incentives and structures are needed to expedite a global shift toward such lower impact production systems?

The collective capacity to mitigate emerging zoonotic disease and AMR risks associated with increasingly complex global animal production chains will be dependent upon a robust understanding of the disease transmission drivers within these global systems. This session will enable a detailed evaluation of the role of animal production in potentiating zoonotic disease emergence and AMR, and will identify commonalities across regions, production contexts, and sectors that can inform applied risk mitigation approaches. While the session will focus on animal production systems, a balance with the role of anti-microbial use in crops, animal feed, and human health will need to be included.

Objectives

- Evaluation of terrestrial and aquatic animal production systems within the context of emerging zoonotic disease and AMR risk
- Understand how projected increases in livestock production in Africa and shifting production contexts in Asia over the 21st century will impact the future of farming systems and the risk of emerging zoonoses and AMR
- Identify common risk threads across regions, production contexts, and sectors that can inform applied risk mitigation approaches
    - Exploration of what is known about the quality and integrity of veterinary medicines - and their supply chains - used in animal production and their contribution to AMR risk.

[6] FAO. 2011. *Mapping supply and demand for animal-source foods to 2030,* T.P. Robinson & F. Pozzi. Animal Production and Health Working Paper. No. 2. Rome

- Review practical options for minimizing risks associated with increased animal production and marketing

Moderator

- **Dennis Carroll**, USAID

Panelists

- **Simplice Nouala**, African Union Interafrican Bureau of Animal Resources
- **Ugo Picaciamarra**, FAO
- **Peter Daszak**, EcoHealth Alliance
- **Dan Schar**, USAID

Note: All speakers to be confirmed

PARALLEL SESSION 1.1 (PS1.1)

Lessons Learned in Managing Emerging Infectious Diseases (EID)

Background

Several outbreaks since 2000 have shaped the way in which we prepare for and respond to infectious diseases outbreaks. The emergence of SARS CoV in the first years of this century was a wakeup call to the global health community followed by H5N1 avian influenza outbreaks and the first influenza pandemic in the 21st century. The renewed IHR (2005) marked a major change in the approach to global health security, going beyond specific diseases to apply to all health risks, irrespective of their origin or source.

Objectives

To present and discuss the management of a selection of recent crisis in different settings and draw lessons for the future. The session will tackle what works, what doesn't work from the political, public health, social and economic perspectives.

The following events will be discussed:

- **Ebola** : management of local and extended outbreaks: comparison of local outbreaks (DRC Uganda) and the epidemic in West Africa (2014-2015) with a particular emphasis on :
  - Community engagement and the socio-cultural aspects of outbreak response;
  - Cross-border collaboration between neighboring countries (surveillance, contact tracing, case management);
  - The role of international assistance;
  - Clinical management and vaccine.
- **MERS**: limiting spread example of Kingdome of Saudi Arabia, Republic of Korea and Thailand, managing the regional and global aspects of MERS-CoV, with a particular emphasis on:
  - Monitoring the health of international travelers and migrant workers;
  - Hospital preparedness
- **Zika and yellow fever** : managing vector borne outbreaks and emerging infectious diseases in Brazil / Angola (Yellow fever) and mitigating the risk of international spread (example of Portugal), with a particular emphasis on:
  - Controlling vectors and other environmental factors;
  - Vaccination and other preventive measures;
  - Effective communication to address public fear and potential panic.
- *Also **potentially discussed** : From SARS to influenza A(H7N9); lessons learned in China, with a particular emphasis on:*
  - *Addressing the human-animal interface and cross-sectoral collaboration;*
  - *Resolving conflicting interests between the commercial and public health sectors*
  - *Strengthening preparedness based on experience of past outbreaks*

Keywords: Ebola, Zika, MERS, Influenza, contact tracing, clinical management, migrations.

Moderator

- **Ron St John**, Public Health Agency of Canada

Panelists

- **Bruce Aylward**, WHO, Special Representative for Ebola Response – Ebola response
- **Adullah Assiri**, KSA MOH – MERS (country of origin)
- Director General, Department of Disease Control, Ministry of Health, Thailand
- **João Paulo Toledo**, Director, surveillance department, Ministry of Health, Brazil
- **Francisco George**, Portugal MOH – yellow fever: stockpiling and preventing importation and spread of infectious viruses

Note: All speakers to be confirmed

PARALLEL SESSION 1.2 (PS1.2)

Strategic Information and the Evolution of Emerging Infectious Diseases: Lessons from the Past and New Opportunities

Background

The last century has witnessed an increase in the frequency of emerging infectious diseases (EID) and antimicrobial resistance (AMR). Climate change, environmental pressure, population movement, population growth and increasing overlaps between human and animal livelihoods have contributed to an acceleration of novel infectious diseases. In addition, the increasing pace of human and animal pathogens resistant to antibiotic therapies raises serious concerns about treatable infections becoming life threatening, raising the death toll and the economic cost to potentially unsustainable level within decades.

In this context, early warning systems and strategic information play a key role in preventing, detecting and responding adequately to emerging zoonosis and antimicrobial resistance. More surveillance systems are needed. New technologies, electronic health records, internet and social media have the potential to provide timely information on emerging infectious diseases and antimicrobial resistance that can supplement traditional surveillance systems. With these new tools, individuals and their communities can play a new role in participatory syndromic surveillance. Nevertheless, there are important caveats that need to be addressed, such as ensuring data privacy, underrepresentation of some categories such as infants, the elderly, or people lacking access to these new technologies.

Objectives

This session will look at the recent changes in strategic information and how can they contribute to current surveillance systems in order to identify appropriate actions and interventions for preparedness and response to emerging infectious diseases and antimicrobial resistance.

Moderator

- TBD

Panelists

- Shweta Bansal, Department of Biology, Georgetown University, Washington, USA
- Laurel Sprague, Executive Director GNP+, The Hague, The Netherlands
- Marcel Salathé, Centre for Infectious Disease Dynamics, Penn State University, Pennsylvania, USA or Caroline Guerrisi Sorbonne University, INSERM
- Margaret D. Straton, Tufts University Initiative for Forecasting and Modelling of Infectious Diseases (InForMID), Medford, Massachusetts, USA or Sarah Del Valle, Los Alamos National Laboratory New Mexico, USA
- Osama Ahmed Hassan, Umea University, Sweden, Public Health Institute, Khartoum, Sudan
- Amy Wesolowski, Centre for Communicable Disease Dynamics, Harvard TH Chan School of Public Health

Note: All speakers to be confirmed

PARALLEL SESSION 1.3 (PS1.3)

Safeguarding Medicines in the Era of AMR: What Do We Know? What Works?

Background

The prevention, detection and mitigation of emerging and re-emerging infectious diseases involve both applying preventive controls in animal production as well as ensuring the safety, efficacy, quality, and appropriate use of vaccines, diagnostics and medicines through secure supply chains and health delivery systems.

Complex and fragmented supply chains, especially in countries and regions with limited regulatory and quality oversight, increase the likelihood of substandard, fraudulent or adulterated medicines entering the market. Poor quality medicines ensure microbial replication in the presence of drug pressure. Substandard and falsified medicines also contribute to lack of efficacy and adverse events, undermining trust in the health system. Inappropriate use of anti-microbials is another driver of AMR. Both poor quality medicines and inappropriate use are preventable and can be addressed through the development of robust regulatory and quality assurance systems, treatment guidelines and enforcement.

While there are major limitations in evidence and best practice in the human health sector, even less is known in the veterinary sector, both with respect to use and quality of antibiotics in animals, and effective controls. Further, environmental factors are beginning to come to light.

Objectives

- Review evidence of what is known about the links between medicines quality and AMR.
- Highlight successful efforts in, and benefits from, strengthening systems that monitor and strive to improve medicines quality.
- Address environmental impacts of antibiotic manufacturing on AMR.
- Relate frameworks for addressing medicines quality and appropriate use in the human sector to the animal sector and discern what lessons and approaches from other initiatives could be mobilized to address these drivers of infectious disease risk and AMR.

Moderator

- **Katherine Bond** – overview of issue/session and introduction

Panelists

- Panelist 1 – Overview of evidence linking medicines quality and use to AMR; directions for more attention and link to current response (Proposed: **Michael Deats**, WHO)
- Panelist 2 – Reflections on effective strategies, approaches and benefits to strengthen medicines quality monitoring and quality assurance systems (Proposed: **Margareth Ndomondo-Sigonda**, Tanzania)

- Panelist 3 – Reflections on veterinary sector; insights into how approaches on drug quality and use in human health sector could be applied in the veterinary health sector (Proposed: **Angkana Sommanustwichai**, London School of Hygiene and Tropical Medicine/IHPP Thailand
- Panelist 4 – **Sasi Jaroenpoj**, Head of Veterinary Medicinal Product, Department of Livestock Development, Ministry of Agriculture, Thailand
- Panelist 5 – Environmental impacts of antibiotic production: Proposed: **Dan Andersson**, Department of Biochemistry and Microbiology, Uppsala University, Sweden
- Panelist/Discussant – Broad overview and reflections on how medicines quality and practices contribute to ID and AMR risk from; experience in outbreaks; and links to current initiatives/broad perspectives (Proposed: **Margaret Hamburg**, National Academies of Medicine)

Note: All speakers to be confirmed

PARALLEL SESSION 1.4 (PS1.4)

Financing Pandemic Preparedness: Where is the Money?

Background

Recent experiences with the Ebola, Zika, and SARS outbreaks, among others, have underscored the need for countries to invest in pandemic preparedness, and to do so not only from a health perspective but also from an economic perspective: the socio-economic cost of outbreaks is often proportionally much larger than the corresponding impact on mortality and morbidity.

The International Working Group on Financing Preparedness (IWG) has recently made several recommendations to integrate pandemic preparedness into international macro-economic and market assessments that determine the availability of concessionary and other international financing eligible lower and middle income countries.

To date, however, what has largely been missing in global and country-level discussions is a systematic understanding about adequacy and modality of *current* financing arrangements for health security. Part of pandemic preparedness is embedded in health financing and service delivery. Part also deals with animal health which is the responsibility of livestock/agriculture sector. In addition to its multisectoral nature, there are contingency financing arrangements for pandemic preparedness that may or may not be linked to how countries manage other natural or man-made disasters. There is also risk that health security and pandemic preparedness may get lost in health financing transition that focuses more on financial protection and access to individual services than public goods.

Given the complexity of pandemic preparedness, better understanding of the current financing landscape would enable an informed dialogue on financing gaps and how best they could be filled given domestic and international fiscal constraints. The nature of health security implies that some of the objectives and functions that may be applicable to a generic health financing system would need to be amended to consider some of the unique characteristics of the specific sub-set of activities that constitute health security.

Objectives

The objective of this session is to discuss issues on financing health security within the broader context of trends in health and public financing more generally. Specifically, the session will:

- Provide an overview of how to conceptualize and estimate financing for health security, including preparedness, response and recovery;
- Present and discuss some preliminary findings on health security financing analysis from select countries, including a 10-year evaluation of OIE PVS Pathway and gap analysis to strengthen/finance veterinary services;
- Examine key domestic policies and interventions to ensure sustainable financing for pandemic preparedness and opportunities for mobilizing domestic and international financing for rapid response.

Moderator

- **Timothy Grant Evans**, Senior Director, Health, Nutrition and Population Global Practice. World Bank Group

Panelists

- **Netsanet Workie**, Senior Health Economist, World Bank Group. *Experiences from Health Security Financing Assessment Tool (HSFAT)*
- **Ronella Abila**, OIE sub-regional representative Southeast Asia. *10 years of experience with OIE PVS Pathway*
- **Eduardo Banzon**, Principal Health Specialist, Asian Development Bank. *Financing Health Security in the Mekong Region*
- **Tran Dac Phu**, General Director, General Department of Preventive Medicine, Vietnam. *Country Experience*
- **Julian Naidoo**, Chief of Party, Wits Health Consortium, South Africa. *Country Experience*
- **Benjamin Rolfe**, CEO, Asia Pacific Leaders Malaria Alliance. *Civil Society perspective*

Note: All speakers to be confirmed

PARALLEL SESSION 1.5 (PS1.5)

One Health on the Move: Nomadic Communities

Background

Fully dependent on their animals for their livelihood and income, pastoralists employ mobility as a key strategy to ensure the availability of pasture and water for their herds, thus increasing their resilience. While their movement allows them to overcome the vagaries of nature prevalent in the harsh environments they inhabit, their remoteness and often trans-boundary livelihoods have made it challenging to access services and engage in decision-making. Pastoralist are at the forefront of the human, livestock and wildlife interface. They are especially vulnerable to zoonotic diseases, because they live in close contact with their animals and often consume raw milk and meat. Furthermore changing environmental conditions also affect the availability of pasture for their animals, and in-turn affect their nutrition status.

The animal-human-environment sectors are interconnected and associated with the emergence of infectious diseases as Middle East Respiratory Syndrome (MERS). Multisectoral approaches such as One Health can help address the challenges at this interface by providing adapted vaccinations campaigns and veterinary services to pastoralists.

Objectives

- To foster a deeper understanding of the health risks faced by mobile pastoral communities, and the challenges they encounter in accessing animal and human healthcare
- To share examples of interventions and policies that tackle pastoralists' health issues at the animal-human-environment interface
- To promote the participation of pastoral communities in health policy decisions and sanitation campaigns

Moderator

- **Gregorio Velasco Gil**, Food and Agricultural Organization of the United Nations

Panelists

- **Asiimwe Benon**, Associate Professor. Makerere University
- **Maty Ba Diao**, Regional Coordinator of the Support Pastoralism in Sahelian Countries project- CILSS.
- **Marite Alvarez**, Pastoral representative. Argentina. Pastoamericas.
- **Taghi Farvar**, Pastoral representative. Iran. Cenesta.

Note: All speakers to be confirmed

PARALLEL SESSION 2.1 (PS2.1)

Beyond MERS and Zika: Are we Prepared for the Next Big Epidemic?

Background

Over the past decade, Ebola, MERS, highly pathogenic avian influenza and, more recently, the Zika virus outbreaks have demonstrated the ability of epidemics to devastate communities through both extraordinary losses of life and severe morbidity as well as adverse social and economic impacts that jeopardize global health security. These recent disease outbreaks have not only made evident countries' lack of preparedness to adequately prevent, detect and respond to epidemics, but also the extent to which measures must cut across governance levels and all sectors of society in order to truly be effective. Furthermore, only one third of countries have met their commitments under the International Health Regulations (IHR). And although several tools and frameworks have been developed (by WHO, USAID, CDC, OIE, etc.) to provide guidance for countries to develop country epidemic preparedness and response plans, these are generally disease specific, have not been updated or tested through routine exercises, remain largely underfunded and are, therefore, not fully operational. As a result, many countries remain unprepared to prevent, detect, mitigate risks and respond to health threats and disease epidemics before they cause devastating consequences in the livelihoods of communities and the economies of countries.

Objectives

- To present country experiences on strengthening IHR core capacities, including efforts for effective coordination, partnership models and financing mechanisms to strengthen health security.
- To identify critical elements needed for sustainable, inclusive, and effective preparedness at country level and propose solutions for more effective epidemic preparedness guidance.
- To discuss gaps in the current guidance and frameworks that need to be filled to develop country epidemic preparedness and response plans.

Moderator

- **John Nkengasong**, Director, Africa CDC

Panelists

- **Isabella Ayagah**, IHR Focal Point, Ministry of Health, Kenya. *Strengthening Pandemic Preparedness across Sectors in Kenya: Lessons Learned & the Way Forward*
- **Ronello Abila**, OIE sub-regional representative Southeast Asia. *Lessons Learned from 10yrs of Implementing the OIE PVS Pathway*
- **Tran Dac Phu**, General Director, General Department of Preventive Medicine, Ministry of Health, Vietnam
- **Casey Barton Behravesh**, Director, One Health Office, U.S. CDC

Note: All speakers to be confirmed

PARALLEL SESSION 2.2 (PS2.2)

AMR: Addressing Excessive and Inappropriate Use of Antibiotics

Background

The tripartite, Food and Agricultural Organization, World Health Organization and World Organization for Animal Health and other relevant organizations had declared Antimicrobial resistance (AMR) a serious and growing global public health threat. The loss of effective antibiotics is reducing an ability to protect people from infectious diseases, with profound impacts on healthcare systems, global trade, agriculture, environment and health sectors. Based on World Bank Group projections of the world economy in 2017-2050, if AMR problems continue at the current pace, the annual global GDP would fall by 1.1-3.8% by 2050 and the global healthcare cost would range from US$ 300 billion to more than US$ 1 trillion.

Though AMR is a natural mechanism of pathogen survival; the excessive and inappropriate use of antibiotics are key drivers of the emergence of antimicrobial resistance. Decision to prescribe antibiotics by health professionals still occurs in the absence of adequate information about the nature of the infection or before the results of diagnostic and sensitivity tests become available. Moreover, the regulation of antimicrobial use is poorly enforced in some areas, such as over-the-counter, unregulated use of antibiotic in agriculture, substandard medicines for both human and animal antibiotics.

Several attempts to optimize use of antibiotics in human and animal sectors have shown in the last decade at global, regional and national levels. To fulfill key action proposed by the Global Action Plan, countries need to strengthen the evidence base through surveillances of AMR and the consumption of antimicrobials, and strengthen regulation of the distribution and use of antibiotics in human and animals. The information on AMR and antibiotic consumption will guide the treatment of patients and inform local and national actions. Thus, antibiotic, as a global public good requires regulation on distribution and use.

It is imperative that PMAC audiences recognize the drivers contributing to excessive and inappropriate use of antibiotics; but more importantly, learn and share practical and successful solutions.

Objectives

The panelists in this session will address the following questions

On problem streams

1. Why there are excessive and inappropriate use of antibiotics in humans, animals and crops (i.e. in citrus for treatment of greening disease), such as self-medication of antibiotic from over-the-counter purchases, inefficiently regulated the use of antibiotic. Stakeholder analysis are helpful to unpack the complexity. Key actors involved in the use of antibiotics:
   a) Demand for antibiotics: patients and farmers,
   b) Supply of antibiotics: pharmaceutical industry, professionals: veterinarians, physicians and pharmacists,

On solution streams

2. What are the good practices and lessons for countries or regional organization such as ECDC and networks such as ESAC and ESVAC, to develop and maintain an effective system for surveillance of AMR, antimicrobial consumption and Point prevalence survey in human, and animal?
3. How evidences of surveillance of antimicrobial consumption are used:
    a. To guide antibiotic prescribing decisions of health professionals
    b. To formulate, support and monitor policies which curb down antimicrobial consumption and promote rational use of antibiotics
4. What are the challenges of use of antibiotics in crops? Is there any monitoring system on impacts of antibiotic use in crops, such as antibiotic resistance in food crops and environment, and antibiotic residue in environment and food crops?
5. How does the regulatory system support the control of antibiotic use?

On recommendations

6. What are the policy interventions on "demand" and "supply" sides, which address the excessive and inappropriate use of antibiotics in developing countries?

Moderator

- **Klara Tisocki**, WHO SEARO

Panelists

- **Otto Cars**, Senior Professor, Founder and senior adviser, ReAct-Action on Antibiotic Resistance, Uppsala University, Sweden
- **Jonathan Rushton**, Professor of Animal Health and Food Systems Economics Epidemiology and Population Health, University of Liverpool
- **Lilit Ghazaryan**, Scientific Center of Drug and Medical Technology Expertise, MoH, Armenia
- **Angkana Sommanustweechai**, Doctoral student at LSHTM on AMR, IHPP Thailand

Note: All speakers to be confirmed

PARALLEL SESSION 2.3 (PS2.3)

Dealing with an Inter-Connected World: Partnerships for Preparedness, Detection and Response during Mass Gatherings

Background

Mass gatherings are recognised to have the potential to enhance spread of infectious diseases as well as being potential targets for deliberate events. Although both these risks are unlikely, the rise of Zika infection in the run up to the Rio 2016 Olympic and Paralympic Games and Middle East Respiratory Syndrome (MERS) in Saudi Arabia highlighted how these events can create a perceived, if not actual, global health threat and a political as well as health challenge.

The inspiration of this session derives from the next three Olympiads (Winter 2018, Summer 2020 and Winter 2022) being in the western pacific region (S Korea, Japan and China respectively). This session will be based on previous sporting mass gatherings such as the Rio Olympics, the London Olympics, and the World Cup, religious gatherings such as the Hajj, and large state events such as the King's funeral in Thailand. The session aims to share learning and best practices from a biosecurity and terrorism perspective and to explore how such mass gathering events can best be planned to minimise any health risks. Many mass gatherings, especially international sporting events, are organised by what are effectively private sector companies and the relationship between the private and public sector partners is vitally important.

Objectives

- To share learning and experience from previous events
- To explore effective risk mitigation strategies
- To examine the health and political interface of mass gatherings, including private sector partners
- To explore how mass gatherings can be used to improve global health security capacity

Moderator

- **Brian McCloskey**, Senior Consulting Fellow, Chatham House; Consultant in Global Health Security, Public Health England; & Professor, Faculty Epidemiology and Population Health, London School of Hygiene and Tropical Medicine

Panelists

- **Tina Endericks**, Director, WHO Collaborating Centre on Mass Gatherings and Global Health Security, Public Health England, London
- **Maurizio Barbeschi**, Mass Gathering Unit, WHO, Geneva
- **Lucille Bloomberg**, National Institute Infectious Diseases, South Africa
- **Badriah Alotaibi**, Global Centre for Mass Gathering Medicine, Riyadh, Saudi Arabia
- Speaker (to be identified) from Thailand Ministry of Health
- **Koji Wada**, National Centre for Global Medicine, Tokyo

Note: All speakers to be confirmed

PARALLEL SESSION 2.4 (PS2.4)

Changing Dynamics: Emerging Infectious Diseases and Antimicrobial Resistance in an Era of Expanding Global Human Population Growth and Movement

Background

The global human population is projected to peak at over 11 billion this century. Accelerated human population growth and corresponding changes in demography, along with associated food and companion animal population increases, are altering disease dynamics and will continue to drive emerging infections and transmission over the course of the next century. This session will explore the connections among infectious disease emergence, antimicrobial resistance (AMR), and changing human and animal population dynamics. We will explore the state-of-the-art in emerging disease and AMR detection and forecasting and answer the question, "How can we minimize emerging disease and AMR risks linked to changing demography."

Objectives

This session aims to explore and address the impacts of growing human and animal populations and unplanned mega-cities and peri-urban settlements on disease emergence, amplification, and global distribution. Accordingly, presenters will also tackle the risks associated with surging global trade and travel and illustrate how forecasting can inform risk mitigation.

Specific Objectives:

- Explore projected demographic trends over the 21st century and their impact on expected zoonotic disease emergence and AMR
- Enhance understanding of how trends in demography will differ regionally; how differences in agricultural productivity and marketing practices will impact emerging disease risk, including spread of AMR; and how purchasing power and animal protein demand will have global supply chain impacts and associated emerging disease risk
- Highlight practical, evidence-driven approaches to defining, forecasting, and mitigating human demographic-driven emerging disease risk

Moderator

- **Jonna A.K. Mazet**, University of California, Davis

Speakers

- **Martin (Marty) Cetron**, Division of Global Migration & Quarantine, US CDC
- **Saber Yezil**, WHO/MoH, Saudi Arabia
- **Thuy Bich Hoang**, Viet Nam, Wildlife Conservation Society
- **Christine Kreuder Johnson**, University of California, USA Davis/Nepal context
- **Evelyn Wesangula**, Global Antibiotic Resistance Partnership-Kenya
- **Kamran Khan**, Associate Professor, Department of Medicine, Division of Infectious Diseases, University of Toronto, Canada
- **Olaniran Alabi**, Nigeria Chief Veterinary Officer

Note: All speakers to be confirmed

PARALLEL SESSION 2.5 (PS2.5)

Reducing the Gap: Addressing Neglected Disease; Neglected Populations

Background

Preventable, endemic diseases are rarely prioritized for surveillance as they do not pose a risk of epidemic or pandemic outbreak. This is a failing on two levels: (1) the presence of preventable diseases acts an indicator of the overall state of the health system; and (2) the knowledge of 'usual' allows for detection of the unusual. Strengthening surveillance and other systems for endemic diseases, infectious or otherwise, provides necessary infrastructure to combat the existing and target the emerging. In addition, most of these subsisting populations live in close proximity with their animals and experience a double burden, disease in their animals and disease in their families and communities. A pro-poor initiative on a massive scale, control of NTDs has much to offer in terms of what can be adapted, innovated and built in low-resource settings most burdened by NTDs in an agenda that makes poverty alleviation its overarching objective and aims to leave no one behind.

The success celebrated for some of the NTDs shows that it is possible to build private-public partnerships that lead to concrete results, such as the Global Partners' Meeting on NTDs based on the theme "Collaborate. Accelerate. Eliminate". This encapsulates an exemplary informal collaboration that marks a 'turning point' in global efforts to control and eliminate poverty-related diseases.

The discussion will center on forging cross-sectoral partnerships to tackle NTDs and "diseases of poverty", and will include a range of elements crucial to an effective collaboration across sectors such as financing, research and development, production and delivery of vaccinations and treatment, disease surveillance, role of local communities and other actors on the field. It will elucidate the incentives of building effective cross-sectoral and public-private partnerships by using the case of NTDs. Lessons may be derived from the NTD experience to other areas requiring cross-sectoral partnerships in health where a population-based intervention is appropriate.

Objectives

Marginalized and neglected populations bear the epidemic risk of infectious diseases especially neglected tropical diseases. They are more exposed to disease vectors as well as have less access to effective and timely health care. Without addressing prevention, detection and response among this segment of the population, the world cannot be safe from infectious disease. This session aims to discuss successful examples of cross-sectoral partnerships across human and animal health sectors to tackle "diseases of poverty" including financing, vaccine development, and distribution as well as delivery. It will also address how to target this neglected segment of the population against the threat of infectious diseases. Intervention based approaches through specific diseases can be discussed as well as tackling access and inclusion into the health system through a social determinants approach. Tackling NTDs is addressing the causes of poverty and the pathways to reach the poorest and most vulnerable in society those that will have slower access to universal health coverage and would be a pathway to strengthen health systems, human, animal and environmental.

Moderator

- Dan Normandeau (TBC)

Panelists

- Mark Bradley, Director Global De-worming , Global Health Programs, GSK
  Or, Klaus Brill, Vice President Corporate Commercial Relations, Bayer Pharmaceuticals
  Or, Alasdair King, Director, Intergovernmental Veterinary Health Merck Animal Health
- Dr Nwankwo Uzoma, Senior Medical Officer and Health Economist, Ministry of Health, Nigeria
- Dr Amila Gunesekera, MD, Medical Officer in charge Rabies treatment National Hospital of Sri Lanka
- Harena Rasamoelina, Veterinary epidemiologist, Indian Ocean Commission
- Representative from local NGO involved in distribution and delivery of vaccines/treatment (TBC)
- Representative from WHO or UN system (TBC)
- Representative from CEPI co-founders or Board (TBC)

Note: All speakers to be confirmed

PARALLEL SESSION 3.1 (PS3.1)

To be updated

Note: All speakers to be confirmed

PARALLEL SESSION 3.2 (PS3.2)

Lessons Learned from a One Health Approach to AMR

Background

Antimicrobial resistance (AMR) is a major threat to global health, the world economy, food safety and food security, and therefore poses a unique challenge to humanity. All countries – regardless of their economic situation, the strength of their health systems or their level of antibiotic consumption – will face disastrous consequences if the spread of AMR is not contained. Global and community solutions are needed to prevent overuse of antibiotics, including development of new vaccines, improved diagnostic tests and, above all, universal access to antibiotics which are affordable and effective against drug-resistant diseases. Antimicrobials also play a significant role in both plant and animal health, and therefore, in global food production. While the important goal of reducing antibiotic usage for growth promotion in animals is increasingly implemented, antibiotics will be needed in maintaining the health of food-producing animals, and the safety of their products.

AMR occurs when disease-causing pathogens (including bacteria, fungi, parasites, or viruses) develop defense mechanisms against the drugs designed to treat them, making these resistant pathogens difficult or even impossible to treat. This resistance is the inevitable result of antimicrobial use and an example of natural selection in practice. The more antimicrobials are used, the less effective they become. Rising levels of AMR are a sign that natural selection is taking place more rapidly than innovation in developing new antimicrobials. If this process is to be reversed, the world must innovate more, but also slow natural selection – by eliminating excess use of all antimicrobials; only using second- and third-level treatments when absolutely necessary; and ensuring appropriate access to treatments.

The importance for countries to develop and implement one health focused national action plans

In line with the Global Action Plan on Antimicrobial Resistance, developed by WHO with participation and endorsement by the OIE and FAO, the development of countries' own National Action Plans (NAPs) on AMR is an essential first step towards establishment of an effective response to combat AMR. At the Sixty-eighth WHA in 2015, Member States committed to have NAPs in place by May 2017. Also in 2015, the OIE World Assembly of Delegates adopted Resolution No 26, committing to development of NAPs in the spirit of "One Health", taking into account the use of antimicrobial in animals and ensuring collaboration with public health officials. In February 2016, WHO, in collaboration with FAO and OIE, developed a manual for developing NAPs on AMR and a set of accompanying tools. The three organizations have been working closely with stakeholders to provide technical support to countries for the effective development of their NAPs.

Sharing Expertise for a Coordinated AMR Response

Ensuring political commitment, engagement and support has been a challenge as understanding of AMR, multisectoral collaboration and the importance of developing and implementing NAPs is still somewhat limited. The identification of best practices in human, animal and plant health continues to play an important role as the world is still learning what works best in particular contexts. WHO is sharing expertise regarding human health and developing communities of practice to support countries with ongoing efforts. Inter-sectoral action, and the complexity of coordination within and across sectors, continues to be a challenge, particularly as countries shift towards NAP implementation.

Global Action Plan for Antimicrobial Resistance

At the Sixty-Eighth World Health Assembly in May 2015, WHO Member States endorsed a global action plan through resolution WHA68.7 to tackle antimicrobial resistance, including antibiotic resistance, the most urgent drug resistance trend.
The AMR global action plan contains five major strategic objectives:

1. to improve awareness and understanding of antimicrobial resistance;
2. to strengthen knowledge through surveillance and research;
3. to reduce the incidence of infection;
4. to optimize the use of antimicrobial agents; and
5. to develop the economic case for sustainable investment that takes account of the needs of all countries, and increase investment in new medicines, diagnostic tools, vaccines and other interventions.

The global action plan, which takes into account the commitment, perspectives and roles of all relevant stakeholders is a plan in which everyone has clear and shared ownership and responsibilities. The endorsement of the plan reflects a global consensus that AMR poses a profound threat to human health.

One Health Approach
Addressing the rising threat of AMR requires a holistic and multisectoral ("One Health") approach because antimicrobials used to treat various infectious diseases in animals may be the same as or similar to those used in humans. Resistant bacteria arising in humans, animals, plants or the environment may spread from one to the other, and from one country to another. One Health recognizes that the health of humans, animals and ecosystems are interconnected. It involves applying a coordinated, collaborative, multidisciplinary and cross-sectoral approach.

The WHO, FAO and OIE speak with one voice and take collective action to minimize the emergence and spread of AMR. The aim is to:

- Ensure that antimicrobial agents continue to be effective and useful to cure diseases in humans and animals;
- Promote prudent and responsible use of antimicrobial agents;
- Ensure global access to medicines of good quality.

Objectives

- To gain a better understanding of how the world can learn from the past 2.5 years of AMR response since the Global Action Plan as we shift from development of AMR strategies towards implementation
- To identify main challenges and successes in implementing national action plans and determine ways to productively more forward

Moderator

- **Martha Gyansa-Lutterodt**, Chief Pharmacist of Ghana, IACG Member

Panelists

- WHO
  - **Marc Sprenger**, Director of AMR Secretariat, WHO
- FAO
  - **Juan Lubroth**, Chief Veterinary Officer, FAO
- OIE
  - **Matthew Stone**, Deputy Director General, OIE
- Professional association – health

  - **Judith Shamian,** President, International Council of Nurses
- Professional association – agriculture
  - **Marco Marzano de Marnis**, Secretary General, World Farmers Association

Note: All speakers to be confirmed

PARALLEL SESSION 3.3 (PS3.3)

Climate Change and Emerging Diseases: The Importance of Resilient Societies

Background

During the long processes of human cultural evolution, population dispersal, and subsequent inter-population contact and conflict, several distinct transitions in human ecology and inter-population interactions have changed profoundly the patterns of infectious disease in human populations. As we move further into the 21st century, the spread and increased lability of infectious diseases, new and old, reflects the impacts of demographic, environmental, technological and other rapid changes in human ecology. Climate change, one of the global environmental changes under way, is anticipated to have a wide range of increased impacts upon the occurrence of infectious diseases affecting human, animal, and plant populations.

Climate and weather patterns affect the distribution and risk of many infectious diseases, including vector-borne diseases such as malaria, Rift Valley fever, plague, encephalitis and dengue fever. Weather patterns also affect the distribution of food- and water-borne diseases and emerging infectious diseases such as West Nile virus, Hantavirus, and Ebola hemorrhagic fever and the sporulation of diseases such as anthrax and other clostridia.

The effect of climate variability on infectious diseases is determined largely by the unique transmission cycle of each pathogen. Transmission cycles that require a vector or non-human host are more susceptible to external environmental influences than those diseases which include only the pathogen and human. Important environmental factors include temperature, altitude, precipitation and humidity. Several possible transmission components include pathogen nature (viral, bacterial, etc.), vector (mosquito, snail, etc.), abiotic physical vehicle (water, soil, etc.), non-human reservoir (mice, deer, etc.), and human host.

Humans are more than passive recipients of climate change-induced health effects. We can play a significant and active role through proactive adaptation and mitigation measures in order to control and alleviate the negative health impacts of climate change. The magnitude of changes in climate variables varies across the globe, posing more challenges and stresses for some groups, societies and populations than others. Given the same magnitude of climate change, some population groups and areas are more vulnerable to the elevated risks due to their lack of the ability and resources to effectively respond to the stresses and challenges, including nutrition, immune status, and access to goods, services, and clean water. Inadequate public policies may be perpetuating the marginalization that increases vulnerability to adverse events or change processes. Given that infectious diseases do not confine themselves within a vulnerable population group, these diseases pose a shared global risk and require a coordinated global effort to reduce their vulnerability to climate change-induced health risks. Importantly, human vulnerability to the changing risks for infectious diseases driven by climate change may be altered through proper adaptation measures. Examples include the continuous evolution of public health programmes, the cyclical re-allocation of financial and health care resources and the pre-emptive alteration of policies following scientific projection of spatial–temporal changes in health risk for human infectious diseases. Early warning systems based on such projections have been proven effective in helping societies take proactive measures to prevent or alleviate the possible health impacts.

Objectives

- Explore projected trends in climate change over the 21st century, and their expected impact on infectious disease emergence/re-emergence and AMR
- Highlight practical, evidence-driven policy and approaches to defining and mitigating human-driven emerging disease risk

Moderator

- **Pradeep Kurukulasuriya**, GEF/GCF, UNDP Bangkok

Panelists

- **Sander Koenraadt**, Wageningen University, Netherlands. Climate change and vector-borne diseases; climate change effects on highland malaria, arboviruses.
- Two panelists from government /NGO partners involved in GEF projects on Strengthening national capacities for health and climate change adaptation. Selected speakers to represent case studies from Nepal **Meghnath Dhimal** (Consultant on leave from MOH) and Bangladesh **Iqbal Kabir** (MOH)
- **Montira J. Pongsiri** PhD, MPH, Senior Research Associate, Planetary Health Science Policy, Cornell University, College of Veterinary Medicine, Dept. of Population Medicine and Diagnostic Sciences
- **Kristie Ebi**, Professor, visiting at Department of Public Health and Clinical Medicine Occupational Medicine, Umea University.

Note: All speakers to be confirmed

PARALLEL SESSION 3.4 (PS3.4)

To be updated

Note: All speakers to be confirmed

PARALLEL SESSION 3.5 (PS3.5)

Policy Coherence: Effective Partnerships for Global Health

Background

The 2030 Agenda for Sustainable Development set ambitious health-related targets to "ensure healthy lives and promote well-being for all at all ages" and "strengthen the means of implementation and revitalise the Global Partnerships for Sustainable Development". To this end, for example, the epidemics of AIDS, tuberculosis, malaria and neglected tropical diseases, as well as effectively addressing the threat of emerging infectious zoonotic diseases will require substantial policy coherence and investments. These are critical for the needed health innovations, as well as the development of systems-wide capacities within countries for the necessary measures of "prevention, detection and response".

While many global efforts have focused on increasing research and development for new health innovations, it is also now clear that there must be a corresponding emphasis on strengthening systems and capacities to deliver the range of needed health services and products. The Ebola outbreak in West Africa was an important reminder of the importance of effective, and continuing, core government functions, within and beyond the health sector. As the global community contemplates responses to address epidemics and infectious diseases, the imperatives for ensuring an integrated approach are clear: effective partnerships are required between the public, private and the community sectors.

This signals a clear need for increased policy coherence, which demands coordination between a broad range of actors; not just between government agencies, private sector and community actors at the national and local levels, but also between those working at the global level, including on innovation, R&D, financing, governance and management. Addressing interconnected elements, and encouraging effective synergies of efforts of stakeholders in the public, private and community sectors, will be critical, not only in effectively addressing infectious and new emerging diseases, but also in helping low- and middle-income countries (LMICs) achieve universal health coverage (UHC) and other health-related targets.

Objectives

In this context, the session aims to stimulate a dialogue between key stakeholders with the aim of identifying how public-private-community partnerships (PPCs) can address the needs of LMICs for effective "prevention, detection and response" to the threat of infectious diseases. The aim is to generate recommendations and proposals that can promote effective policy coherence and public-private-community partnerships at all levels. It is proposed that the discussions focus on three key, inter-related elements, as follows:

Policy coherence

- How can cross sectoral, multidisciplinary approaches at the national, regional and global levels be effected and prioritised?
- Which are key factors in facilitating policy, operational delivery environment and effectiveness for such approaches?
- What are relevant experiences and lessons learnt from existing projects and initiatives?
- What are the means to promote adoption of evidenced-based best practices and transferable lessons learned for policy coherence, including South-South approaches and strategies?

Effective partnerships

- What can we learn from existing PPC partnerships in terms of their contribution to the prevention, detection and response to infectious diseases?
- Are there experiences outside the health arena that are transferable?
- How can such partnerships be further strengthened?
- What are the right incentives for collaboration at different levels?
- What are the key considerations for ensuring the sustainability of PPC partnerships?

Evaluation and measuring success

- How can evaluation of PPC partnerships be undertaken?
- How do we measure success; e.g., what should be the matrix of success and effectiveness?
- Can there be evidence-based assessments of investments in innovation and R&D? And their eventual delivery in countries, including best practice, data and knowledge sharing?

Moderator

- **Tenu Avafia**, Team Leader, HIV, Health and Development Team, UNDP

Speakers

- **Mandeep Dhaliwal**, Director of HIV, Health and Development Team, UNDP
- **Hayato Urabe**, Director of Investment Strategy & Management, Global Health Innovative Technology (GHIT) Fund
- **Chalermsak Kittitrakul**, AIDS Access Thailand

Panelists

- **Yodi Mahendradhata**, Director, Center for Health Policy and Management, Universitas Gadjah Mada, Indonesia
- **Mwele Ntuli Malecela**, Director, WHO Regional Office for Africa
- **Richard Kock**, Professor of Wildlife Health and Emerging Diseases at the Royal Veterinary College, University of London, UK
- **Osman Dar**, Project Director, One Health Project, Centre on Global Health Security, London

Note: All speakers to be confirmed

PARALLEL SESSION 4.1 (PS4.1)

Moving Forward and Outward: Progress in Implementation of Global Frameworks and Initiatives

Background

Historically, international organizations, academia and others have provided regulations, standards or guidance to the global community (e.g., International Health Regulations, OIE Terrestrial Animal Health Code, and Codex Alimentarius). However, the challenge at all levels (i.e., globally, regionally, nationally and locally) has been in the actual implementation of these regulations, standards or guidance with the available resources and existing infrastructures. In response to requests from national authorities and as a result of breakdowns or delays in global, regional, national and local responses to emergent diseases, the global community has moved forward to develop frameworks and advance initiatives that further support national and local authorities in their efforts to prevent, detect and respond to human, animal and environmental health concerns. Critical to the utility and effectiveness of these frameworks and initiatives is the ability to build synergy among multiple stakeholder efforts and to address the needs of individual countries and communities.

Objectives

- To present a selection of global frameworks and initiatives, discuss the challenges and successes in their implementation and draw lessons to build sustainable, inclusive and effective preparedness and response systems.
- To discuss how these different global frameworks may (or may not) build upon each other or provide opportunities for synergies in supporting national and local capacity building efforts.

Moderator

- **Julie R. Sinclair**, CDC One Health Liaison to the OIE
- **Ronello C. Abila**, OIE SubRegional Representative for Southeast Asia

Panelists

- Development and implementation of the WHO's Joint External Evaluation (JEE) and role in implementation of the International Health Regulations and building national capacity (Mozambique as case study) – **Ali Ahmed Yahaya**, WHO
- OIE Performance of Veterinary Services (PVS) Missions and future course – **John Stratton**, OIE
- WHO Research and Development Blueprint – **Young-Mee YEE**, member of Advisory Group National of Health, Korea Centers for Disease Control and Prevention
- Global Rabies Initiative business plan – **Bernadette Abela-Ridder**, WHO

Note: All speakers to be confirmed

PARALLEL SESSION 4.2 (PS4.2)

Multi-sectoral Partnerships for Action on AMR

Background

Antimicrobial Resistance (AMR) respects no borders and has become an increasing threat to all countries - developed and developing alike. Common infections become untreatable, devastating infectious diseases become much more difficult to contain and standard medical procedures become a challenge. Thus, AMR has a major negative impact on growth and global economic stability. Given the breadth of impact from AMR, the only effective means to address AMR sustainably is through multisectoral action and partnership; however, challenges have been identified as to how stakeholders from different sectors can meaningfully come together to produce action and change. Innovative new approaches are needed to truly harness the potential of all people and perspectives, particularly those most vulnerable.

The UN Sustainable Development Goals (SDGs) recognize the importance of AMR (paragraph 26 of the Declaration). The attainment of many of them will depend on the availability of and access to affordable and effective antimicrobial medicines and other technologies such as diagnostic tests. AMR seriously threatens the health and lives of vulnerable populations, such as newborns, children, and women, as well as sustainable food and agriculture production and a healthy environment. AMR is reducing our ability to protect the health of animals and therefore is threatening safe and sustainable food and agriculture.

In a tripartite approach, WHO, the Food and Agriculture Organization (FAO) and the World Organization for Animal Health (OIE) recognize that addressing health risks at the human–animal-plant-ecosystems interfaces requires strong partnerships among entities that may have different perspectives and much work is currently ongoing.

On 21 September 2016, the President of the UN General Assembly convened a one-day high-level meeting at the UN Headquarters on AMR with the participation of Member States, non-governmental organizations, representatives of civil society, the private sector and academic institutions. The primary objective of the meeting was to summon and maintain strong national, regional and international political commitment in addressing AMR and the meeting emphasized the important role and responsibilities of governments, as well as the roles of non-State actors, the private sector and relevant inter-governmental organizations, particularly the WHO, FAO and OIE in establishing, implementing and sustaining a cooperative global, multi-sectoral and cross-sectoral approach.

Objectives

- How can the world come together to meaningfully and effectively address AMR in a sustainable way and in particular, engage non-traditional partners?
- Multisectoral partnerships have been identified as essential for addressing AMR – how can the world now move from planning to action at both the international and local levels?
- How does addressing AMR contribute to the attainment of the SDG's? How to effectively engage all relevant sectors: environment, food, employment, poverty reduction, agriculture, development partners, academia, private sector, etc.?
- How can the voice of all people be heard, particularly those marginalized and most vulnerable?
- What are the issues and opportunities around ensuring linkage between global and community/country-level partnerships? How can partnerships focus on possibilities for

meaningful collaboration, action on the ground and specific problems affecting communities rather than focusing only on the broader policy levels?

- What are some good practices and lessons learned from past multisectoral collaborations that could be applied to collaborations on AMR?

Moderator

- **Matthew Stone**, Deputy Director General, OIE

Panelists

- Civil society representative
  Arturo Quizhpe Peralta, Head, ReAct Latin America and Dean of the Faculty of Medical Science at University of Cuenca, Ecuador
  Stefano Nobile, Focal Point for Health, Caritas International, Vatican City
- Stakeholder perspective
  Maria Lettini, Director, FAIRR
- Country representative
  Ana Marie Garfin, National TB Control Program Manager, Department of Health, Phillippines
- WHO
  Marc Sprenger, Director of AMR Secretariat, WHO
- Representative from the interagency coordination group
  Jaana Husu-Kallio, Member of IACG, Permanent Secretary, Ministry of Agriculture and Forestry, Finland

Note: All speakers to be confirmed

PARALLEL SESSION 4.3 (PS4.3)

Community Systems: the Bedrock of Responses to EID and AMR

Background

Community preparedness and response to emerging infectious diseases (EID) and antimicrobial Resistance (AMR) is critical to the health outcomes of individuals. In HIV, people both living with and affected by HIV have been at the forefront of providing treatment preparedness to promote health-seeking behavior, improve adherence and other health outcomes, whilst advocating for increased availability, accessibility and uptake of key viral load diagnostics as well as 2nd and 3rd line antiretroviral therapy. In Malaria, civil societies work with other stakeholders to address artemisinin resistance in Southeast Asia via educating communities about the hazards of substandard drugs and organizing public awareness campaigns to complete a 3-day treatment course and on measures to prevent further spread of resistant pathogen strains. Similarly in tuberculosis, community-based outpatient treatment of MDR-TB in resource poor settings yield higher cure rates and facilitated better referrals to other health services required by TB affected communities. Furthermore, lessons learned from the early response to Ebola in West Africa have recognised the problem of sidelining community engagement as a key factor contributing to failure of the early emergency health programs to meet the needs and realities confronting affected populations in the region.

Today, prevention, detection and response to EID relies significantly on an effective surveillance system which starts at the community level with effective mechanisms in place to ensure linkage into national level health systems reporting. The Ebola crisis highlights the importance of integrated community case management (iCCM) and the roles of the network of community health workers and community leaders in early and better case reporting, contact tracing and bringing people into care, whilst reducing stigma and discrimination associated with the virus. Community-based control and preventive behaviours for vector control is recognized as a key pillar in disease response and preparedness for Zika and other mosquito-borne diseases. The use of innovative technologies in the response to EID by communities and community health workers contributed to the prompt control of the outbreak by providing a valuable platform for early warning and guiding early actions.

Objectives

The session aims to explore community roles in preparedness and response to EID and AMR, concentrating on lessons and approaches deployed in disease-specific programs, such as HIV, TB, Malaria, Ebola and Zika, whilst underscoring the importance of focusing on people, i.e. ensuring that systems for health involve the affected community and promotes community action as part of the overall health system critical for identifying, reporting and responding to emergency health threats.

The session is designed to generate discussions on commonalties and contexts of community action, and to reflect on emerging challenges that still persist in response to EID and AMR from the community perspectives, as well as to identify practical solutions drawing the lessons learned from community responses to the epidemics of HIV, TB, Malaria and to the most recent outbreaks of Ebola and Zika across the globe.

Moderator

- **RD Marte**, Asia Pacific Coalition of AIDS Service Organizations or Alessandra Nilo of GESTOS

Panelists

- **Othman Mellouk**, International Treatment Preparedness Coalition, HIV treatment advocate and educator, Morocco
- **Lina Kharn**, ARC Cambodia, Malaria Consortia, Cambodia
- **Anton Basenko**, Eastern Europe and Central Asia Network of People who Inject Drugs (ENPUD), Ukraine
- **Bhargavi Rao**, MSF-Holland, U.K
- **Alessandra Nilo**, GESTOS, Brazil
- **Abdulai Sesay**, Civil Society Movement Against Tuberculosis, Sierra Leone
- **Kannikar Kijtiwatchakul**, NHS Board member, Thailand

Note: All speakers to be confirmed

PARALLEL SESSION 4.4 (PS4.4)

Finding the Win-Win Solutions for Better Health from Better Food Systems

Background

The surging global demand for animal source foods and rapid growth rates in livestock and aquaculture production are being met with a range of approaches including both aggressive consolidations of production and marketing chains into intensive, large-scale commercial operations, as well as expansion of extensive, small- and medium-scale production systems. Most current approaches contain inherent vulnerabilities. How can the present food systems be reconfigured to feed the growing human population without leading to unintended health consequences for people, animals and the ecosystem? All the stakeholders in these food systems from production, marketing and consumption need to be actively involved in developing coherent and comprehensive approaches where almost everyone can benefit—i.e. collaborative win-win solutions.

Objectives

- Build upon the existing evidence base for the broad collateral benefits realized when longer term investments in shifting production toward reduced impact practices is achieved
- Review cases from the field of how these production shifts were achieved, the methodologies used in measuring the impact realized, and how the impacts were translated into advocacy efforts influencing policy and decision making
- Identify strategies for scaling up these approaches involving the critical stakeholders in a broad range of food systems based on animal production contexts

Moderator

- **Peter Black**, United Nations Food and Agriculture Organization

Speakers

- Farming organization representative representing small/medium size producers: **Andrey Susanto**, Indonesia
- Large producer: **Randal Giroux**, Cargill
- Consumer organization representative: **Niyada Kiatying-Angsulee**, Thailand
- Pharmaceutical industry representative: Elanco, **Kerry Keffaber**, Chief Veterinarian, Scientific Affairs and Policy.
- Knowledgeable Food Systems expert: **Robyn Alders**, University of Sydney, Australia.

Note: All speakers to be confirmed

PARALLEL SESSION 4.5 (PS4.5)

Bringing Solutions into Focus: Harnessing the Power of an Economic Lens

Background

Beyond the tragic loss of human life, the economic impact attributable to epidemics and pandemics can be catastrophic. SARS, $30 billion; Pandemic H1N1: $40 billion; Ebola: $2.8 billion in the three West African economies alone. Recent estimates place the inclusive costs from a moderately severe influenza pandemic at $570 billion annually, within the range projected for the annual cost associated with global climate change.[7] And, without intervention, the cumulative economic impact from anti-microbial resistance (AMR) through 2050 is projected to exceed $100 trillion (two-thirds of which is in low- and middle-income countries), substantially more than current annual global economic output.[8]

Despite a repeated pattern of costly response, the economic case for investing in proactive, preventive measures targeting a reduction in the pressures that facilitate disease emergence has not been widely adopted. A yearly investment of $1.9-3.4 billion to strengthen animal and human public health systems would yield a global public benefit estimated at over $30 billion annually through avoided economic damages associated with pandemics.[9] High return on investment is expected even if only a portion of pandemics are prevented, and strengthened One Health capacity in countries may confer additional benefits via improved prevention and control of endemic disease and AMR. However, challenges in mobilizing capital; an anemic evidence base and difficulty in translating evidence into policy advocacy with budget decision-makers; competing priorities for scarce health systems funding; and inequitable distribution of costs and benefits across sectors and stakeholders are all amongst the impediments to adopting the economic case for investing in preventive approaches.

Recent efforts designed to address these challenges have employed a range of approaches. Structures prioritizing risk avoidance and transference are being developed (e.g. multi-sectoral health security planning and capacity investments; epidemic/pandemic insurance structures). Also underway are new models capturing the economic impact of disease emergence as a function of land use, which will enable the disease regulatory role of ecosystems to be fairly valued and incorporated into payment for environmental services frameworks. And global financing structures promoting targeted, multi-sectoral systems strengthening and incentivizing investments in preparedness are being established.

[7] http://www.nber.org/papers/w22137

[8] O'Neill. Antimicrobial Resistance: Tackling a crisis for the health and wealth of nations. Review on Anti-Microbial Resistance. February 2015

[9] World Bank. People, Pathogens and Our Planet: Economics of One Health. 2012.

Objectives

- Highlight successful practices and approaches that have demonstrated promise in fostering decision making informed by economic analyses;
- Profile structures with proven utility in transcending the identified challenges, including resource prioritization and inequitable sectoral cost and benefit distribution;
- Discuss approaches that strengthen the economic evidence base for investments in proactive, preventive disease mitigation approaches; and
- Review policy and regulatory options, such as tax and incentive structures, that can contribute to a favorable investment environment for more wide scale adoption of risk mitigation approaches

Moderator

- **Dan Schar**, Regional Emerging Infectious Disease Advisor, USAID Regional Office

Panelists

- **Gavin Yamey**, Duke University Global Health Institute
  Introduction/overview; making the investment case for a preventive, One Health approach; challenges and opportunities in financing preparedness
- **Ramanan Laxminarayan**, The Center for Disease Dynamics, Economics, & Policy
  Global consumption of antimicrobials in animal production, costing antimicrobial growth promoter phase out, and catalyzing fit-for-purpose, enforceable AMU policies
- **Carlos Zambrana-Torrelio**, EcoHealth Alliance (A328)
  Analyzing the economics of disease emergence from deforestation to support better practices in the extractive industries and reduce pandemic risk
- **Nita Madhav**, Metabiota
  Catastrophe modeling and pandemic insurance: approaches to managing risk and incentivizing mitigation postures
- **Victoria Fan**, University of Hawai‘i at Mānoa.
  Expected economic losses from potentially vaccine preventable epidemics and pandemics

Note: All speakers to be confirmed

From: Katie Leahy >
Sent: Tuesday, July 25, 2017 9:18 AM EDT
To: kityrob >; ian.mendenhall ;
joram.buza ; vkapur >;
ecohealthalliance.org ecohealthalliance.org
; Kading,Rebekah >; lelincdc
; l.urushadze < ; tamar _kutateladze@
; spwa ; abelwade
c_demetria < >; tigga.kingston
>; cryanp >; dreeder >;
gavin.smith >; nisreen.hmoud >
CC: Stokes, Martha M CIV (US) < >; Lancaster, Mary J CIV (US)
; Gamboa, Omar Maj USAF DTRA J3-7 (US) >; Sander,
William E CTR (US) l>; Caitlin Devaney >
Subject: GBA Products and Action Items
Attachment(s): "GBA Executive Summary_rev2.docx","TORFTA_GBA_v14.docx","GBA_TORFTA Editing Form.xlsx"

Note: this email is best viewed in HTML

Greetings, GBA Steering Committee!

As promised we compiled a couple products and action items from our inaugural meeting on the 29th.

The All Partners Access Network (the site we will use for document sharing and editing) is live and the Executive Summary from our meeting, revised TORFTA, and TORFTA editing sheet have been uploaded. Here are the directions for access:

1. Go to www.apan.org
2. Click, “Create Account” (green button, upper right)
3. Use preferred work email and create password
4. Notify Will Sander once you have created your account; he will invite you to join the GBA SharePoint

For your ease, I have also attached the products that were hung on APAN:

1. An Executive Summary of the 29 June meeting for your files. This lists out key discussions, action items, and participants from the meeting.
2. Revised TORFTA (v14); **NOTE:** the plan for this document is to open a one week editing period for comments. If possible, edits and comments are due back NLT 31 July. After that, the official Version 1 of the GBA will be published.

Here are some requests that we have of you; if you have ideas on any or all of these items, please respond to this email:

1. We need suggestions for a next meeting and would like your suggestions; we will plan to release all options to the group in one week from now for vote. Here are some suggestions to get us started:
   a. International Congress on Pathogens at the Human and Animal Interface (ICOPHAI) 7-9 November 2017, Doha, Qatar https://icophai.org/
   b. Participatory Epidemiology Network for Animal and Public Health (PENAPH) – 10-12 January 2018, Chiang Mei, Thailand https://penaph.net/second-penaph-conference-participatory-approaches-in-animal-health-public-health-one-health-and-ecohealth/
   c. Others??
2. We need suggestions for Network names and would like your suggestions; we will plan to release the options to the group in one week from now for vote. Here are some suggestions to get us started:
   a. Global Alliance for Bat-borne Pathogens (GABP)
   b. Global Bat Pathogen Disease Network (GBPDN)
   c. Bat Alliance Trust Disease Network (BAT-DN)
   d. Others??
3. We need nominations for co-chairs, seek your suggestions; we will plan to release nominees in one week from now for vote.

Katie Leahy
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MEETING OVERVIEW

BACKGROUND

In 2013, the Defense Threat Reduction Agency (DTRA) Cooperative Biological Engagement Program (CBEP) began leveraging, enhancing, and convening research networks to accelerate its programmatic and research driven targets and end states. CBEP uses this approach as a way to connect its active funded research projects with other projects to help influence effective change for global health security; translating data into policy. Further, by using relationship-based research networks around the globe, made up of interdisciplinary relationships, it will allow for novel and transformative scientific solutions for the world's largest infectious disease threats.

The Global Bat Alliance (GBA) is a CBEP research network that connects multidisciplinary and One Health expertise to address challenges and threats posed by bat-associated pathogens of security concern. The GBA maintains the standards of all research networks that are supported by CBEP, in which members convene as a body of experts and researchers to: (1) share information, data, samples, and protocols; (2) coordinate research activities; (3) build training events and awareness-building workshops at all levels of decision-making authority; (4) develop community standards and best research practices; (5) create mentorship-based opportunities for students, trainees, and early-career researchers to convene, present, and share ideas; (6) establish a community of international research leaders and champions; and (7) reduce outbreak / transmission risk.

Some of the world's most deadly emerging zoonotic diseases are found in bats, including Nipah, Hendra, and Marburg viruses. There are a number of factors which make bats unique disease reservoirs, including their social behavior, distinct physiology and metabolism, ability to travel long distances, nocturnal activity, species diversity, and long life span (10-20 years, compared with a rat's average life of two years).[1] These special bat characteristics, coupled with the impact of human mediated interactions and environmental changes, create research challenges to understanding the bat's role in the global zoonotic disease ecology, which is further complicated by being difficult animals to control within a typical laboratory setting. The GBA creates opportunities for policy makers, researchers, conservationists, funders, and students to identify community challenges, develop priority research lists and associated action plans that target needs and gaps, and work at all levels to build awareness of bat-associated disease burden and transmission risks to improve the prevention, detection, diagnosis, and reporting of pathogens of security concern.[2]

EXECUTIVE SUMMARY

On June 29, 2017, CBEP convened a group of multidisciplinary and One Health-focused research scientists, conservationists, and medical / veterinary practitioners for a one-day meeting in Fort Collins, Colorado to discuss organization and objectives for a bat-related research-based network (the complete agenda for the meeting may be found in Annex B). The representatives and experts in attendance work

[1] Hayman, David T.S., "As the bat flies," *Science* 02 Dec 2016: Vol. 354, Issue 6316, pp. 1099-1100 http://science.sciencemag.org/content/354/6316/1099

[2] Schountz, Tony, "Immunology of Bats and Their Viruses; Challenges and Opportunities," *Viruses,* 2014 Dec; 6(12): 4880-4901. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4276934/

in CBEP regions (a full list of participants may be found in Annex A). The meeting was held at the University Center for the Arts, at Colorado State University, in concurrence with the 2nd International Symposium on Infectious Diseases of Bats.

The meeting began with an introduction to CBEP's mission and its use of networks as a way to foster coordination across regions and build sustainable connections through research. The two CBEP science leads, Drs. Mary Lancaster and Marty Stokes, outlined their vision to enhance regional and global research capacity, which starts with a complete understanding of the existing research landscape. CBEP believes this approach mitigates duplication of effort, by working with and building off of existing relationships; this could include an amalgamation of individuals, institutions, or other communities of practice. The CBEP representatives emphasized that their broad objective is to fuse actively funded expertise and projects to better inform and drive global, regional, and national health security policies.

Following an introduction, the CBEP leads facilitated a conversation to build consensus on ways to organize and administrate the network through a Terms of Reference for Trusted Agents (TORFTA). A draft of the TORFTA was emailed to participants in advance of the meeting so the discussions were analytical and substantive. The meeting ended with notes for a new draft that participants agreed could be virtually edited via SharePoint.

The discussions regarding the TORFTA led to other discussions about the objectives for the network, which were revised in-real-time. The group agreed on the following objectives for the GBA:

- Facilitate interdisciplinary relationships and collaboration to identify research goals and needs for bat-associated disease research and disease threat reduction;
- Unify CBEP regions to create a common action plan that yields collaborative and sustainable projects that achieve the following end states: (1) better informed policy-makers; (2) better informed scientific community regarding funding targets and gaps in areas of research and development; (3) better defined threat to global health security from bat-associated pathogens; and (4) improved national, regional, and global capacity to detect and respond to pathogens of security concern; and
- Enable better communication, coordination, and outreach at the research and conservation interface.

The meeting ended with a thorough discussion about the research focus areas for the group. The meeting participants self-nominated into Working Groups to serve as research mentors (note: a list of working groups and mentors is outlined under the Research Focus Areas section of this document). The group agreed that discussions about priorities within the Working Groups should occur at the next steering committee meeting.

The first meeting of the GBA was a success. Participants readily took part in discussions and shared ideas from their respective multidisciplinary backgrounds. Many had experience forming similar research-based networks, and they appeared energized to solve global challenges related to spillover opportunity of bat-borne pathogens of security concern. While there were many unresolved topics of conversation (e.g., a new name for the network), the group agreed that they would communicate virtually on these subjects through email and SharePoint interaction, initiated by CBEP. They agreed to nominate and vote for individuals to serve as co-chairs of the Steering Committee as well as identifying an opportunity to meet again within the calendar year (note: a full list of outlying issues and recommendations for action may be found in the Action Items section of this document).

RESEARCH FOCUS AREAS

WORKING GROUP 1: HOST / PATHOGEN BIOLOGY AND INTERACTIONS

- Bat physiology and immunology
- Bat pathogen community biology (co-infections, co-morbidities)
- Distribution of pathogens among species

WORKING GROUP 1 RESEARCH MENTORS

- Dr. Joram Buza, Nelson Mandela African Institute of Science and Technology, Tanzania
- Dr. Vivek Kapur, Penn State University, U.S.
- Dr. DeeAnn Reeder, Bucknell University, U.S.

WORKING GROUP 2: PATHOGEN SURVEILLANCE, DIAGNOSTIC CAPACITY, AND EPIDEMIOLOGY

- Molecular epidemiology
- Distribution of pathogens geographically and phylogenetically
- Detection, diagnosis, and reporting of bat-associated pathogens

WORKING GROUP 2 RESEARCH MENTORS

- Dr. Catalino Demetria, Research Institute for Tropical Medicine, Philippines
- Dr. Jon Epstein, EcoHealth Alliance, U.S.
- Dr. Tamar Kutateladze, National Center for Disease Control and Public Health, Georgia
- Dr. Lela Urushadze, National Center for Disease Control and Public Health, Georgia
- Dr. Supaporn Wacharapluesadee, WHO CC for Research and Training in Viral Zoonoses, King Chulalongkorn Memorial Hospital, Thailand
- Dr. Abel Wade, National Veterinary Laboratory, Cameroon

WORKING GROUP 3: ECOLOGY SETTING (BAT, DOMESTICATED ANIMALS, AND WILDLIFE INTERFACE)

- Bat behavior, distribution, and movement
- Domesticated animals and wildlife behavior, distribution, and movement impact on interaction with bats.
- The effect of anthropogenic disturbance and modification

WORKING GROUP 3 RESEARCH MENTORS

- Dr. Paul Cryan, United States Geological Survey (USGS) Fort Collins Science Center, U.S.
- Dr. Tigga Kingston, Texas Tech University, U.S.
- Dr. Robert Kityo, Makerere University, Uganda
- Dr. Rebekah Kading, Colorado State University, U.S.

WORKING GROUP 4: HUMAN-BAT INTERACTIONS, RISK CHARACTERIZATION

- Hunting and commodity chain (e.g., bushmeat, guano, and pet trade)
- Ecotourism
- Interactions in human dwellings

WORKING GROUP 4 RESEARCH MENTORS

- Dr. Kevin Olival, EcoHealth Alliance, U.S.
- Dr. Ian Mendenhall, Duke/NUS, Singapore

ACTION ITEMS

The following Action Items were recorded and compiled by the organizational and administrative support staff of CBEP / Executive Committee for the GBA.

ACTION	APPROACH FOR COMPLETION WITH DATES	RESPONSIBLE AGENTS
Generate and send out options for new network name	(1) Send email to steering committee members soliciting options (with one week deadline) – 18 July (2) Preview options with Executive Committee – 25 July (3) Send all name options to group via polling application – 26 July	(1) Leahy (GSE) (2) Leahy (3) Leahy
Generate and send out solicitation for co-chair nominations	(4) Send request to steering committee members soliciting nominations (with one week deadline) in combination with the email from Task (1) (5) Preview options with EC – 25 July (6) Send all nominations to group for voting via polling application – 26 July	(4) Leahy (5) Leahy (6) Leahy
Generate and send out solicitation for next meeting conference opportunities and dates	(1) Send request to steering committee members soliciting nominations (with one week deadline) in combination with the email from Task (1) (2) Preview options with EC – 25 July (3) Send all nominations to group for voting via polling application – 26 July	(7) Leahy (8) Leahy (9) Leahy
Update TORFTA with recommendations from meeting	(4) Send invitation to steering committee members with editing options via APAN SharePoint – 19 July (5) Send Editing Form with above email – 19 July (6) Open editing period for one week – 19- 26 July (7) Collect comments and negotiate updates with EC 26-31 July	(10) Sander (CTR A&AS) (11) Sander (12) Sander (13) Sander / Leahy
Create CV Format for new members	(8) Create a CV Format (9) Upload to APAN	(14) Leahy (15) Sander
Finalize fact sheet	(10) Finalize fact sheet with updates from discussions (11) Send to PAO for review	(16) Leahy (17) Sander

ANNEX A – PARTICIPANTS

The following participants attended or were invited to attend the GBA Kickoff Meeting in Fort Collins, Colorado on 29 June 2017.

STEERING COMMITTEE MEETING INVITEES, DID ATTEND		
Kityo	Robert	Makerere University, Uganda
Mendenhall	Ian	Duke-NUS, Singapore
Buza	Joram	Nelson Mandela African Institute of Science and Technology (NM-AIST) (attended virtually)
Kapur	Vivek	Penn State University (attended virtually)
Olival	Kevin	EcoHealth Alliance
Epstein	Jonathan	EcoHealth Alliance
Kading	Rebekah	Colorado State University
Urushadze	Lela	National Center for Disease Control and Public Health (NCDC) Georgia
Kutateladze	Tamar	National Center for Disease Control and Public Health (NCDC) Georgia
Wacharapluesadee	Supaporn	WHO CC for Research and Training in Viral Zoonoses, King Chulalongkorn Momorial Hospital, Thailand
Wade	Abel	National Veterinary Laboratory of Cameroon (LANAVET)
Demetria	Catalino	RITM, Philippines
Kingston	Tigga	Texas Tech University
Cryan	Paul	USGS Fort Colliins Science Center
Reeder	DeeAnn	Bucknell University
INVITEES, DID NOT ATTEND		
Smith	Gavin	Duke-NUS, Singapore
Alhmoud	Nesreen	Royal Scientific Society
CBEP AND CBEP CONTRACTOR INVITEES, DID ATTEND		
Lancaster	Mary	DTRA CBEP
Stokes	Marty	DTRA CBEP
Gamboa	Omar	DTRA CBEP
Sander	Will	CTR A&AS Booz Allen
Leahy	Katie	GSE
Devaney	Caitlin	GSE

ANNEX B – MEETING AGENDA

The following agenda was set for the meeting. The majority of discussions focused on administration, organization, and focus of the network. The group did not get to the topics to prioritize research gaps and set action plans with short and long-term milestones and deliverables. Event facilitators organized questions and prompts for those sessions, which they will use for the next GBA meeting.

Time	Agenda Topic and Facilitator or Speaker	Expected Outcomes
0930 – 1000	**Welcome and Introductions**	
1000 – 1015	**Global Bat Alliance Overview** *Dr. Mary Lancaster (Africa Science Lead)* *Dr. Marty Stokes (SEA Science Lead, CBEP)*	• Review discussions leading up to this meeting • Discuss how this meeting is an opportunity to formalize the central / steering committee node for the distributed network • Emphasize that the steering committee shall focus on mentorship and connecting individuals and institutions across the globe
1015 – 1045	**Review Charter and Move to Agreement** *TBD*	• Vote to accept organizational document for steering committee • Unanimous (??) acceptance • We will advertise intent ahead of meeting • We will convene a meeting on 7 June to review and discuss the draft TORFTA
1045 – 1115	**Identify and discuss research focus areas** *TBD*	• Group will identify and discuss overarching focus areas and sub focus areas • Steering committee and invitees shall self nominate to groups and agree to serve as research mentors for the groups
1115 – 1230	**Breakout: Prioritize research needs and gaps** *TBD*	• Group will breakout into their research focus areas and begin identifying needs and gaps • Groups will then work to prioritize their lists
1230 – 1330	**Working Lunch** *TBD*	• Buffett • Convene back as a group, hold discussions about the overarching objectives of the alliance • Discuss One Health and Vector-based International meetings as an opportunity to re-convene semi-annually

1330 – 1400	**Breakout: Draft timelines and workplans** *TBD*	• Begin drafting short and long-term timelines and workplans for each focus area • Short-term milestones could include identifying key researchers and networks • Long-term milestones could include training events and focus area meetings
1400 – 1430	**Closing / review of actions** *TBD*	• Close-out meeting / 5min brief out for each group (2 slides) • Review action items and next steps

	A	B	C	D
1		**Reference (page #, line #)**	**Commenter** **Date** (Last, F/ mm-dd)	**Comment/** **Recommendation**
2				
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	E	F	G	H
1	**Level**	**Responder/ Date**		
2	(Critical, Substantive, Administrative)	(Last, F/ mm-dd)	**Response**	**Resolution**
3				
4		YELLOW AREAS TO BE FILLED OUT BY REPRESENTATIVES OF THE EXECUTIVE COMMITTEE		
5				
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TERMS OF REFERENCE FOR TRUSTED AGENTS OF THE GLOBAL BAT ALLIANCE

1. BACKGROUND

In 2013, the Defense Threat Reduction Agency (DTRA) Cooperative Biological Engagement Program (CBEP) began leveraging, enhancing, and convening research networks to accelerate its programmatic and research driven targets and end states. CBEP uses this approach as a way to connect its active funded research projects with other projects to help influence effective change for global health security; translating data into policy. Further, by using relationship-based research networks around the globe, made up of interdisciplinary relationships, it will allow for novel and transformative scientific solutions for the world's largest infectious disease threats.

The Global Bat Alliance (GBA) is a CBEP research network that connects multidisciplinary and One Health expertise to address challenges and threats posed by bat-associated pathogens of security concern. The GBA maintains the standards of all research networks that are supported by CBEP, in which members convene as a body of experts and researchers to: (1) share information, data, samples, and protocols; (2) coordinate research activities; (3) build training events and awareness-building workshops at all levels of decision-making authority; (4) develop community standards and best research practices; (5) create mentorship-based opportunities for students, trainees, and early-career researchers to convene, present, and share ideas; (6) establish a community of international research leaders and champions; and (7) reduce outbreak / transmission risk.

Some of the world's most deadly emerging zoonotic diseases are found in bats, including Nipah, Hendra, and Marburg viruses. There are a number of factors which make bats unique disease reservoirs, including their social behavior, distinct physiology and metabolism, ability to travel long distances, nocturnal activity, species diversity, and long life span (10-20 years, compared with a rat's average life of two years).[1] These special bat characteristics, coupled with the impact of human mediated interactions and environmental changes, create research challenges to understanding the bat's role in the global zoonotic disease ecology, which is further complicated by being difficult animals to control within a typical laboratory setting. The GBA creates opportunities for policy makers, researchers, conservationists, funders, and students to identify community challenges, develop priority research lists and associated action plans that target needs and gaps, and work at all levels to build awareness of bat-associated disease burden and transmission risks to improve the prevention, detection, diagnosis, and reporting of pathogens of security concern.[2]

2. GBA MISSION AND VISION

The GBA brings together a multidisciplinary and One Health-focused group of scientists, policy makers, research scientists, and medical/veterinary practitioners with interests in bat-related research involving pathogens of security concern. The network builds on community standards and best practices for research. The GBA identifies and shares information on research funding opportunities offered by multiple institutions. Most importantly, this network fosters international relationships among

[1] Hayman, David T.S., "As the bat flies," *Science* 02 Dec 2016: Vol. 354, Issue 6316, pp. 1099-1100 http://science.sciencemag.org/content/354/6316/1099

[2] Schountz, Tony, "Immunology of Bats and Their Viruses; Challenges and Opportunities," *Viruses,* 2014 Dec; 6(12): 4880-4901. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4276934/

collaborators, agencies, and organizations, which can produce long-term, sustainable partnerships that withstand changes in government and organization budgets, priorities, postures, and policies.

All members, or "Trusted Agents" of the Alliance play a role in operationalizing the objectives of the GBA, strengthening linkages and reducing overlap in global research on high-priority pathogens of bats (especially zoonoses) to maximize the efficient use of expertise and resources and accelerate the coordinated development of better disease surveillance and control methods.

3. OBJECTIVES

CBEP created a standard framework of objectives that it uses for its research networks, which is outlined in the Background Section of this document. The specific, research-focused objectives of the GBA are as follows:

- Facilitate interdisciplinary relationships and collaboration to identify research goals and needs for bat-associated disease research and disease threat reduction; and
- Unify CBEP regions to create a common action plan that yields collaborative and sustainable projects that achieve the following end states: (1) better informed policy-makers; (2) better informed scientific community regarding funding targets and gaps in areas of research and development; (3) better defined threat to global health security from bat-associated pathogens; and (4) improved national, regional, and global capacity to detect and respond to pathogens of security concern
- Enable better communication, coordination, and outreach at the research and conservation interface

4. APPROACH

The Terms of Reference for Trusted Agents (TORFTA) establishes ground rules and responsibilities for all members – known heretofore as "Trusted Agents" (TAs) of the GBA. The leadership structure of the GBA is made up of subject matter experts who serve as mentors and function as independent, trusted advisors and honest brokers for research within the GBA.

All TAs function within an organizational structure that consists of an Executive Committee (EC), a Steering Committee (SC), and four subject matter-focused Working Group (WG) subcommittees. The GBA employs a bottom-up design. This is an organizational approach that encourages ideas, solutions, and projects to start with TAs within the WGs. The ideas, solutions, and projects will filter through the WG mentors, who then link people, ideas, solutions, and projects together at the SC level; ultimately, this approach will (1) foster lasting relationships at an individual or institutional level, and (2) yield better data outcomes and/or larger fields of study. A visual representation of the responsibilities and organizational flow of the GBA is found in Figure 1.

Roles and responsibilities of the TAs within Committees and Working Groups are as follows:

4.1 Working Groups (WGs)

The WGs serve as subdivisions of the GBA designed to foster multinational and multidisciplinary participation and meet the wide spanning research challenges associated with bat-borne diseases. TAs from the SC serve as research mentors and subject matter experts within each WG, providing guidance on projects.

There are limited barriers to entry for becoming a TA in the GBA and joining a WG. Non-steering committee members should work or reside in CBEP engaged countries, which can be found in Annex B, and may be students, entry to mid-level career professionals, or anyone interested in

contributing to the bat research community. Entry for indviduals who do not work or reside in CBEP engaged countries will be considered by the EC on a case-by-case basis. Non-steering committee TAs do not have term limits, but are encouraged to collaborate, contribute, and participate evenly across the WGs. TAs receive invitation or nomination to participate in a WG by members of the EC or SC.

The WGs focus on the following research areas *(**note:** these focus areas were agreed upon at the GBA kickoff in Fort Collins, CO 29 June 2017*):

Working Group 1: Host / pathogen biology and interactions; specifically:

1. Bat physiology and immunology
2. Bat pathogen community biology (co-infections, co-morbidities)
3. Distribution of pathogens among species

Working Group 2: Pathogen surveillance, diagnostic capacity, and epidemiology; specifically:

1. Molecular epidemiology
2. Distribution of pathogens geographically and phylogenetically
3. Detection, diagnosis, and reporting of bat-associated pathogens

Working Group 3: Ecology setting (bat, domesticated animals, and wildlife interface); specifically:

1. Bat behavior, distribution, and movement
2. Domesticated animals and wildlife behavior, distribution, and movement impact on interaction with bats.
3. The effect of anthropogenic disturbance and modification

Working Group 4: Human-bat interactions; specifically:

1. Human behavioral risk characterization
2. Hunting and commodity chain (e.g., bushmeat, guano, and pet trade)
3. Ecotourism
4. Interactions in human dwellings

4.2 Steering Committee (SC)

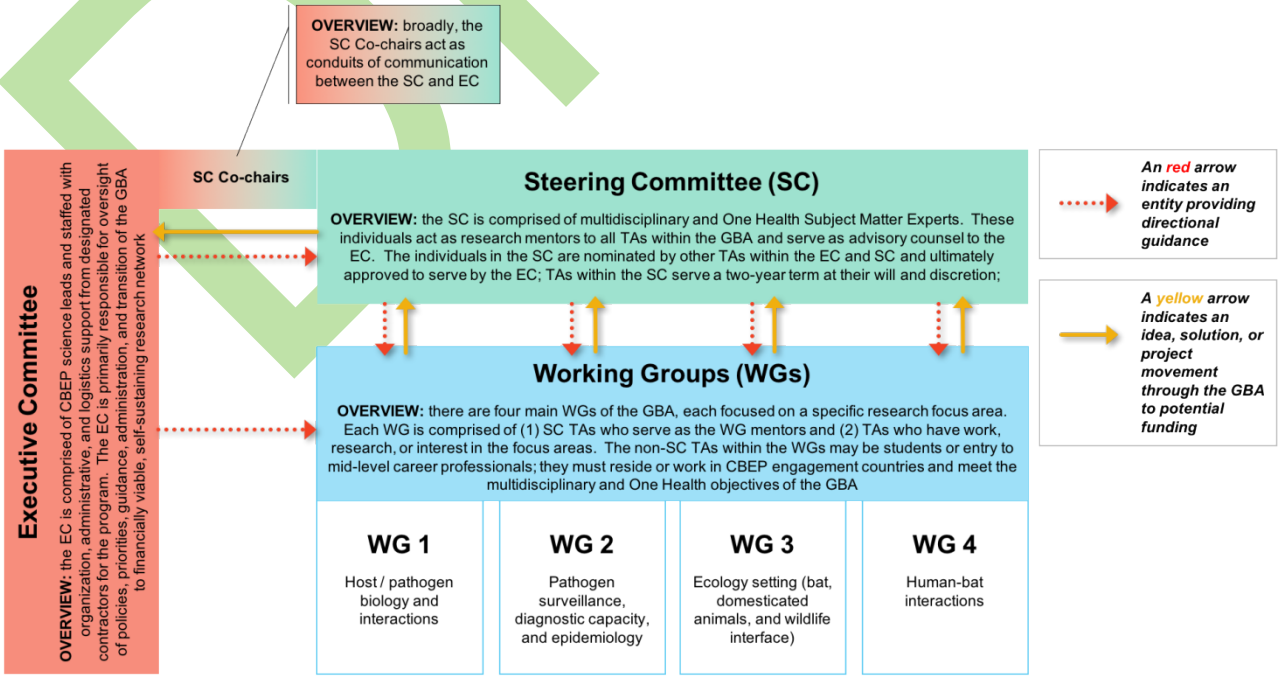
The SC includes multidisciplinary subject matter experts. They fill two important roles to operationalize the objectives of the GBA, (1) acting as advisory counsel to the EC for global bat research (providing analysis of research gaps and needs and priority targets for future funds) and (2) serving as scientific mentors within WGs.

TAs within the SC advise on the scientific merit of proposals to the EC and assist with implementation per TORFTA guidance and EC direction. The selection process for SC membership gathers a multidisciplinary body of global representation, both geographically and across the bat research spectrum. Two SC Co-chairs are elected to serve as communication between the SC and EC. Their roles and responsibilities are outlined in more detail later in this section.

TAs are nominated to join the SC by active members of the SC and EC. The inaugural SC was gathered together by the EC on 29 June 2017 in Fort Collins, Colorado. There is a two-year term limit for a TA in the SC, however, they have the option to leave and nominate a replacement at any time and with sufficient notification to the SC Co-chairs.

The SC is responsible for the following items (at a minimum):

- Act as a scientific coordinating body for the GBA
- Consider and provide analysis on the scientific merit of proposals at the direction of the EC
- Serve as subject matter experts and research mentors for implementation of accepted GBA-endorsed projects
- Work within WGs to gather information on challenges, and propose research priorities to EC
- Identify possible conflicts of interest and make recommendations to SC Co-chairs and EC (e.g., one solution might be a temporary hiatus from the GBA or from service on the SC for a period of time)
- Annually review and make recommendations on policy and guidance of the GBA, which could include revision of the objectives, terms of reference, terms for membership, or structure of the GBA
- Work with the EC to determine challenges for transition to a self-sustaining network, which could include sources and means of political and financial support
- Define objectives, schedules, milestones, and deliverables of the WGs, as well as identifying need for proposing establishment of new or closing-out existing WGs
- Support WGs in organizing gap analyses and research prioritization
- Promote interactions between WGs
- Assess and report progress of the WGs to other members of the SC and EC
- Develop and encourage exchange of protocols and best practices, and agree on standard operating procedures, good research practice, and roadmap to reach GBA goals (short and long-term)
- Establish compliance rules for ethical practice, create training SOP



NOTE: *CBEP considers all contributors and participants of the GBA as "members" of the network; designating the term "Trusted Agents" (TAs) to all individuals regardless of role, affiliation, seniority, or responsibilities*

FIGURE 1 ORGANIZATIONAL STRUCTURE AND RESPONSIBILITIES OF THE GBA

SC Co-chairs: Two members of the SC are chosen by majority voting during annual meeting of the EC and SC. All other TAs on the SC have two-year term limits; however, the Co-chairs hold one-year term limits. These two individuals serve as the communication node between the EC and SC. They engage with the WG mentors that serve on the SC from the bottom-up, to identify candidates and projects. Other responsibilities include:

- Coordinate with EC organization and administration staff to arrange meeting schedule for EC/SC (virtual and in-person)
- Identify opportunities to broaden the network, e.g., conference attendance, paper presentations, etc.
- Communicate EC requirements to SC and set standards for good management practices within WGs
    - Reports
    - Schedules
    - Membership distribution
    - Information flow
- Communicate EC requirements to SC and set standards for good management practices within WGs
- At the direction of the EC, act as a spokesperson for the network and interact with complimentary fields of study outside the network
- Work with the EC to determine and seek other funding opportunities
- Communicate regularly with EC on potential risks to self-sustainability of the network
- Advise the EC on potential conflicts of interest and recommended courses of action

4.3 Executive Committee (EC)

The EC ultimately sets policy and guidance for the GBA. It is chaired by the CBEP Science Leads from Africa and Southeast Asia and staffed with organization, administrative, and logistics support from designated contractors assigned to the program. The EC is primarily responsible for oversight of GBA governance policies and guidelines, which includes funding decisions, research priorities, adjudication of potential conflicts of interest, and GBA membership at all levels of participation. As such, the EC is the sole decision-making body of the research network for funding.

The EC is comprised of members from the CBEP Research Program, therefore, the details regarding program requirements and processes for funding can be found in Annex A of this document and should be used as a resource for all GBA Trusted Agents who wish to submit projects to CBEP.

The EC and their team are broadly responsible for the following tasks (at a minimum):

- Review and approve objectives and goals for the GBA
- Review and approve Steering Committee and Working Group schedules and deliverables
- Provide organizational, administrative, and logistics support for meetings, conferences, and training events (virtual and in-person) of the GBA SC and WGs

- Work with Chairman and Deputy Chairman of the SC on marketing, communication, and outreach with other experts, fields of study, policy makers, international organizations, non-governmental organizations, and other networks
- Disseminate network information to all TAs, which could include newsletters, website links, press releases, and dates for upcoming meetings and conferences (inside and outside the network)
- Build connections with other funding agencies and organizations
- Convene a bi-annual research review for four focus areas of the network
- Measure network performance goals
- Score indicators of network transition to self-sustainability readiness

5. GOVERNANCE AND MEMBERSHIP

5.1 Accountability

The overarching duty of the GBA is to develop multi-disciplinary and multi-national, hypothesis driven, research projects and training opportunities that meet the prioritized challenges defined by the EC under advice from the SC with the goal of outlining community standards of practice. All TAs are accountable for the following:

- TAs must be familiar with the TORFTA and the mandate of the committees or WGs on which they serve
- TAs must promote a culture of responsible practice for scientific research
- TAs must work towards the short and long-term goals for the benefit of the GBA with a particular emphasis on the foci that fall within their WG
- TAs on the SC are selected for their breadth of experience, insight and knowledge, integrity and character, and sound and independent judgment; therefore, they are expected to bring these personal qualities to their role on the SC and apply impartial judgment to help the EC make informed and independent decisions

5.2 Conflicts of Interest

The TORFTA document chooses the National Academy of Sciences (NAS) definition of Conflict of Interest: “a conflict of interest in research exists when the individual has interests in the outcome of the research that may lead to a personal advantage and that might therefore, in actuality or appearance compromise the integrity of the research.”

No member of the Steering Committee may participate in a discussion where such participation would give rise to a potential conflict of interest. As defined in section 4.1, the EC shall review all situations and decisions insofar as a financial obligation is at stake. SC members may leave their term of service on the SC if they wish to participate in a funding opportunity that would otherwise be perceived as a conflict of interest. SC TAs must recuse themselves if any personal advantage, not just those of financial benefit, is perceived. Any member of the SC may discuss possible conflicts of interest with the EC before recusing themselves or stepping down from their term of service.

The EC arbitrates final decisions regarding potential conflicts of interest. With advice from the SC Co-chairs, they will determine if a recusal, resignation, or termination is required. The EC will determine the terms of recusal on a case-by-case basis, which could include being directed to

abstain from any or all of the following: (1) meetings; (2) votes; (3) exchange of information; or (4) other correspondence. Ultimately, the EC advocates for complete transparency within the GBA, with an emphasis on early and frequent communication about any matter that could be perceived as a conflict of interest; this approach will mitigate ethics concerns and should eliminate the need for termination of service.

5.3 Selecting **TAs**

As stated in previous sections, all members of the GBA are referred to as "Trusted Agents" (TAs) of the network. TAs must reflect the One Health, multi-disciplinary, and multi-national nature of the GBA. There are no term limits for non-committee associated TAs, who are allowed to participate at will in accordance with terms of the TORFTA, additional selection rules are as follows:

5.3.1 ***Terms of service –*** *none*

5.3.2 ***Eligibility*** *– representation from each CBEP region must be maintained*

5.3.3 ***Nomination process –*** *nominated or invited to participate by the EC or SC at conferences, meetings, or electronically*

5.3.4 ***Selection process –*** *reviewed by members of the EC under advisement of the SC*

5.4 Selecting SC TAs

The SC includes TAs that are regarded as subject matter experts in their fields of research. TAs of the SC agree to the following rules for selection:

5.3.5 ***Terms of service –*** *2 years, no term limit*

5.3.6 ***Eligibility*** *– representation from each CBEP region must be maintained*

5.3.7 ***Nomination process –*** *nominated biennially (or as needed or requested by EC and SC Co-chairs); nomination process takes place in-person or virtually, selection is achieved through majority vote*

5.3.8 ***Selection process –*** *upon nomination, potential applicant will submit an application, which will be reviewed for relevancy by members of the EC and SC Co-chairs*

5.5 Consensus

A quorum within the GBA is constituted by 2/3 approval within the SC, and rounded up when the number is uneven. The SC may decide by consensus or majority vote to ask other TAs to join a meeting to exchange information, material, or knowledge. The SC may establish sub-committees consisting of three or more of its members to conduct training or outreach (or any effort not explicitly within the stated focus areas of the SC and WGs). However, the Co-chairs should be informed of these efforts to communicate the need and seek approval from the EC.

ANNEX A: APPLYING FOR FUNDING VIA EXECUTIVE COMMITTEE / CBEP

A.1 CBEP Research Scope

In order for CBEP to remain relevant, agile, and sustainable, research projects must be aimed at threat reduction objectives and demonstrate a clear nexus with the biosurveillance mission. The scope of CBEP research priorities include (but are not limited to):

- Understanding the ecology and epidemiology of pathogens of security concern, including HHS and USDA Biological Select Agents and Toxins and pathogens of pandemic potential, emerging, and re-emerging infectious diseases (e.g., avian influenza [low and highly pathogenic], African swine fever, Middle East Respiratory Syndrome (MERS), Ebola)
- Differentiating infectious diseases presenting clinical signs and symptoms similar to those of pathogens of security concern (e.g., influenza-like illness, acute febrile illness, fever of unknown origin)

CBEP will not support research projects that have no clear link to its threat reduction mission, are not sustainable for the partner country, or propose activities constituting Dual Use Research of Concern. These and other requirements and constraints are outlined in the figure below.

CBEP Fundamental Research Scope	
In Scope	**Out of Scope**

Projects that demonstrate:
• Clear relationships to pathogens of security concern
  ○ U.S. Biological Select Agents *
  ○ Pathogens of pandemic potential
  ○ Pathogens with potential to be weaponized
  ○ Emerging or re-emerging infectious diseases
  ○ Differentiating pathogens of security concern from agents with similar clinical signs and symptoms
• Links to threat reduction mission
• Support of BS&S and biosurveillance capabilities that reduce the threat of pathogens of security concern
  ○ Rapid, accurate, and safe detection, diagnoses, and reporting
• Alignment with both CBEP and partner country infectious disease priorities
• Use of sustainable techniques, procedures, and approaches in appropriate facilities
	Projects that focus on:
	• Dual-Use Research of Concern (DURC)
	• Diagnostic assay / novel technology
	• Development **
	• Medical countermeasures, including vaccine development
	• Non-infectious diseases
	
	Projects that contain:
	• Establishment of new pathogen repositories
	• No link to pathogens of security concern
	• No clear alignment to threat reduction mission
	• Use of unsustainable techniques, procedures, or inappropriate facilities
	  ○ Requires use of supplies or resources not available in country

	• No clear research question or hypothesis • No potential to generate knowledge that may result in scientific publications

* Pathogens on the HHS and USDA Biological Select Agent and Toxins List

** Field or country-specific validation of new diagnostic assays, novel technologies or equipment may be in scope if meeting other in-scope criteria

A.2 Applying for DTRA CBEP Research Funding

CBEP Research Objectives and Scope

DTRA CBEP is continuously seeking new collaborators, partners and international partners to conduct cooperative biological research to inform and enhance disease surveillance and global health security. Projects that are hypothesis-driven and contain substantive engagement with and contribution by partner country governments, institutions and scientists are appropriate for CBEP research funding. Research projects that support CBEP objectives in partner countries include those that promote One Health, improve disease surveillance, enhance understanding of endemic pathogens, explore the microbial ecology of endemic organisms, and enhance host country capabilities in support of World Health Organization International Health Regulations and World Organization for Animal Health reporting standards. Pathogens of interest include Biological Select Agents and Toxins, pathogens of pandemic potential, pathogens with the potential to be weaponized, emerging and re-emerging infectious diseases, and pathogens that are co-syndromic with associated select agent etiologies such as Influenza-Like Illness or Acute Febrile Illness. CBEP does not support research topics that involve Dual- Use Research of Concern or focus on disease agents that are sexually transmitted, non-infectious, or do not pose a threat to global health security.

Research projects supported by CBEP must align with CBEP's overarching goals to reduce the threat to U.S. and global health security and are expected to produce results suitable for scientific publication.

Applying to the Broad Agency Announcement (BAA) and Government Call

CBEP welcomes research funding applications from domestic and foreign academic, private, and government institutions, and has multiple solicitations available for proposals.

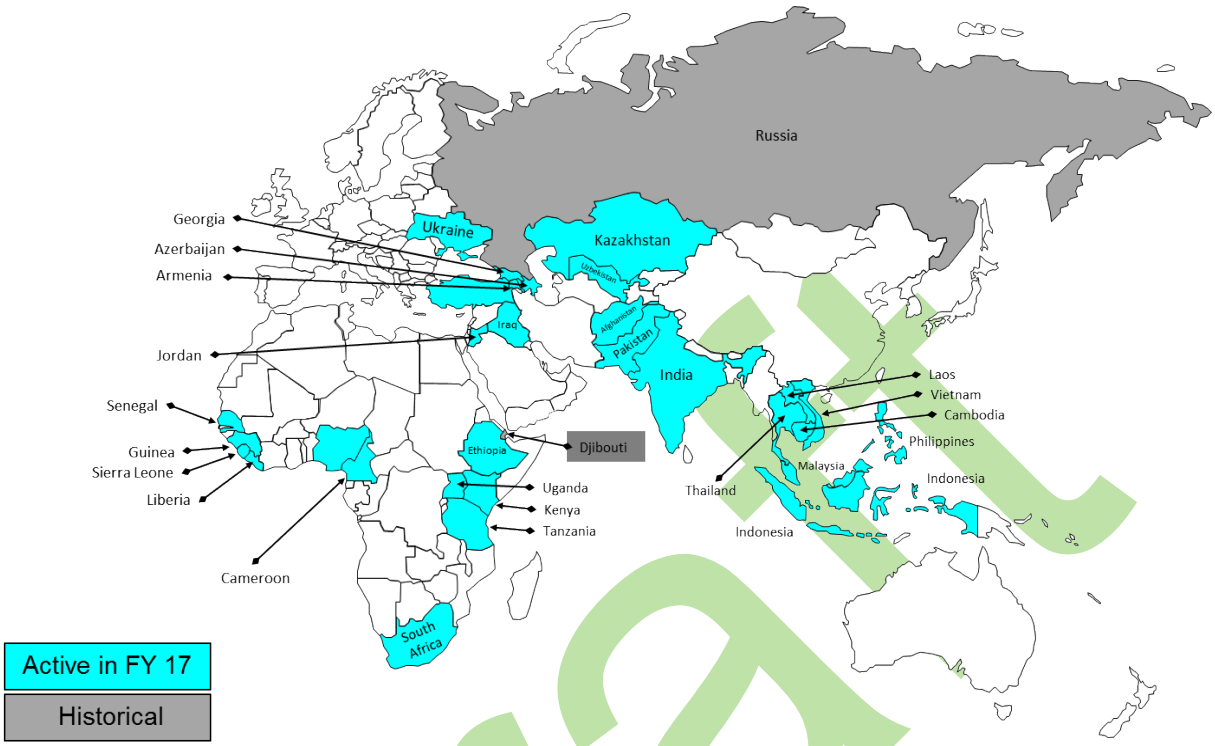
- Academic institutions, non-governmental organizations, industry, foreign laboratory equivalents, and members of the private sector must apply through Thrust Area 6: Cooperative Counter Weapons of Mass Destruction (CWMD) Research with Global Partners of the Fundamental Research to Counter Weapons of Mass Destruction (FRCWMD) – BAA (HDTRA1-14-24- FRCWMD-BAA).
- U.S. Government partners and Federally Funded Research and Development Centers (FFRDCs) must apply through Thrust Area 6 of the FRCWMD Government Call (HDTRA1-12-17- FRCWMD-Call).

All research ideas MUST be pre-coordinated through submission of an abstract to HDTRA1-FRCWMD-TA6@mail.mil prior to submitting a white paper. White papers (aka Phase I proposal) must be submitted and a full proposal (aka Phase 2 Proposal) invited prior to submission of a full proposal. Phase 1 and

Phase 2 proposals to the FRCWMD-BAA must be submitted through www.grants.gov. Phase 1 and Phase 2 proposals to the FRCWMD-Call must be submitted through www.dtrasubmission.net. White papers and proposals will be peer reviewed in accordance with the evaluation criteria published in the BAA and Call and in coordination with appropriate CBEP Regional and Country Managers. To be successful, a white paper and/or proposal must align with both the DTRA/SCC-WMD CBEP mission and regional priorities.

Detailed instructions for the FRCWMD-BAA and the FRCWMD-Call can be found through the solicitation links at www.dtrasubmission.net. Please ensure that you are downloading and reviewing the latest amended full announcement for the most accurate information and instructions. Offerors may submit questions of an administrative nature for BAA to HDTRA1-FRCWMD-A@mail.mil or for Service Call to HDTRA1-FRCWMD-C@mail.mil.

ANNEX B: CBEP ENGAGEMENT COUNTRIES



From: Katie Leahy >
Sent: Tuesday, August 22, 2017 8:17 PM EDT
To: Robert Kityo >; Ian Mendenhall >; Joram Buza >; Vivek Kapur >; Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Kading,Rebekah ; Lela Urushadaze ; Lela Urushadaze ; Tamar Kutateladze >; Supaporn Wacharapluesadee >; Abel Wade >; Catalino Demetria >; Tigga Kingston >; Paul Cryan >; DeeAnn Reeder ; Gavin Smith < Nisreen Alhmoud
CC: Lancaster, Mary J CIV (US) l>; Stokes, Martha M CIV (US) Sander, William E CTR (US) >; Caitlin Devaney <
Subject: GBA Update and Request

All,

On behalf of Dr. Mary Lancaster and Dr. Marty Stokes, we would like to thank everyone, for your responses over the last couple weeks! Based on your feedback, we have a few announcements and one request:

Based on committee consensus, the group chose our next event to coincide with the Participatory Epidemiology Network for Animal and Public Health (PENAPH) on 10-12 January 2018, in Khon Kaen, Thailand. Details will be forthcoming, but please visit the hyperlink for further information (https://penaph.net/second-penaph-conference-participatory-approaches-in-animal-health-public-health-one-health-and-ecohealth/).

We did not receive additional nominations to serve as co-chairs, so we are pleased to announce our first Steering Committee Co-chairs: Dr. Jon Epstein from EcoHealth Alliance and Dr. Vivek Kapur from Penn State University. We will be setting up coordination calls with our two co-chairs, so you can expect communication and direction from them in the future.

Finally, one request; we did not have a majority vote selection for our organization's name, which leaves us with two options:

Option 1 Bat-associated Pathogen and Ecology Research Network (BPERN) and

Option 2 Global Alliance for Bat-borne Pathogens (GABP).

Please respond to this email with your selection no later than 24 August. We will tally the votes and make an announcement thereafter.

Thank you, again, for signing up to the APAN site and being so responsive to the request. We will be loading the first documents and drafts to the site (e.g., the TORFTA and community fact sheet) in the next couple weeks. You may expect email from us with information concerning our next meeting in January and planning discussions leading up to that meeting.

V/r,

Katie Leahy
Program Manager | Global Systems Engineering
5881 Leesburg Pike, Suite 506
Baileys Crossroads, VA 22041

http://globalsyseng.com

From: Katie Leahy
Sent: Monday, June 12, 2017 9:53 AM EDT
To: Prof. Joram Buza ; "Devaney, Caitlin (US)" >; "Stokes, Martha M CIV (US)" >; "Kevin Olival, PhD" ; "Leahy, Catharine (US)" "Lancaster, Mary J CIV (US)" ; "Sander, William E CTR (US)" >; Vivek Kapur Jon Epstein @ecohealthalliance.org>; gavin.smith ; Ian MENDENHALL PhD >; kityrob >; Kading,Rebekah ; Caitlin Devaney >; mary dugan

Subject: Global Bat Alliance Follow-up
Attachment(s): "GBA Database[1].xlsx"

All,

As a follow-up to last week's GBA call, please find a very rough draft spreadsheet of the information we have collected for the GBA. Please take a look and modify or add to the list as needed.

We are in the process of updating the Terms of Reference and will get a second draft of that out to the group in the next day.

V/r,

Katie Leahy

	A	B	C	D
1	Title	Website	Location	Mission
2	African Bat Conservation (ABC)	http://www.africanbatconservation.org	Africa (Malawi)	ABC conducts applied research, conservation, and education to bring bats the conservation agenda and conserve bats in Africa.
3	Bats Without Borders	http://www.batswithoutborders.org	Africa (Namibia, Botswana, South Africa)	Bats Without Borders aims to support research and conservation action, community engagement, and capacity building that contribute to the conservation of southern African bats
4	Health for Animals and Livelihood Improvement (HALI) Project	http://haliproject.org	Africa (Tanzania)	The HALI Project is a collaborative research and capacity building program investigating health at human-animal-environment interfaces in Tanzania. HALI is an international team of researchers, professionals, students, volunteers, and community members working together to better understand the interactions among humans, animals, and their shared environments in Tanzania.
5	Bat Conservation Trust	http://www.bats.org.uk/index.php	Europe (London)	The Bat Conservation Trust supports over 100 local bat groups and 6000 members and works with volunteers, scientists, industry and government both locally and nationally on a range of projects.
6	North American Society for Bat Research (NASBR)	https://www.nasbr.org	North America	NASBR promotes the study and conservation of bats by facilitating communication and collaboration among scientists, educators, and the general public. The society holds an annual meeting called the North American Symposium on Bat Research.
7	Indian Bat Conservation Research Unit (IBCRU)	http://ibcru.org	South Asia (India)	IBCRU is established to provide an organization support for Bat research, conservation, capacity building and outreach in India. It aims to prepare a detailed database on bat ecology in the country.
8	Southeast Asian Bat Conservation Research Unit	http://www.seabcru.org	Southeast Asia	SEABCRU gathers people with existing expertise to share experiences among and countries, refine research and protocols that can lead to integration and synthesis across the region, and link research processes and outputs with conservation effects.
9	Center for International Forestry Research (CIFOR) Bushmeat Research Initiative (BRI)	http://www.cifor.org/bushmeat/	Southeast Asia (Indonesia)	BRI brings together diverse researchers and practitioners to generate and share knowledge on bushmeat harvesting, marketing, and consumption across Latin America, Africa, and Asia. BRI and partner scientists work to strengthen the evidence base for effective interventions and to identify knowledge gaps and main areas where further work is required.
10	Bat Conservation International (BCI)	http://www.batcon.org	USA (headquartered in Austin, Texas and Washington, D.C.)	BCI's mission is to conserve the world's bats and their ecosystems to ensure a healthy planet. The organization conducts work in Africa, Asia, Latin America, Oceania, and USA-Canada regions.

	A	B	C	D	E
1	Last Name	First Name	Organization	5/31/20175/31/2017	Website/ Linkedin
2	Al-Hmoud	Nisreen	Royal Scientific Society (RSS) of Jordan Center for Excellence in Biosafety, Biosecurity, and Biotechnology	nisreen@rss.gov.jo	Linkedin: https://jo.linkedin.com/in/nisreen-al-hmoud-15a0a78b
3	Chaber	Anne-Lise	Zoological Society of London, Royal Veterinary College University of Liège, Belgium	alchaber@hotmail.com	Linkedin: https://www.linkedin.com/in/anne-lise-chaber-17257b3a
4	Daszak	Peter	U.S. EcoHealth Alliance	daszak@ecohealthalliance.org	Website: https://www.mailman.columbia.edu/research/center-infection-and-immunity/peter-daszak-phd
5	Davies	Glyn	WWF-UK (previously Zoological Society of London)	gdavies@wwf.org.uk	Linkedin: https://www.linkedin.com/in/glyn-davies-82691989
6	Demetria	Catalino	Philippine Department of Health - Research Institute for Tropical Medicine (RITM)	c_demetria@yahoo.com.ph	Linkedin: https://ph.linkedin.com/in/catalino-demetria-51636b49
7	Douangngeun	Bounlom	Lao National Animal Health Laboratory (NAHL)	bounlom@gmail.com	
8	Epstein	John	U.S. EcoHealth Alliance	epstein@ecohealthalliance.org	Company website bio: http://www.ecohealthalliance.org/personnel/dr-jonathan-epstein-2 Linkedin: https://www.linkedin.com/in/jonathan-h-epstein-26111723 Twitter: https://twitter.com/epsteinjon
9	Fa	John E.	Center for International Forestry Research (CIFOR) Bushmeat Initiative & Manchester Metropolitan University	jfa949@gmail.com jfa@durrell.org	LinkedIn: https://www.linkedin.com/in/jfa01 CIFOR website: http://blog.cifor.org/author/john-e-fa/ CV: http://www.iccs.org.uk/wp-content/docs/FaCV.pdf
10	Hughes	Tom	U.S. EcoHealth Alliance (Malaysia)	tom.hughes@ecohealthalliance.org	Company website bio: http://www.ecohealthalliance.org/personnel/tom-hughes

	F	G	H
1	Research	Country of Origin	Location of Research
2	Biosafety, Water and Food Safety, Genetically Modified Organisms	Jordan	MENA region
3	transboundary animal diseases, ecosystem health, livestock production system (extensive and intensive), wildlife and livestock's epidemiology as well as zoonotic diseases. Bushmeat importation chains/ trafficking	UAE	UK, UAE, Belgium
4	His achievements include identifying the bat origin of SARS, and the underlying drivers of both Nipah and Hendra virus emergence. He confirmed the first case of a species extinction due to disease, and identified chytridiomycosis as the cause of amphibian declines around the globe.	USA	n/a (disease specific)
5	biodiversity, wildlife conservation, bushmeat trade ("Bushmeat and Livelihoods: Wildlife Management and Poverty Reduction")	UK	Africa (Sierra Leone, Kenya, Cameroon), Southeast Asia (Malaysia)
6	Genetics, Molecular Biology, Evolutionary Biology, Rabies (https://www.researchgate.net/profile/Catalino_Demetria/publications)	Philippines	Philippines
7	Brucellosis, Influenza, Zoonotic Diseases, Rabies	Mongolia (based on his attendance of Mongolian State Univesity for undergrad: http://www.onehealthsea.org/lacanet/coordination-and-partners/partners)	Lao PDR
8	Dr. Jonathan Epstein studies Nipah and Ebola virus, along with SARS, and other diseases that have emerged within Asia and Africa. Jon is part of a large international collaboration that is investigating the ecology of Nipah virus in Bangladesh, where outbreaks occur in people almost every year with mortality rates reaching 100%. The focus of this research is to better understand the factors that cause this lethal virus to emerge, and to develop models to predict and prevent future outbreaks.	USA	Southeast Asia, Africa
9	Zoology, Evolutionary Biology, Biodiversity, Conservation Biology, Human Ecology, Biogeography, Large-Scale Economy, Community Processes, Behavioural Ecology, Vetebrate Ecology (https://www.researchgate.net/profile/John_E_Fa)	England	Africa
10	Study of Zoonotic Infections among Persons Exposed to Wild Animals Tom began working with EcoHealth Alliance in June 2005 on the Nipah virus research project in Malaysia. In 2007, he took on the new role of coordinating the Study of Zoonotic Infections among Persons Exposed to Wild Animals in Malaysia, to determine if close contact with wild animals results in the transfer of zoonotic diseases. In 2010, Tom became the PREDICT Malaysia country coordinator for USAID's Emerging Pandemic Threats program. The aim of this research is to create an early warning system for potential zoonotic disease spillover into livestock and humans. Tom is working closely with partners from the Ministry of Health, the Department of Wildlife and National Parks, the Department of Veterinary Services, Sabah Wildlife Department and local universities to develop personnel and laboratory capacity and establish sustainable disease surveillance systems.	England	Southeast Asia (Malaysia)

	A	B	C	D	E
11	**Kading**	Rebekah	Uganda CDC/ Colorado State University	Rebekah.Kading@colostate.edu	Linkedin: https://www.linkedin.com/in/rebekah-kading-63453556
12	**Karesh**	William	U.S. EcoHealth Alliance	karesh@ecohealthalliance.org	Company website bio: http://www.ecohealthalliance.org/personnel/dr-william-karesh Linkedin: https://www.linkedin.com/in/williamkaresh Twitter: https://twitter.com/dr_wildlife
13	**Kilonzo**	Christopher	University of California, Davis HALI Project (Health for Animals and Livilihood Improvement)	ckilonzo@ucdavis.edu	University Bio: http://www.wifss.ucdavis.edu/?page_id=673 LinkedIn: https://www.linkedin.com/in/christopher-kilonzo-01158334
14	**Kityo**	Robert	Makere University/ Uganda	kityrob@gmail.com	Linkedin: https://www.linkedin.com/in/robert-kityo-8a288a39
15	**Kupur**	Vivek	Penn State University/ Tanzania	vkapur@psu.edu	Linkedin: https://www.linkedin.com/in/vivek-kapur-6290649a
16	**Lee**	Tien Ming	Princeton University	tienl@princeton.edu tienminglee@gmail.com	Researcher Bio: http://cred.columbia.edu/about-cred/people/affiliated-researchers/tien-ming-lee/ CV: http://cred.columbia.edu/files/2015/02/TLee_CV_for_CRED.pdf
17	**Linder**	Joshua	James Madison University	linderjm@jmu.edu	Institution Staff Profile: http://www.jmu.edu/socanth/anth/linderj.shtml Personal website: http://www.joshua-linder.com/
18	**Mazet**	Jonna	University of California, Davis HALI Project (Health for Animals and Livilihood Improvement)	jkmazet@ucdavis.edu	University Bio: http://www.vetmed.ucdavis.edu/faculty/results.cfm?fid=14802
19	**Mendenhall**	Ian	Singapore Duke-NUS	ian.mendenhall@duke-nus.edu.sg	Linkedin: https://www.linkedin.com/in/ian-mendenhall-0391ab23
20	**Nasi**	Robert	Center for International Forestry Research (CIFOR) Bushmeat Initiative	r.nasi@cgiar.org	LinkedIn: https://id.linkedin.com/in/robert-nasi-5338b650 CIFOR Bio: http://www.cifor.org/scientific-staff-detail/984/robert-nasi/

	F	G	H
11	Research studies on virus discovery and arbovirus surveillance of bats in Uganda, Entebbe bat virus, bat biosurveillance, Zika	USA	Africa
12	Zoonotic disease research; animal and human health linkages with wildlife Global surveillance systems for emerging diseases Impact reduction efforts for diseases such as Ebola, measles and tuberculosis on humans and endangered animal species (Congo basin)	USA	over 45 countries from Argentina to Zambia
13	Epidemiology and ecology of zoonotic foodborne pathogens in domestic ruminants and synanthropic wild animals https://www.researchgate.net/profile/Thomas_Stopka/publication/259494854_Illegal_animal_and_bush_meat_trade_associated_risk_of_spread_of_viral_infections/links/56711f0608ae5252e6f3d68f.pdf	Kenya	Africa (Tanzania)
14	Ebola, Entebbe bat Virus, bat biodiversity research, bat biosurveillance research, wildlife ecology/ biology, zoology	Uganda	Africa
15	Molecular biology, microbial pathogenomics: including host response to infection, molecular epidemiology: including the study of population genetics of microbes,	India	Africa
16	Bushmeat in East, South, and Southeast Asia https://books.google.com/books?hl=en&lr=&id=lnWTCgAAQBAJ&oi=fnd&pg=PP5&dq=bushmeat+asia&ots=LJRXRw8ETB&sig=Imrmzg-QwV7Z1cWEnalvhJ9XU20#v=onepage&q=bushmeat%20asia&f=false	Singapore	Asia
17	bushmeat hunting, trade and consumption long term research program in Cameroon Taylor , G., Scharlemann, J.P.W., Rowcliff, M.,…Linder, J.M., et al. (accepted). Synthesising bushmeat research effort in West and Central Africa: an introduction to a new regional database. Conservation Biology.	USA	Cameroon
18	Epidemiology, One Health, Pathogen Pollution, Marine and Coastal Conservation, Emerging Infectious Diseases, Land Use Change, Climate Variability, Wildlife Health	USA	Africa (Tanzania), Nepal, India
19	bat-borne pathogen surveillance, virus evolution, Astrovirus, Ebola, viral immunity	USA	Southeast Asia
20	Sustainable use of tropical forests, more sustainabile livelihoods and better designated forest policies. (https://www.researchgate.net/profile/Robert_Nasi)	France	Africa, Asia, & the Pacific

	A	B	C	D	E
21	**Nichol**	Stuart	U.S. CDC, Viral Special Pathogens Branch (VSPB)	stn1@cdc.gov	CDC branch website: https://www.cdc.gov/ncezid/dhcpp/vspb/
22	**Olival**	Kevin	U.S. EcoHealth Alliance	olival@ecohealthalliance.org	Company website bio: http://www.ecohealthalliance.org/personnel/dr-kevin-j-olival Linkedin: https://www.linkedin.com/in/kevin-olival-4986237 Twitter: https://twitter.com/nycbat
23	**Paige**	Sarah	University of Wisonsin-Madison & Public Health Institute	spaige1@gmail.com sarah.paige@wisc.edu	Company Website: http://ghi.wisc.edu/person/paige-sarah/ LinkedIn: https://www.linkedin.com/in/sarahpaige
24	**Pinedo-Vasquez**	Miguel	Columbia University & Center for International Forestry Research (CIFOR)	map57@columbia.edu	University Bio: http://www.columbia.edu/~map57/Pinedo_vasquez.html LinkedIn: https://www.linkedin.com/in/miguel-pinedo-vasquez-89740151
25	**Rowcliffe**	Marcus	Institute of Zoology, Zoological Society of London	marcus.rowcliffe@ioz.ac.uk	https://www.zsl.org/users/marcus-rowcliffe
26	**Scharlemann**	Jorn	University of Sussex	J.Scharlemann@sussex.ac.uk	Twitter: https://twitter.com/jpws2 http://www.sussex.ac.uk/lifesci/scharlemannlab/index
27	**Sigouin**	Amanda	Center for Biodiversity and Conservation (CBC)	asigouin@amnh.org	CBC Staff profile: http://www.amnh.org/our-research/staff-directory/amanda-sigouin/
28	**Simon**	Edson	Philippine Department of Health - Research Institute for Tropical Medicine (RITM)	Email sent to RITM requesting contact info	Linkedin: https://www.linkedin.com/in/edson-michael-simon-09861942

	F	G	H
21	Viral special pathogens; Highly infectious disease research; molecular virology; microbiology and immunology Ebola virus, Marburg virus, Lassa fever virus, Rift Valley fever virus, Crimean-Congo hemorrhagic fever virus, other Arenavirus and Hantavirus species, and additional recently identified and emerging viral species.	USA	Africa
22	Dr. Olival has been at the forefront of recent international investigations to understand the origins and transmission pathways of: Middle East Respiratory Syndrome coronavirus (MERS-CoV) in Saudi Arabia; Ebola Reston virus in the Philippines; and Nipah virus in Bangladesh and Malaysia. He has managed wildlife conservation and disease research projects across Southeast Asia for over 10 years, with a strong focus on bat research. Dr. Olival's role as Senior Research Scientist at EcoHealth Alliance involves coordinating the modeling and analytics research; integrating evolutionary and ecological theories to understand the drivers of disease emergence; and managing zoonotic disease surveillance efforts in Thailand and Indonesia under the USAID PREDICT project.	USA	Southeast Asia
23	"Beyond Bushmeat: Animal Contact, Injury, and Zoonotic Disease Risk in Western Uganda" (https://www.researchgate.net/profile/Sarah_Paige) (https://www.researchgate.net/profile/Sarah_Paige/publications) (http://research-information.bristol.ac.uk/files/32571511/Beyond_Bushmeat_Manuscript_EcoHealth_2014.pdf)	USA	Uganda
24	Bushmeat harvest, patterns and effects of smallholder management of tropical ecosystems and landscapes. https://books.google.com/books?hl=en&lr=&id=BsTHBQAAQBAJ&oi=fnd&pg=PP5&dq=bushmeat+asia&ots=2mxM45mWPk&sig=8lwKN1eQi0mOZwN2X1WqGRnDF0M#v=onepage&q=bushmeat%20asia&f=false	USA (unconfirmed)	Amazonia
25	Modelling bushmeat harvesting systems, trade and sustainability along a Ghanian bushmeat commodity chain, bushmeat supply chains (Guinea), surveying bushmeat cupply and demad in the Sanaga-Cross region of Nigeria and Cameroon, bushmeat survey/studies in Sierra Leone, Roads andbushmeat trade in Gabon, Monitoring international bushmeat trade- imports to Europe	UK	Scotland / Madagascar/ West & Central Africa
26	Modelling global biodiversity and ecosystems	UK	UK, Panama
27	Wildlife trade, bushmeat in Asia with a focus on local livelihoods, biocultural approaches to conservation, capacity development and all aspects of the wildlife trade http://www.amnh.org/our-research/staff-directory/amanda-sigouin/	USA	Asia
28	Rabies Resarch Group: umaresearch on human and animal rabies using a One-Health approach. It aims to provide support to the National Rabies Prevention and Control Program of the Departments of Health and Agriculture through its multi-disciplinary research activities, laboratory capabilities, rabies referral center and animal bite clinic, training programs, advocacy and as technical advisers to the program. The current focus of research activities include clinical trials on human biological products, epidemiology of human rabies, analysis of treatment failures, dog ecology studies, molecular epidemiology and development/evaluation of diagnostic tests/reagents. Ebola related Laboratory Waste Management, Decontamination and Laboratory Emergencies	Philippines	Philippines

	A	B	C	D	E
29	**Swamy**	Varun	Duke University & San Diego Zoo Institute for Conservation Research	varunswamy@gmail.com	Website: mddforestdynamics.org CV: http://mddforestdynamics.org/wp-content/uploads/2016/10/VARUN-SWAMY-CV.pdf
30	**Swanepoel**	Bob	University of Pretoria	bob.swanepoel@up.ac.za	University Page: http://www.up.ac.za/the-genomics-research-institute/article/1929285/speakoutup
31	**Vora, MD**	Neil	Centers for Disease Control and Prevention	wii8@cdc.gov nvora@health.nyc.gov	Speaker Bio: https://www.aspenideas.org/speaker/neil-vora Twitter: https://twitter.com/neilvora_md
32	**Wacharapluesadee**	Supaporn	Nueroscience Center for Research and Development, WHO Collaborating Center for Research and Training in Viral Zoonoses at Chulalongkorn University	spwa@hotmail.com	Linkedin: https://th.linkedin.com/in/supaporn-wacharapluesadee-377ba755 Conference Bio: http://www.pmaconference.mahidol.ac.th/index.php?option=com_docman&task=doc_download&gid=763
33	**Wade**	Abel	Cameroon National Veterinary Laboratory (LANAVET)	abelwade@gmail.com	Linkedin: https://cm.linkedin.com/in/wade-abel-56261932
34	**Watt**	Frank	Duke - National University of Singapore (NUS) Centre for Ion Beam Applications Professor	gmsfw@nus.edu.sg (https://myaces.nus.edu.sg/srd/BrwsStfDtl?STF=226) phywattf@nus.edu.sg (http://www.ciba.nus.edu.sg/pages/people_academic.html)	
35	**Wright**	Scott	USGS	swright@usgs.gov	https://www.nwhc.usgs.gov/staff/scott_wright.jsp

	F	G	H
29	Regeneration dynamics of tropical forests, plant-animal interactions, effects of hunting-induced defaunation on forest plant communities, DNA barcoding and phylogenetic analysis, demographic modeling, interdisciplinary strategies for maintaining ecological integrity of tropical forests. Bushmeat harvest in tropical forests: Knowledge base, gaps and research priorities (http://www.cifor.org/library/5098/bushmeat-harvest-in-tropical-forests-knowledge-base-gaps-and-research-priorities/)	USA	Peru
30	Virology, Ebola, Marburg virus, Duvenhage virus, Lassa fever, Rift Valley fever and Crimean-Congo haemorrhagic fever Zoonotic and vector-borne agents as cause of undiagnosed disease of humans, farm and wild animals in southern Africa; pathogen discovery; development of microbiological/molecular and immunological investigatory tools; epidemiology of vector-borne diseases including seasonal circulation of agents in vectors and vertebrates, and the role of climate	South Africa	Africa
31	Zoonotic diseases, Emerging Infectious Diseases, "Assessment of potential zoonotic disease exposure and illness related to an annual bat festival," "Human Infection with a Zoonotic Orthopoxvirus in the Country of Georgia," Raccoon rabies virus variant transmission through solid organ transplant." (http://europepmc.org/abstract/med/24739343) (https://www.researchgate.net/profile/Neil_Vora)	USA (unconfirmed)	Africa
32	Viral Encephalitis and Zoonoses (https://www.researchgate.net/profile/Supaporn_Wacharapluesadee)	Thailand	Southeast Asia
33	Microbiology, Epideiological Analysis, Agricultural Science, Contagious Bovine Pleuropneumonia (https://www.researchgate.net/profile/Wade_Abel)	Cameroon (unconfirmed)	Cameroon
34	Applying nuclear-based physics to biomedical problems, development of proton beam technology (proton microscopy and proton beam writing) and applications in biomedicine (https://www.researchgate.net/researcher/38914183_Frank_Watt)	England	England / Singpore
35	Biotoxins, comparative veterinary pathology, diseases of marine mammals, wildlife disease ecology	USA	USA

	A	B	C	D
1	Title	Author	Publish Date	Summary Review
2	"Bat Astroviruses: Towards Understanding the Transition Dynamics of a Neglected Virus Family	Kerstin Fischer	17-Feb-17	This article overviews current findings regarding Astroviruses in bats, humans, and livestock. Since 2008, a growing number of bat species have been found to carry Astroviruses with a noticeable prevalence and diversity. Fischer calls for virologists, bat ecologists, and zoologists to create an interdisciplinary research environment for Astroviruses, specially those transmitted by bats.
3	Identification of a Lineage D Betacoronavirus in Cave Nectar Bats in Singapore and an Overview of Lineage D Reservoir Ecology in SE Asian Bats"	Ian Mendenhall	16-Sep-16	Bats are reservoirs for several different coronaviruses that lead to SARS and MERS outbreaks. This article examined bat urine and feces to look for coronavirus sequences in six species of bats. They found a new strain closely related to D Betacoronavirus. The study helped scientists better understand coronavirus evolution and host specificity.
4	Flavivirus Infections of Bats: Potential Role in Zika Virus Ecology"	Rebekah Kading	22-Aug-16	Kading studies bats with flaviviruses as vectors contributing to emerging viruses in human populations and the potential role of bats in the sylvatic transmission of Zika virus.
5	"Optimizing Viral Discovery in Bats"	Cristin Young, Dr. Kevin Olival	11-Feb-16	This article synthesizes the published data from 2007-2013 on viral discovery studies in bats. They specifically examine factors that increase success of viral discovery in bats while also studying particular trends and patterns of infection across host taxa and viral families. They found that detection methods have changed, with a decrease in serological assays such as ELISA, and an increase in the use of molecular methods, primarily PCR. Lethal sampling does not appear to increase success in obtaining positive viral detection. Viral prevalence and detection vary by specimen type and host taxonomy, therefore increasing the number of bat species sampled is likely to increases the number of viruses found.
6	Molecular evidence of Ebola Reston virus infection in Philippine bats	Tom Hughes	17-Jul-15	This article provides the results of a surveillance mission conducted in order to gather evidence of Ebola Reston virus in Philippine Bats. The team surveyed multiple locations across the country and used serology as well as molecular assays to test for infections. In all, 464 Bats representing 21 different species were captured and tested. Of the samples captured and tested in Bulatan, all sera were negative, and all swabs were negative. 5 oropharyngeal swabs produced potentially positive results, with 3 full positive (all positive results came from the same species Miniopterus schreibersii). The samples showed a close relationship to sequences found in Philippine pigs, off by one single nucleotide. This relationship poses a serious risk due to recent discovery of Ebola in Chinese pigs. The team concluded that Ebola virus infection is taxonomically widespread in Philippine bats, but more surveillance needs to be conducted in order to pin down specific geographic regions and specific species.
7	"Detection of Entebbe Bat Virus After 54 Years"	Rebekah Kading, Robert Kityo	8-May-15	Kading and Kityo studied the evolution of the Entebbe (ENTV) bat virus from 1957 to 2011 to determine ecological and genetic factors influencing the evolution and transmission of bat and mosquito borne flaviviruses. They created a maximum likelihood tree based on nucleotide frame sequencing. Studying the patterns and evolution of ENTV may provide insight into the ecological and genetic factors influencing the evolution and transmission of other bat-borne and mosquito-borne flaviviruses.
8	"Characteristics and Risk Perceptions of Ghanaians Potentially Exposed to Bat-Borne Zoonoses through Bushmeat"	Alexandra Kamins, J Rowcliffe	30-Sep-14	The authors interviewed 577 Ghanaians to identify the characteristics of bat hunters and consumers, and the perceived risk of people involved in the bat-bushmeat trade. Interviewees held little belief of disease risk from bats and the authors found notable discrepancies between stated preference and reported behaviors. Identifying gaps in perceived risk and actual risk can inform management plans and draw on social context and gender roles to best mitigate the spread of disease. It also allows for targeted education initiatives to correct misconceptions about demand and risk associated with bat meat.
9	"Filoviruses in Bats: Current Knowledge and Future Directions"	Kevin Olival, David Hayman	17-Apr-14	Olival and Hayman review the ecology, epidemiology, and natural history of Filoviruses, specifically Ebolavirus and Marburgvirus. They conclude by emphasizing the need for unified, global surveillance for filo viruses in wildlife and advocate for more multi-disciplinary approach to understand the dynamics in bat populations that lead to outbreaks.

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1	Source Format	URL	Location	CBEP Region	Focus Area	Tags
2	Journal Publication	https://www.google.com/url?sa=t&rct=j&q=&esrc=s&source=web&cd=3&ved=0ahUKEwif8ouez5rUAhUJKyYKHYUzAQ4QFgg2MAI&url=http%3A%2F%2Fwww.mdpi.com%2F1999-4915%2F9%2F2%2F34%2Fpdf&usg=AFQjCNHce6WEbBcRdqxmCfMt3In7bcCT2Q	n/a (global)	n/a	Virus / host relationship	astrovirus
3	Journal Publication	http://onlinelibrary.wiley.com/doi/10.1111/tbed.12568/full	Singapore	PACOM	Virus / host relationship	SERS, MERS, coronavirus
4	Journal Publication	http://www.ajtmh.org/content/95/5/993.short	n/a (global)	n/a	Virus / host relationship	flavivirus, Zika
5	Journal Publication	http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0149237	n/a	n/a	Virus / host relationship	ELISA, viral discovery
6	Journal Publication	http://virologyj.biomedcentral.com/articles/10.1186/s12985-015-0331-3	Philippines	PACOM	Bat, livestock ,and wildlife interactions	Ebola Reston, pigs
7	Journal Publication	http://www.ajtmh.org/content/93/3/475.long	Uganda	AFRICOM	Virus / host relationship	Entebbe, ENTV, flavivirus,
8	Journal Publication	http://link.springer.com/article/10.1007/s10393-014-0977-0	Ghana	AFRICOM	Commodity chain and trade routes	Bushmeat, trade, gender roles
9	Journal Publication	http://www.mdpi.com/1999-4915/6/4/1759Filoviruses	n/a	n/a	Ecological change and effects	Ecology, filovirus

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10	Foraging Behaviour and Landscape Utilisation by the Endangered Golden-Crowned Flying Fox (Acerodon jubatus), The Philippines	Tom Hughes	21-Nov-13	This article details a study conducted to better understand the foraging behavior and travel patterns of the Golden Crown Flying Fox (Acerodon jubatus) in the Philippines. Understanding these patterns is vital to efforts of conservation of the endangered species, and predicting disease/virus emergence. The team captured multiple flying foxes in order to log body characteristics, test for disease and viruses, and imbed a gps tracking logger. The loggers revealed repetitive travel patterns to numerous foraging sites. The repetitious behavior causes an increased excretion of viral loads on feed and landscape that can lead to transmission to other wildlife leaving humans vulnerable to exposure. New foraging sites were discovered during the study that are close to popular roadways and human travel. Regional discoveries of zoonosis in related species in neighboring Indonesia reveal a risk of spreading Nipah and SARS.
11	"Middle East Respiratory Syndrome Coronavirus in Bats, Saudi Arabia"	Ziad memish, Kevin Olival, John Epstein	Nov-13	Bat CoVs are typically host specific, however, MERS-related CoVs have reportedly been found in many bat families. The authors created a phylogenetic tree showing genetic relatedness between coronaviruses identified in bat samples. The team tested bats in Saudi Arabia for the MERS CoV sequence and determined the prevalence of MERS in the area. The MERS CoV sequence was only detected in one bat but a broad distribution of MERS cases were found throughout the Middle East, thus denoting the possiblity of hosts other than bats. Future work should investigate additional bat and other wildlife species and domestic animals for CoV infection and potential linkage to human disease.
12	Risk Factors for Nipah Virus Infection among Pteropid Bats, Peninsular Malaysia	Tom Hughes	1-Jan	This article details a cross-sectional and longitudinal study to determine distribution of seropositivity to Nipah Virus among vampryrus and hypomelanus bats in peninsular Malaysia. The study found that the Pteropus species serves as the natural reservoir for NiV in Malaysia. The study showed that seroprevalence of NiV was higher in female bats that were pregnant, carrying a pup, and lactating. The study shows that vampryus bats are more commonly seropositive due to high mobility coupled with cross-border movement.
13	"A Longitudinal Study of the Prevalence of Nipah Virus in Pteropus lylei Bats in Thailand: Evidence for Seasonal Preference in Disease Transmission	Supaporn Wacharapluesadee	1-Mar	Over 90% of Nipah outbreaks have occurred during the first 5 months of the year and morbidity and mortality have increased in subsequent outbreaks. Although direct contact during breeding was believed to be an important transmission factor, this study seems to show that there may be other mechanisms responsible for transmission than direct contact during breeding in the same roost. Greater virus shedding over extended periods of time and the highest peak of virus detection in May when offspring start to separate may suggest that there may be mechanisms other than direct contact during breeding that cause spillover. Knowledge of seasonal preferences will help to better explain the dynamics of Nipah virus transmission and have implications for disease management
14	"*Pteropus vampyrus*, a hunted migratory species with a multinational home-range and a need for regional management"	John Epstein, Kevin Olival	25-Aug-09	This article looks at the challenges of managing migratory species that pose a threat to public health, specifically relating to the Malayan flying fox Pteropus vampyrus. Bats often move across borders within Southeast Asia and require regional management plans across their migratory range. This species of bat is also often hunted for food, sport, and medicine. Epstein et al. used roost site surveys, satellite telemetry, and data from hunter license sales and population protection models to assess the current sustainability of the flying fox population.
15	"Bats as bushmeat: a global review"	Simon Mickleburgh, Kerry Waylen, Paul Racey	1-Apr-09	This questionnaire and literature review gives an overview of bat hunting in the Old World tropics. Fruit bats of the genus Pteropus are the most widely eaten in Asia, likely because they roost in fruit trees and their whereabouts are predictable. Voluntary controls on hunting have assisted in preserving bat populations. The authors recommend continued surveys of the extent to which bats are used as bushmeat to inform conservation and health efforts. These surveys will help indicate why the meat is in demand, the effectiveness of regulation, and where to fill in gaps of education.
16	"Studies of Reservoir Hosts for Marburg Virus"	Robert Swanepoel	Dec-07	The authors examined a mine in northeastern Democratic Republic of the Congo to determine the hosts likely responsible for an outbreak of Marburg hemorrhagic fever. There was a clear link between breeding patterns of the bats and the occurrence of Marburg hemorrhagic fever. Outcome of virus infection, carrier status, and shedding of virus are influenced by bat age, reproductive status, diet, and type of bat. An evolutionary distinction may exist between cave-roosting bats as hosts of MARV and forest bats as host of Ebola virus. The authors recommend experimental infections in colonized bats to provide more clarity.

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10	Journal Publication	http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0079665	Philippines	PACOM	Ecological change and effects	Acerodon jubatus,
11	CDC Emerging Infectious Diseases Journal	https://wwwnc.cdc.gov/eid/article/19/11/13-1172_article	Saudi Arabia	CENTCOM	Virus / host relationship	CoV, Saudi Arabia, MERS
12	Journal Publication	https://www.researchgate.net/publication/233974164_Risk_Factors_for_Nipah_Virus_Infection_among_Pteropid_Bats_Peninsular_Malaysia	Malaysia	PACOM	Virus / host relationship	Nipah, hypomelanus
13	Journal Publication	http://online.liebertpub.com/doi/abs/10.1089/vbz.2008.0105	Thailand	PACOM	Virus / host relationship	Nipah, Pteropus lylei, Thailand
14	Journal Publication	http://onlinelibrary.wiley.com/doi/10.1111/j.1365-2664.2009.01699.x/full	Malaysia (SEA)	PACOM	Bat, livestock ,and wildlife interactions	Pteropus vampyrus, Malaysia
15	Journal Publication	https://www.researchgate.net/publication/231949029_Bats_as_Bushmeat_A_Global_Review	n/a (global)	n/a	Commodity chain and trade routes	Pteropus, fruit bat. Hunting
16	CDC Emerging Infectious Diseases Journal	https://wwwnc.cdc.gov/eid/article/13/12/07-1115_article	Democratic Republic of the Congo	AFRICOM	Virus / host relationship	Congo, Marburg hemorrhagic fever, MARV, cave-roosting

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17	"Bat Nipah Virus, Thailand"	Supaporn Wacharapluesadee	Dec-05	Scientists surveyed Thailand s bat population to test for Nipah virus. Nipah virus RNA was found in bat saliva and urine, suggesting the persistence of Nipah virus infection in Thai bats. Many of the Thai bat species that carry the Nipa virus antibodies live near the borders of Malaysia and Cambodia. Countrywide surveillance is therefore needed to clarify the epidemiology of Nipah virus infections in relation to host, seasonal, and geographic attributes.
18	"Quantifying the Bat Bushmeat Trade in North Sulawesi, Indonesia, with Suggestions for Conservation Action"	Susan M. Tsang	1/26/2015	Tsang desired to assess local cultural attitudes towards bats for the formulation of a targeted conversation campaign. The article discusses the conducted survey and results, suggesting church engagement, student ambassador programs, meat substitution, and local conservation initiatives as potential next steps of conservation action.
19	"Understanding the Bushmeat Market: Why Do People Risk Infection from Bat Meat?"	Olivier Restif, James Wood, Alexandra Kamins	9-Oct-14	This article discusses the findings of Dr. Kamins and her colleages after they interviewed 577 people across southern Ghana, including hunters, vendors, and consumers of bat meat. Hunters use a variety of means to capture bats, but none reported using any sort of protective measures while hunting. Cooking bats is also done in a variety of ways, as the bushmeat serves as both subsistence and luxury food. The article concludes by calling for partnerships with local communities in Ghana to help find effective and sustainable solutions which align with economic needs.
20	Wildlife Trade and Human Health in Lao PDR: An Assessment of the Zoonotic Disease Risk in Markets.	Bounlom Douangngeun	23-Mar-16	This article is an assessment of the zoonotic disease risk of the bushmeat trade in Lao PDR. An observational survey was conducted from 2010-2013 in order to gather details about the volume of bushmeat markets, species sold, price, and market biosafety. Seven markets with the highest volumes were included in the study; 1,937 animals representing twelve different taxonomic families were observed for sale. The 12 taxonomic families represented have been documented to carry over 36 zoonotic pathogens. The 36 diseases documented include: rabies, SARS, Leptospirosis and Tuberculosis. Insectovous Bats were one of the taxa families observed, known to host 9 different zoonotic pathogens. The author noted a strong possibility of humans spreading the diseases due to high volume of regional and foreign visitors to the markets, and poor biosafety measures of the market (lack of hand washing and cleaning of tables, generally poor market cleanliness, selling wildlife alongside other fresh produce presents risks for food contamination and infection of humans with pathogens).
21	The Prevalence of Contagious Bovine Pleuropneumonia (CBPP) in Cameroon: A Case Study in Garoua Central Abattoir, Cameroon	Wade Abel	1-Jan-16	This article discusses the findings of a year long prevalence study of contagious bovine pleuropneumonia (CBPP) conducted among slaughtered cattle in Cameroon. The article includes a breakdown of the different species of cattle and the rate of prevalence of each species. The prevalence rate was astronomically greater in cattle between the ages of 5-10 as compared to cattle aged 0-5 and 10 years and above. CBPP is a chronic disease, meaning more cattle harbor the causative agent with time due to multiple exposure. The age at which the prevalence rate is greatest is also the age at which slaughter is greatest due to quantity of meat to be harvested. The results prove the endemic nature of CBPP, and the prevalence rates observed in Cameroon are significantly higher than Nigeria.
22	Eating and conserving bushmeat in Africa	John E. Fa, Robert Nasi	12/16/2015	This article plots a map of the most favorable regions for Ebola in Africa. The authors used known environmental and zoogeographic descriptors and biogeographic approaches; mainly, the authors used current models for Ebola distribution in Africa, and the mammalian distribution. The authors started out by mapping the environmentally favored regions for Ebola, then mapped the areas of expected exposure in mammals. The map shows that mammalian biogeography contributes to explaining distribution of Ebola; Ebola is more widespread than initially predicted. The goal of the article is to show the importance of biogeography in collaboration with virologacial, zoogeographical, and environmental information. Article states the importance of the role the bush meat market plays in the transmission of Ebola from wildlife to humans.
23	"Long-Term Urban Market Dynamics Reveal Increased Bushmeat Carcass Volume Despite Economic Growth and Prospective Environmental Legislation on Bioko Island, Equatorial Guinea"	Drew Cronin, Joshua Linder	31-Jul-15	This article analyzed the dynamics of the bushmeat market on Bioko Island, Equatorial Guinea in the context of economic growth, political events, and changes in legislation. Bushmeat hunting and availability increased as GDP and disposable income increased. They believe the emergence of a luxury market was driven by the immigration of people non-native to Bioko with a cultural preference for bushmeat. Hunting also increased following unenforced legislation.

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17	CDC Emerging Infectious Diseases Journal	https://wwwnc.cdc.gov/eid/article/11/12/05-0613_article	Thailand	PACOM	Virus / host relationship	Nipah, Thailand, Malaysia, Cambodia
18	Journal Publication	http://www.sciencedirect.com/science/article/pii/S2351989415000049	Indonesia	PACOM	Commodity chain and trade routes	Indonesia,
19	Journal Publication	http://www.cam.ac.uk/research/news/understanding-the-bushmeat-market-why-do-people-risk-infection-from-bat-meat	Ghana	AFRICOM	Commodity chain and trade routes	Ghana, hunting, cooking
20	Journal Publication	http://www.pubfacts.com/detail/27008628/Wildlife-Trade-and-Human-Health-in-Lao-PDR-An-Assessment-of-the-Zoonotic-Disease-Risk-in-Markets	Lao PDR	PACOM	Commodity chain and trade routes	Lao PDR, trade market
21	Journal Publication	https://www.researchgate.net/publication/290136798_The_Prevalence_of_Contagious_Bovine_Pleuropneumonia_CBPP_in_Cameroon_A_Case_Study_in_Garoua_Central_Abattoir_Cameroon	Cameroon	AFRICOM	Bat, livestock ,and wildlife interactions	Contagious Bovine Pleuropneumonia, Cameroon
22	Journal Publication	https://www.researchgate.net/publication/309636107_Eating_and_conserving_bushmeat_in_Africa	Africa (generally)	AFRICOM	Bat, livestock ,and wildlife interactions	Ebola
23	Journal Publication	http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0134464	Equatorial Guinea	AFRICOM	Commodity chain and trade routes	Equatorial Guinea, market

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24	Ebola and bushmeat: myth and reality	John E. Fa	20-May-15	The author addresses some common misconceptions about bush meat and its connection to the spread of the Ebola Virus. First, the article addresses the threat Ebola poses on human populations. While the outbreak is severe, the death toll is estimated to cease at 10,000 as compared to 500,000 from malaria. Bush meat is key mechanism from which humans come in contact with pathogens, however, it is not a major risk for spreading Ebola to new areas such as the U.S. and Europe via the bush market due to long travel times and the common process of smoking the meat; the greater threat for transmission to new areas is person to person contact. Bats play a large role in transmitting pathogens; however, Ghana trades 100,000 bats per year for bush meat and yet has no cases of Ebola despite the presence of Ebola in the bats there.
25	"Synthesizing Bushmeat Research Effort in West and Central Africa: A New Regional Database"	G Taylor, J Scharlemann, Marcus Rowcliffe, Noelle Kumpel, Joshua Linder	Jan-15	The authors created a database for bushmeat off take, consumption, and trade in West and Central Africa. They collected data on 177 species from 275 sites across 11 countries over 30 years. The database helps identify patterns and drivers of bushmeat harvesting as well as informing future research priorities.
26	The harvest of wildlife for bushmeat and traditional medicine in East, South and Southeast Asia: Current knowledge base, challenges, opportunities and areas for future research	Tien Ming Lee, Robert Nasi, Miguel Pinedo-Vasquez	11-Nov-14	This paper provides an overview of the bushmeat market in Asia, with particular attention to the Southeast Asia region. The author outlines the bushmeat crisis currently facing the continen and defines the crisis as the overexploitation of wildlife and the recognition that the outcomes are undesirable both for conservation efforts as well as sociocultural needs. Large volumes of bushmeat transport, such as the illegal trade network that exist in most countries of Asia, leave the continent vulnerable to the spread of pathogens. As it pertains to Southeast Asia, the high concentration of illegal wildlife trade make the region a hotspot for future emerging infectious diseases. Solutions for limiting the illegal bushmeat trade include community education on risk factors that coincide with consumption, such as the SARS epidemic. The key to limiting the spread of infectious pathogens through bushmeat is to stop the illegal market and have all trade regulated by increasing border security.
27	"Beyond Bushmeat: Animal Contact, Injury, and Zoonotic Disease Risk in Western Uganda"	Sarah Paige	25-Mar-14	Paige examines activities other than hunting that bring people into contact with wildlife in sub-Saharan Africa, focusing on patterns of injuries from animals and contact with nonhuman primates. The study found that men are at higher risk for animal injury than women, and people living near forest habitats are at highest overall risk. Unlike similar studies, Paige found that touching a carcass was the primary form of primate contact in her population as opposed to butchering or eating bushmeat. This study shows that risky contact with wildlife occurs in landscapes other than forests with routine bushmeat hunting.
28	"Illegal Animal and (Bush)Meat Trade Associated Risk of Spread of Viral Infections"	Christopher Kilonzo	1-Jan-14	This article is a review of collaborative research done into the bushmeat industry around the globe. The issue lays with the developing high demand of bushmeat in developed countries. An increase in the demand leads to attempts to increase supply, furthering the amount of human contact with bush meat through hunting, butchering, and consumption. The expanded industry increases cross-species contact and transmission of diseases. The cross-species contact of Non Human Primates is believed to be the origin of Ebola. The problem is widespread in Southeast Asia specifically due to densely populated areas and access to biologically diverse ecosystems. Bush meat trade is also believed to be the origin of HIV/AIDS. The path forward includes culturally appropriate health education, conservation efforts, supply/demand focused intervention, and a surveillance tool.
29	"The bushmeat trade in African savannas: Impacts, drivers, and possible solutions"	Peter Lindsey, Guy Balme, Matthew Decker	Apr-13	This article looks at the spatial and temporal trends in occurrence of bushmeat hunting. Patterns include focusing efforts on protected areas with rarer animals, and areas where wildlife congregate such as near water, game trails, or fruit trees. Factors found to facilitate the bushmeat trade include political instability and demand for wildlife for traditional use. Potential solutions include incentivizing alternative livelihoods, providing alternative protein and carbohydrate supplies, and enforcing land-use regulations and protections. Combinations of various interventions are necessary and may vary among sites.
30	"Uncovering the fruit bat bushmeat commodity chain and the true extent of fruit bat hunting in Ghana, West Africa"	A. Kamins, Marcus Rowcliffe	Dec-11	The authors study the mechanisms by which bushmeats get to consumers, specifically following the African straw-colored fruit bat Eiodlon helvum. They estimate 128,000 bats are sold each year. Bats do not follow the normal commodity chain for bushmeat and are primarily sold through markets places (not restaurants) which makes bats often overlooked and underrepresented by many surveys.

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24	Journal Publication	https://www.researchgate.net/publication/276937390_Ebola_and_bushmeat_myth_and_reality	n/a	n/a	Commodity chain and trade routes	Ebola, market
25	Journal Publication	http://www.sciencedirect.com/science/article/pii/S0006320714004182	Africa	AFRICOM	Commodity chain and trade routes	trade market
26	Journal Publication	https://play.google.com/store/books/details?id=lnWTCgAAQBAJ&rdid=book-lnWTCgAAQBAJ&rdot=1&source=gbs_vpt_read&pcampaignid=books_booksearch_viewport	Asia (generally)	PACOM	Commodity chain and trade routes	trade market
27	Journal Publication	http://research-information.bristol.ac.uk/files/32571511/Beyond_Bushmeat_Manuscript_EcoHealth_2014.pdf	Africa (sub-Saharan)	AFRICOM	Bat, livestock ,and wildlife interactions	human contact, uganda
28	Journal Publication	https://www.researchgate.net/profile/Thomas_Stopka/publication/259494854_Illegal_animal_and_bush_meat_trade_associated_risk_of_spread_of_viral_infections/links/56711f0608ae5252e6f3d68f.pdf	Africa (generally)	AFRICOM	Commodity chain and trade routes	trade market, ebola, HIV/AIDS
29	Journal Publication	https://www.ewt.org.za/WILDLIFETRADE/bushmeat/Lindsey%20et%20al.%202013%20The%20bushmeat%20trade%20in%20African%20savannas.pdf	Africa (central / west)	AFRICOM	Commodity chain and trade routes	hunting
30	Journal Publication	http://www.sciencedirect.com/science/article/pii/S000632071100348X	Ghana	AFRICOM	Commodity chain and trade routes	trade market, Eiodlon helvum

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31	"The Scale of Illegal Meat Importation from Africa to Europe via Paris"	Anne-Lise Cambers, Marcus Rowcliffe	7-Jun-10	This article conducts a systematic survey of customs seizures of bushmeat, livestock meat, and fish carried by passengers arriving at Paris Roissy-Charles de Gaulle airport from sub-Saharan Africa. They estimate that 62 tons of meat and fish were imported from sub-Saharan Africa into a Paris airport over one week. The authors recommend better incentivizing customs officers to search for meat and increase penalties and fines for those found importing illegal meat.
32	"Incentives for Hunting: The Role of Bushmeat in the Household Economy in Rural Equatorial Guinea"	Noelle Kumpel, Marcus Rowcliffe,	Apr-10	It is important to understand the role of bushmeat within the wider rural economy in order to create effective policy regarding conservation and safety. They found that bushmeat is a necessity good with consumption and expenditure on bushmeat related less than proportionately to income. 60% of poor-to-middle income households hunted and traded bushmeat while richer households had other income-generating activities. Thus, hunting serves as an important source of fallback income for men without the alternative of preferable alternative opportunities.
33	"Bushmeat and International Development"	Glyn Davies	Jun-02	Conservation agencies and development agencies often have difficulty relating despite overlapping goals and interests. Davies recommends regulating bushmeat trade as a way of conserving natural resources and sustainably providing economic growth.
34	Agouti on the wedding menu: Bushmeat harvest, consumption and trade in a post-frontier region of the Ecuadorian Amazon	Miguel Pinedo-Vasquez, Robert Nasi	2015	This article serves as an analysis of the bushmeat market in Ecuador. The evidence gathered shows that the country of Ecuador has established laws both protecting the act of subsistence hunting in local rural markets, and has outlawed the sale of bushmeat for public consumption. The overexploitation of larger game has created foundation, and forests have begun to flourish with more desirable small game species. Nationally, the government of Ecuador recognizes the importance of hunting and bushmeat for economic and cultural purposes, and protects the act in its constitution. Strict enforcement creates an underground market. Ecuador also has a well regulated system of biodiversity, and interviews show that respondents to surveys recognize the importance of conservation. The bushmeat market in Ecuador has provided no evidence of foreign or national sales. The authors detail the importance of regulating bushmeat trade based on local necessities and not general national statistics.
35	"The harvest of wildlife for bushmeat and traditional medicine in East, South, and Southeast Asia"	Amanda Sigouin	2014	Asia has a booming but often illegal wildlife trade that drives the bushmeat crisis. The high concentration of illegal wildlife trade seizures in Southeast Asia make the region a hot spot for emerging infectious diseases. The lack of infrastructure, technical capacity, and political stability will make addressing the bushmeat crisis difficult. The book continues to view the bushmeat crisis through the lenses of food insecurity, traditional medicine, and urbanization. They conclude with recommendations and research opportunities to address each aspect of the issue.
36	Bushmeat harvest in tropical forests Knowledge base, gaps and research priorities	Varun Swamy, Miguel Pinedo-Vasquez	2014	This article presents the current statistics and research of the global bushmeat market. The goal of the article is to shift focus of future research to the topic of sustainability. The authors review past and present attempts to improve sustainability through management and intervention. Nearly 150,000 people living in forest ecosystems and 5 million people living in afrotropics consume upwards of 5 million tons of wild bush meat a year. Large animals that provide a lot of meat are the most targeted, often have lowest reproductive cycles, leading to unsustainable hunting levels. The bushmeat market has created a luxury demand, nearly 5 tons of unregulated bushmeat is smuggled through Paris airport every week. Strict control of licenses and arms has been successful in Malaysia, hunter education programs successful in Brazil, and community-based management successful in Peru.
37	"Bushmeat and Livelihoods: Wildlife Management and Poverty Reduction"	Glyn Davies, David Brown	2007	In this book, Davies analyzes the bushmeat market as both a threat to wildlife conservation and a significant component of livelihood for many people. Davies focuses on the human dimension of the debate because the values of wildlife often conflict with cultural and human societal values. The book explores both of these dimensions to best align and reconcile the varying priorities.
38	"Molecular and Mathematical Modeling Analyses of Inter-island Transmission of Rabies into a Previously Rabies-free Island in the Philippines"	Kentaro Tohma, Mariko Saito, Catalino Demetria	Mar-16	This article investigates the inter-island transmission of rabies in the Philippines using phylogenetic and modeling approaches. They found a lag time of several months to a year from rabies introduction to initial case detection, thus creating difficulties in identifying the initial introductory event. Molecular epidemiology can detect occasional introduction events from genetic information and can reveal how often spillover events happen, thus providing useful data for improving rabies control strategies.

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31	Journal Publication	http://onlinelibrary.wiley.com/doi/10.1111/j.1755-263X.2010.00121.x/full	Africa (sub-Saharan)	AFRICOM	Commodity chain and trade routes	trade market
32	Journal Publication	http://link.springer.com/article/10.1007/s10745-010-9316-4	Equatorial Guinea	AFRICOM	Commodity chain and trade routes	Equatorial Guinea, market
33	Journal Publication	http://www.jstor.org/stable/3061204?seq=1#page_scan_tab_contents	n/a	n/a	Commodity chain and trade routes	trade market
34	Journal Publication	http://www.cifor.org/library/5730/agouti-on-the-wedding-menu-bushmeat-harvest-consumption-and-trade-in-a-post-frontier-region-of-the-ecuadorian-amazon/	Ecuador	SOUTHCOM	Commodity chain and trade routes	trade market, ecuador, harvest
35	Book	https://books.google.com/books?hl=en&lr=&id=lnWTCgAAQBAJ&oi=fnd&pg=PP5&dq=amanda+sigouin&ots=LJRYMyaGSH&sig=QFjecWfhWaiocKqJOU7dnri6qMQ#v=onepage&q=amanda%20sigouin&f=false	Asia	PACOM	Commodity chain and trade routes	trade market, harvest, southeast asia
36	Journal Publication	http://www.cifor.org/publications/pdf_files/OccPapers/OP-114.pdf	n/a (global)	n/a	Commodity chain and trade routes	trade market
37	Book	https://books.google.com/books?hl=en&lr=&id=JGkEXrG3srwC&oi=fnd&pg=PP2&dq=Glyn+Davies+bushmeat&ots=cj3KIvBzrn&sig=vYAfXpFauSxxQ90zq3dlSyc5lq4#v=onepage&q=conclusion&f=false	n/a	n/a	Commodity chain and trade routes	trade market, conservation
38	Journal Publication	http://www.sciencedirect.com/science/article/pii/S1567134815300666	Philippines	PACOM	Virus / host relationship	rabies, Philippines

	A	B	C	D
39	Molecular Epidemiology of Rabies Viruses Circulating in Two Rabies Endemic Provinces of Laos, 2011–2012: Regional Diversity in Southeast Asia	Bounlom Douangngeun	31-Mar-15	A study conducted in order to gain knowledge about epidemiology and genetic characteristics of circulating rabies viruses in Laos. The data gathered showed gradual growth of positive rabies samples between 2004-2011. The study includes a Phylogenetic tree stating the bat origin rabies viruses form their own cluster. Further, there are three distinct viral lineages currently circulating the country. The genetic makeup of the strains show relation to those found in neighboring countries, indicating a shared ancestry. Due to size of the country, movement of people, and the number of dog , it is likely that multiple lineages and clusters of rabies will circulate Lao PDR.
40	Rabies Death Attributed to Exposure in Central America with Symptom Onset in a US Detention Facility - Texas, 2013	Neil Vora	9-May-14	This article details the case of a 28 year old Guatemalan Nationals diagnosed with rabies infection while in custody at a U.S. Immigration Detention Center in Texas. The case study illustrates the possibility of human to human transmission of rabies through exposure to mucus membranes, open wounds, saliva, tears, or nervous tissue.
41	"Genetic Diversity and Geographic Distribution of Genetically Distinct Rabies Viruses in the Philippines"	Mariko Saito, Hitoshi Oshitani, Catalino Demetria	4-Apr-13	This study performed a molecular analysis of rabies viruses using animal brain samples. They found multiple strains diverged and divided from different island groups in the Philippines. The results suggest the viruses evolved independently in each geographic area without frequent introduction into other areas. Application includes the idea of geographically targeted vaccination in the different island groups.
42	"A Seroepidemiologic Study of Reston Ebolvairus in Swine in the Philippines"	Yusuke Sayama, Catalino Demetria	23-Feb-12	This article aimed to clarify how REBOV infection was spread among swine during epizootics. The study used multiple serological assays to test the swine and confirm they are susceptible for REBOV infection. The serological assays should also be useful for future surveillance or a serological survey of REBOV infection in swine.
43	"Trapid Detection of Rabies Virus by Reverse Transcription Loop-Mediated Isothermal Amplification"	Bazartseren Boldbaatar, Catalino Demetria	30-Mar-09	A sensitive, specific, and reliable diagnosis is important in diagnosing rabies. A direct fluorescent antibody (DFA) test is the most frequently used test in animals while reverse-transcription polymerase chain reaction (RT-PCR) is most common in humans. Both of these tests require expensive equipment and can be difficult to adopt in developing countries. This study developed reverse-transcription loop-mediated isothermal amplification (RT-LAMP) as a less resource-intensive rapid and reliable test for rabies in both humans and animals.
44	"Wildlife Trade and Global Disease Emergence"	William Karesh	Jul-05	Global trade in wildlife can result in disease transition that threatens human disease outbreaks, livestock, native wildlife populations, and the health of ecosystems. Instead of eradiating these dangerous pathogens or the species that carry them, Karesh et al. suggest decreasing the contact rate among species, specifically in wildlife trade. Wildlife markets are generally networks with major hubs that provide practical control opportunities. Karesh also argues that focusing on markets is a cost-effective way to decrease the spread of diseases.
45	"The Impact of a Monthly Rest Day on Avian Influenza Virus Isolation Rates in Retail Live Poultry Markets in Hong Kong"	K. Y. Kung, Y. Guan	14-Apr-02	Live poultry markets act as a reservoir for many diseases that are passed between animals and humans. This study found that the isolation rate of avian influenza (AI) was significantly lower after a day of rest in the markets where stalls were completely emptied, cleaned, and restocked. This was not true for all diseases, as Newcastle disease virus was not affected by this intervention.
46	"Integrated Assessment Models for Ecologists: the Present and the Future"	Michael Harfoot, Jorn Scharlemann	11-Aug-13	Integrated assessment models (IAMs) are useful for analyzing socio-environmental factors in ecological and biodiversity modeling. The authors review four IAMs and identify challenges for implementation among ecologists. The IAM community and ecological community would both benefit from greater collaboration to align incentives.

	E	F	G	H	I	J
39	Journal Publication	http://journals.plos.org/plosntds/article/file?id=10.1371/journal.pntd.0003645&type=printable	Lao PDR	PACOM	Virus / host relationship	rabies, Lao PDR
40	Journal Publication	https://www.researchgate.net/publication/281926873_Rabies_Death_Attributed_to_Exposure_in_Central_America_with_Symptom_Onset_in_a_US_Detention_Facility_-_Texas_2013	USA	NORTHCOM	Virus / host relationship	rabies, Guatamala, united states
41	Journal Publication	http://journals.plos.org/plosntds/article?id=10.1371/journal.pntd.0002144	Philippines	PACOM	Virus / host relationship	rabies, Philippines
42	Journal Publication	http://bmcvetres.biomedcentral.com/articles/10.1186/1746-6148-8-82	Philippines	PACOM	Virus / host relationship	Ebola Reston, pigs, REBOV
43	Journal Publication	https://www.researchgate.net/profile/Catalino_Demetria/publication/26239699_Rapid_Detection_of_Rabies_Virus_by_Reverse_Transcription_Loop-Mediated_Isothermal_Amplification/links/02e7e526f47b96e35a000000.pdf	n/a	n/a	Virus / host relationship	ravies, DFA test
44	CDC Emerging Infectious Diseases Journal	https://wwwnc.cdc.gov/eid/article/11/7/05-0194_article	n/a	n/a	Commodity chain and trade routes	trade market
45	Journal Publication	https://www.researchgate.net/publication/5412305_The_Impact_of_a_Monthly_Rest_Day_on_Avian_Influenza_Virus_Isolation_Rates_in_Retail_Live_Poultry_Markets_in_Hong_Kong	Hong Kong	PACOM	Virus / host relationship	Avian influenza, Hong Kong
46	Journal Publication	http://onlinelibrary.wiley.com/doi/10.1111/geb.12100/full	n/a	n/a	n/a	IAM

From: Caitlin Devaney
Sent: Wednesday, June 21, 2017 3:01 PM EDT
To: ian.mendenhall >; joram.buza vkapur >; @ecohealthalliance.org ; gavin.smith ; Kading,Rebekah ; Lela Urushadze >; Tamar Kutateladze >; S Wacharapluesadee ; Wade Abel >; Kingston, Tigga < >; DeeAnn Reeder >; Jon Epstein ecohealthalliance.org>
CC: Lancaster, Mary J CIV (US) >; Stokes, Martha M CIV (US) >; Sander, William E CTR (US) ; Katie Leahy

Subject: Global Bat Alliance Meeting 29 JUNE Document for Review
Attachment(s): "TORFTA_GBA_v10.docx","GBA Meeting Overview_29June2017_v2.docx"

All,

Ahead of the Inaugural GBA Steering Committee Meeting next Thursday, we wanted to pass along the attached revised version of the Terms of Reference for Trusted Agents for your review. We will work to finalize this document during our meeting. The agenda for the meeting (this has not changed) is also attached for your reference.

Please let us know if you have any questions. Looking forward to seeing you all at our meeting next week!

v/r,
Caitlin Devaney

Caitlin Devaney
Project Manager | Global Systems Engineering
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Baileys Crossroads, VA 22041

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Global Bat Alliance Meeting

Overview (objectives and agenda)
29 June 2017

Meeting objectives (proposed)

1. Finalize GBA Terms of Reference for Trusted Agents (TORFTA)
2. Identify bat research focus areas and associated mentorship leads for each area
3. Prioritize research needs and gaps for each focus area and identify correlating researchers, institutions, other networks / alliances, and funding entities
4. Draft short and long-term timelines and workplans for each focus area
5. Determine steering committee convening schedule and Cohort II / III / IV training schedule

Focus areas (proposed)

- Virus / host relationship
- Commodity chain and trade routes
- Ecological change and effects
- Bat, livestock, and wildlife interactions

Note: these focus areas are not regionally based as previously discussed, in an effort to build towards the overarching objective of a multi-regional, multi-disciplinary network; they will be the subject of discussion during the 29 June GBA Meeting in Fort Collins

Agenda

Time	Agenda Topic and Facilitator or Speaker	Expected Outcomes
0930 – 1000	**Welcome and Introductions**	
1000 – 1015	**Global Bat Alliance Overview** *Dr. Mary Lancaster (Africa Science Lead)* *Dr. Marty Stokes (SEA Science Lead, CBEP)*	• Review discussions leading up to this meeting • Discuss how this meeting is an opportunity to formalize the central / steering committee node for the distributed network • Emphasize that the steering committee shall focus on mentorship and connecting individuals and institutions across the globe
1015 – 1045	**Review Charter and Move to Agreement** *TBD*	• Vote to accept organizational document for steering committee

		• Unanimous (??) acceptance • We will advertise intent ahead of meeting • We will convene a meeting on 7 June to review and discuss the draft TORFTA
1045 – 1115	**Identify and discuss research focus areas** *TBD*	• Group will identify and discuss overarching focus areas and sub focus areas • Steering committee and invitees shall self nominate to groups and agree to serve as research mentors for the groups
1115 – 1230	**Breakout: Prioritize research needs and gaps** *TBD*	• Group will breakout into their research focus areas and begin identifying needs and gaps • Groups will then work to prioritize their lists
1230 – 1330	**Working Lunch** *TBD*	• Buffet • Convene back as a group, hold discussions about the overarching objectives of the alliance • Discuss One Health and Vector-based International meetings as an opportunity to re-convene semi-annually
1330 – 1400	**Breakout: Draft timelines and workplans** *TBD*	• Begin drafting short and long-term timelines and workplans for each focus area • Short-term milestones could include identifying key researchers and networks • Long-term milestones could include training events and focus area meetings
1400 – 1430	**Closing / review of actions** *TBD*	• Close-out meeting / 5min brief out for each group (2 slides) • Review action items and next steps

PROPOSED TERMS OF REFERENCE FOR TRUSTED AGENTS OF THE GLOBAL BAT ALLIANCE

1. BACKGROUND

The Global Bat Alliance (GBA) will serve as a platform to identify and connect interdisciplinary expertise to address challenges and threats posed by bat-associated pathogens of security concern. Specifically, the GBA shall convene a body of experts and researchers to: (1) share information, data, samples, and protocols; (2) coordinate research activities; (3) build training events and awareness-building workshops at all levels of decision-making authority; (4) develop community standards and best research practices; (5) create mentorship-based opportunities for students, trainees, and early-career researchers to convene, present, and share ideas; and (6) establish a community of international research leaders and champions.

Some of the world's most deadly emerging zoonotic diseases are found in bats, including Nipah, Hendra, and Marburg viruses. There are a number of factors which make bats unique disease reservoirs, including their social behavior and mutual grooming patterns, ability to travel long distances, nocturnal activity, species diversity, and long life span (10-20 years, compared with a rat's average life of two years).[1] These characteristics make bats very difficult to study within traditional controlled laboratory settings and create research challenges to understanding their roles in the global zoonotic disease ecology. The GBA will create opportunities for policy makers, researchers, funders, and students to identify research challenges, develop priority lists and associated action plans to target needs and gaps, and work at all levels to build awareness of bat-associated disease burden and transmission risks to improve the prevention, detection, diagnosis, and reporting of pathogens of security concern.[2]

2. GBA MISSION AND VISION

The GBA shall bring together scientists, policy makers, and medical/veterinary practitioners with interests in bat-related research involving pathogens of security concern. The network will build on community standards and best practices for research. The GBA will identify and share information on research funding opportunities offered by multiple institutions. Most importantly, the alliance will foster international relationships among collaborators, agencies, and organizations, which can produce long-term, sustainable partnerships that withstand changes in government and organization budgets, priorities, postures, and policies.

The Trusted Agents of the alliance with play a role in operationalizing the GBA, strengthening the linkages and reducing overlap in the global research effort on high-priority diseases of bats (especially

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[1] Hayman, David T.S., "As the bat flies," *Science* 02 Dec 2016: Vol. 354, Issue 6316, pp. 1099-1100 http://science.sciencemag.org/content/354/6316/1099

[2] Schountz, Tony, "Immunology of Bats and Their Viruses; Challenges and Opportunities," *Viruses,* 2014 Dec; 6(12): 4880-4901. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4276934/

zoonoses) to maximize the efficient use of expertise and resources and accelerate the coordinated development of disease surveillance and control methods.

3. OBJECTIVES

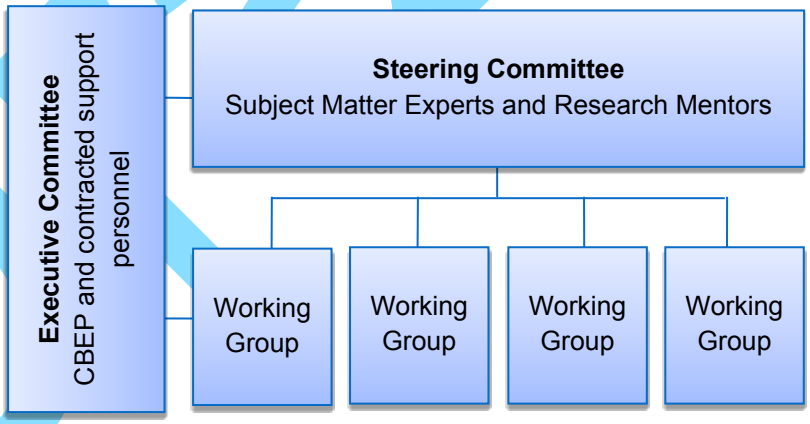
The objectives of the GBA are as follows:

- Facilitate interdisciplinary collaboration to identify research goals and needs for bat-associated disease research and disease threat reduction; and
- Unify CBEP regions to create a common action plan that yields collaborative projects that achieve the following end states: (1) better informed policy-makers; (2) better informed scientific community regarding funding targets and gaps in areas of research and development; and (3) better defined threat to global health security from bat-associated pathogens

4. APPROACH

The Terms of Reference for Trusted Agents (TORFTA) will convene subject matter experts to serve as mentors and function as independent, trusted advisors and honest brokers for research within the GBA. Trusted Agents will function within an organizational structure that consists of an Executive Committee, a Steering Committee, and four subject matter focused Working Groups.

4.1 The **Executive Committee (EC)** will be chaired by the CBEP Science Leads from Africa and Southeast Asia with organizational and administrative support from designated contractors for the program. The EC shall be responsible for developing GBA governance policies and guidelines, which includes funding decisions and approval of nominations for individuals to serve on the Steering Committee (SC) and within the Working Groups. As such, the EC shall be the sole decision-making body regarding funding while the SC shall be a separate body that makes recommendations on research priorities and targets to the EC. Since the EC will be comprised of members from the CBEP Research Program, the details regarding program requirements and processes for funding can be found in Appendix A of this document and should be used as a resource for all GBA members who wish to submit projects to CBEP.



The EC and their team shall additionally be responsible for the following tasks (at a minimum):

- Establish broad objectives and goals for the GBA
- Organize and facilitate meetings for the GBA
- Provide secretarial support for all virtual and in-person meetings for the GBA
- Prepare materials on request

- Disseminate information including (but not limited to) newsletters, website links, press releases, meetings and conferences
- Coordinate with other funding agencies and organizations

4.2 The **Steering Committee (SC)** shall include scientific experts that shall act as the scientific coordinating body for global bat research, provide research gap analysis, and priority setting to the EC, as well as considering the scientific merit of proposals from the EC and assist with their implementation as per the terms of reference. As such, the selection process for SC membership seeks to cultivate a balanced body of globally representative individuals, both geographically and across the bat research spectrum. The SC shall be responsible for the following items (at a minimum):

- Act as a scientific coordinating body for the GBA
- Consider the scientific merit of proposals from the EC
- Serve as subject matter experts and research mentors for implementation of accepted GBA-endorsed projects
- Propose research priorities
- Review and make recommendations on any matter involving an alteration in the mandate, terms of reference, membership, or structure of the GBA
- Review, discuss, and make recommendations for the logistics requirements of the GBA, sources and means of political and financial support, and its capability to function correctly in the future
- Define missions and submissions of the Working Groups (WGs), as well as identifying need for proposing establishment of new or closing-out existing WGs
- Supporting WGs in organizing gap analyses and research prioritization
- Promote interactions between WGs
- Assess and report progress of the WGs to other members of the SC and EC
- Develop and encourage exchange of protocols and best practices, and agree on standard operating procedures, good research practice, and roadmap to reach GBA goals (short and long-term)

4.2.1 Participate in semi-annual meetings. Meetings will normally take place twice annually in a place and at a time that is convenient for participants to a bat-relevant conference or meeting. The Chair (*please note: a more in-depth discussion concerning the SC "Chairman" will take place at the 29 June meeting; this document will be updated live in accordance with the outcomes of those discussions*) may convene meetings at other times when they find support of at least two thirds of the members of the Steering Committee. These meetings can be virtual or in-person. The Secretary is responsible for ensuring that the agenda of the meeting is made available to the members no later than one week before the meeting.

4.2.2 Develop recommendations. Business will be conducted by careful and considered deliberation leading to recommendations to the GBA. Recommendations shall be decided by consensus where possible. Consensus means that after deliberation all members support a particular point of view. Where consensus is not achieved, recommendations

shall be decided by simple majority vote of members voting on the question. In the case of a tied vote, the person acting as Chair shall be entitled to a second or deciding vote.

4.2.3 Attain consensus. A quorum is constituted by half of the number of individuals composing the Steering Committee rounded up when the number in the Steering Committee is uneven. The Steering Committee may decide by consensus or majority vote to ask parties who are not members of the Steering Committee to participate in a meeting so that they can provide relevant information, material, or knowledge. The Steering Committee may establish sub-committees consisting of 3 or more of its members and refer to them any matter in the Steering Committee's mandate. It may co-opt other GBA participants onto such committees.

4.3 The **Working Groups (WGs)** shall serve to divide the GBA into multi-disciplinary, multi-national focus areas to meet the research challenges associated with bat-borne diseases. Members of the SC shall serve as research mentors and subject matter experts within each WG. There will be no term limits, as WG members are encouraged to contribute and participate indefinitely. GBA members shall be nominated to participate in a WG by members of the EC or SC. The WGs will focus on the following focus areas (*please note, these focus areas are very much in draft form and will be the subject of discussion during the 29 June GBA Meeting in Fort Collins)*:

- Virus / host relationship
- Commodity chain and trade routes
- Ecological change and effects
- Bat, livestock, and wildlife interactions

5. GOVERNANCE AND MEMBERSHIP

5.1 Accountability

The overarching duty of the GBA is to develop multi-disciplinary and multi-national, hypothesis driven, research projects that meet the prioritized challenges defined by the Executive Committee under advice from the Steering Committee. Accountabilities of the GBA EC, SC, and Members include the following:

- Each member shall be familiar with the TORFTA and the mandate of the committees or WGs on which they serve
- Each member shall promote a culture of responsible practice for scientific research
- Each member shall work towards the short and long-term goals for the benefit of the GBA with a particular emphasis on the foci that fall within their WG
- Members of the SC are selected for their breadth of experience, insight and knowledge, integrity and character, and sound and independent judgment; therefore, they are expected to bring these personal qualities to their role on the SC and apply impartial judgment to help the EC make informed and independent decisions

5.2 Conflicts of Interest

This terms of reference document chooses the National Academy of Sciences (NAS) definition of Conflict of Interest: "a conflict of interest in research exists when the individual has interests in the

outcome of the research that may lead to a personal advantage and that might therefore, in actuality or appearance compromise the integrity of the research."

No member of the Steering Committee may participate in a discussion where such participation would give rise to a potential conflict of interest. As defined in section 4.1, the EC shall review all situations and decisions insofar as a financial obligation is at stake. SC members may leave their term of service on the SC if they wish to participate in a funding opportunity that would otherwise be perceived as a conflict of interest. SC members may recuse themselves if any personal advantage, not just those of financial benefit, is perceived. Any member of the SC may discuss possible conflicts of interest with the EC before stepping down from their term of service.

5.3 Selecting Committee Members

The SC and members of the WGs shall include members that reflect the multi-disciplinary and multi-national nature of the GBA. There are no term limits for members of the GBA, who are allowed to participate at will in accordance with terms of the TORFTA. However, members of the SC follow other rules for selection:

- ***5.3.1*** ***Terms of service –*** *2 years, no term limit*
- ***5.3.2*** ***Eligibility*** *– representation from each CBEP region must be maintained*
- ***5.3.3*** ***Nomination process –*** *nominated at the end of even calendar years by peers (members of the GBA) at GBA research review meetings or electronically*
- ***5.3.4*** ***Selection process –*** *reviewed by members of the EC under advisement of the SC*

(*please note: a more in-depth discussion concerning the scope of the total number of SC members will take place at the 29 June meeting; this document will be updated live in accordance with the outcomes of those discussions*)

APPENDIX A: APPLYING FOR FUNDING VIA EXECUTIVE COMMITTEE / CBEP

A.1 CBEP Research Scope

In order for CBEP to remain relevant, agile, and sustainable, research projects must be aimed at threat reduction objectives and demonstrate a clear nexus with the biosurveillance mission. The scope of CBEP research priorities include (but are not limited to):

- Understanding the ecology and epidemiology of pathogens of security concern, including HHS and USDA Biological Select Agents and Toxins and pathogens of pandemic potential, emerging, and re-emerging infectious diseases (e.g., avian influenza [low and highly pathogenic], African swine fever, Middle East Respiratory Syndrome (MERS), Ebola)
- Differentiating infectious diseases presenting clinical signs and symptoms similar to those of pathogens of security concern (e.g., influenza-like illness, acute febrile illness, fever of unknown origin)

CBEP will not support research projects that have no clear link to its threat reduction mission, are not sustainable for the partner country, or propose activities constituting Dual Use Research of Concern. These and other requirements and constraints are outlined in the figure below.

CBEP Fundamental Research Scope

In Scope	Out of Scope

Projects that demonstrate:
• Clear relationships to pathogens of security concern
  ○ U.S. Biological Select Agents *
  ○ Pathogens of pandemic potential
  ○ Emerging or re-emerging infectious diseases
  ○ Differentiating pathogens of security concern from agents with similar clinical signs and symptoms
• Links to threat reduction mission
• Support of BS&S and biosurveillance capabilities that reduce the threat of pathogens of security concern
  ○ Rapid, accurate, and safe detection, diagnoses, and reporting
• Alignment with both CBEP and partner country infectious disease priorities
• Use of sustainable techniques, procedures, and approaches in appropriate facilities
	Projects that focus on:
	• Dual-Use Research of Concern (DURC)
	• Diagnostic assay / novel technology
	• Development **
	• Medical countermeasures
	• Non-infectious diseases
	
	Projects that contain:
	• Establishment of new pathogen repositories
	• No link to pathogens of security concern
	• No clear alignment to threat reduction mission
	• Use of unsustainable techniques, procedures, or inappropriate facilities
	  ○ Requires use of supplies or resources not available in country
	• No clear research question or hypothesis

	• No potential to generate knowledge that may result in scientific publications

* Pathogens on the HHS and USDA Biological Select Agent and Toxins List

** Field or country-specific validation of new diagnostic assays, novel technologies or equipment may be in scope if meeting other in-scope criteria

A.2 Applying for DTRA CBEP Research Funding

CBEP Research Objectives and Scope

DTRA CBEP is continuously seeking new collaborators, partners and international partners to conduct cooperative biological research to inform and enhance disease surveillance and global health security. Projects that are hypothesis-driven and contain substantive engagement with and contribution by partner country institutions and scientists are appropriate for CBEP research funding. Research projects that support CBEP objectives in partner countries include those that promote One Health, improve disease surveillance, enhance understanding of endemic pathogens, explore the microbial ecology of endemic organisms, and enhance host country capabilities in support of World Health Organization International Health Regulations and World Organization for Animal Health reporting standards. Pathogens of interest include Biological Select Agents and Toxins, pathogens of pandemic potential, emerging and re-emerging infectious diseases, and pathogens that are co-syndromic with associated select agent etiologies such as Influenza-Like Illness or Acute Febrile Illness. CBEP does not support research topics that involve Dual- Use Research of Concern or focus on disease agents that are sexually transmitted, non-infectious, or do not pose a threat to global health security.

Research projects supported by CBEP must align with CBEP's overarching goals to reduce the threat to U.S. and global health security and are expected to produce results suitable for scientific publication.

Applying to the Broad Agency Announcement (BAA) and Government Call

CBEP welcomes research funding applications from domestic and foreign academic, private, and government institutions, and has multiple solicitations available for proposals.

- Academic institutions, non-governmental organizations, industry, foreign laboratory equivalents, and members of the private sector must apply through Thrust Area 6: Cooperative Counter Weapons of Mass Destruction (CWMD) Research with Global Partners of the Fundamental Research to Counter Weapons of Mass Destruction (FRCWMD) – BAA (HDTRA1-14-24- FRCWMD-BAA).
- U.S. Government partners and Federally Funded Research and Development Centers (FFRDCs) must apply through Thrust Area 6 of the FRCWMD Government Call (HDTRA1-12-17- FRCWMD-Call).

All research ideas MUST be pre-coordinated through submission of an abstract to FRCWMD-TA6@dtra.mil prior to submitting a white paper. White papers (aka Phase I proposal) must be submitted and a full proposal (aka Phase 2 Proposal) invited prior to submission of a full proposal. Phase 1 and Phase 2 proposals to the FRCWMD-BAA must be submitted through www.grants.gov. Phase 1 and Phase 2 proposals to the FRCWMD-Call must be submitted through www.dtrasubmission.net. White papers and proposals will be peer reviewed in accordance with the evaluation criteria published in the

BAA and Call and in coordination with appropriate CBEP Regional and Country Managers. To be successful, a white paper and/or proposal must align with both the DTRA/SCC-WMD CBEP mission and regional priorities.

Detailed instructions for the FRCWMD-BAA and the FRCWMD-Call can be found through the solicitation links at www.dtrasubmission.net. Please ensure that you are downloading and reviewing the latest amended full announcement for the most accurate information and instructions. Offerors may submit questions of an administrative nature to HDTRA1-FRCWMD-A@dtra.mil, and of a technical nature to FRCWMD-TA6@dtra.mil.

From: Sander, William E CTR (US)
Sent: Tuesday, June 27, 2017 4:27 PM EDT
To: kityob ; ian.mendenhall >; Prof. Joram Buza ; Vivek Kapur < ; Kevin Olival, PhD ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; gavin.smith Kading,Rebekah ; lelincdc >; l.urushadze ; tamar_kutateladze ; spwa >; abelwade ; c demetria ; Kingston, Tigga >; nisreen.hmoud ; cryanp >; dreeder

CC: Lancaster, Mary J CIV (US) >; Stokes, Martha M CIV (US) >; Gamboa, Omar Maj USAF DTRA J3-7 (US) katie.leahy >; Caitlin Devaney
Subject: Global Bat Alliance Steering Committee meeting - info
Attachment(s): "TORFTA_GBA_v10.docx","GBA Meeting Overview_29June2017_v2.docx"

On behalf of Mary Lancaster and Marty Stokes, we're excited to convene the first in-person meeting of the Steering Committee for the Global Bat Alliance.

As friendly reminders of what to expect:

- Convene on Thursday, June 29th, in room 142 of the University Center for the Arts (same building as the conference)
- Start at 9:30AM local time (room will be open by 9AM)
- Working lunch (lunch provided) - vegetarian option included
- Plan to end the meeting at 2:30PM local time
- For those of you calling in, we will get that information to you within the next day.

I have attached again our agenda as well as the Terms of Reference for Trusted Agents for your reference and review.

If you have any questions, do not hesitate to reach out to any of us in the CC line. The number below is my cell phone.

Best,

Will Sander, DVM, MPH, DACVPM, PMP
Veterinary Specialist
Booz Allen Hamilton
CTR A&AS Support Contractor

Global Bat Alliance Meeting

Overview (objectives and agenda)
29 June 2017

Meeting objectives (proposed)

1. Finalize GBA Terms of Reference for Trusted Agents (TORFTA)
2. Identify bat research focus areas and associated mentorship leads for each area
3. Prioritize research needs and gaps for each focus area and identify correlating researchers, institutions, other networks / alliances, and funding entities
4. Draft short and long-term timelines and workplans for each focus area
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Focus areas (proposed)

- Virus / host relationship
- Commodity chain and trade routes
- Ecological change and effects
- Bat, livestock, and wildlife interactions

Note: these focus areas are not regionally based as previously discussed, in an effort to build towards the overarching objective of a multi-regional, multi-disciplinary network; they will be the subject of discussion during the 29 June GBA Meeting in Fort Collins

Agenda

Time	Agenda Topic and Facilitator or Speaker	Expected Outcomes
0930 – 1000	**Welcome and Introductions**	
1000 – 1015	**Global Bat Alliance Overview** *Dr. Mary Lancaster (Africa Science Lead)* *Dr. Marty Stokes (SEA Science Lead, CBEP)*	• Review discussions leading up to this meeting • Discuss how this meeting is an opportunity to formalize the central / steering committee node for the distributed network • Emphasize that the steering committee shall focus on mentorship and connecting individuals and institutions across the globe
1015 – 1045	**Review Charter and Move to Agreement** *TBD*	• Vote to accept organizational document for steering committee

		• Unanimous (??) acceptance • We will advertise intent ahead of meeting • We will convene a meeting on 7 June to review and discuss the draft TORFTA
1045 – 1115	**Identify and discuss research focus areas** *TBD*	• Group will identify and discuss overarching focus areas and sub focus areas • Steering committee and invitees shall self nominate to groups and agree to serve as research mentors for the groups
1115 – 1230	**Breakout: Prioritize research needs and gaps** *TBD*	• Group will breakout into their research focus areas and begin identifying needs and gaps • Groups will then work to prioritize their lists
1230 – 1330	**Working Lunch** *TBD*	• Buffet • Convene back as a group, hold discussions about the overarching objectives of the alliance • Discuss One Health and Vector-based International meetings as an opportunity to re-convene semi-annually
1330 – 1400	**Breakout: Draft timelines and workplans** *TBD*	• Begin drafting short and long-term timelines and workplans for each focus area • Short-term milestones could include identifying key researchers and networks • Long-term milestones could include training events and focus area meetings
1400 – 1430	**Closing / review of actions** *TBD*	• Close-out meeting / 5min brief out for each group (2 slides) • Review action items and next steps

PROPOSED TERMS OF REFERENCE FOR TRUSTED AGENTS OF THE GLOBAL BAT ALLIANCE

1. BACKGROUND

The Global Bat Alliance (GBA) will serve as a platform to identify and connect interdisciplinary expertise to address challenges and threats posed by bat-associated pathogens of security concern. Specifically, the GBA shall convene a body of experts and researchers to: (1) share information, data, samples, and protocols; (2) coordinate research activities; (3) build training events and awareness-building workshops at all levels of decision-making authority; (4) develop community standards and best research practices; (5) create mentorship-based opportunities for students, trainees, and early-career researchers to convene, present, and share ideas; and (6) establish a community of international research leaders and champions.

Some of the world's most deadly emerging zoonotic diseases are found in bats, including Nipah, Hendra, and Marburg viruses. There are a number of factors which make bats unique disease reservoirs, including their social behavior and mutual grooming patterns, ability to travel long distances, nocturnal activity, species diversity, and long life span (10-20 years, compared with a rat's average life of two years).[1] These characteristics make bats very difficult to study within traditional controlled laboratory settings and create research challenges to understanding their roles in the global zoonotic disease ecology. The GBA will create opportunities for policy makers, researchers, funders, and students to identify research challenges, develop priority lists and associated action plans to target needs and gaps, and work at all levels to build awareness of bat-associated disease burden and transmission risks to improve the prevention, detection, diagnosis, and reporting of pathogens of security concern.[2]

2. GBA MISSION AND VISION

The GBA shall bring together scientists, policy makers, and medical/veterinary practitioners with interests in bat-related research involving pathogens of security concern. The network will build on community standards and best practices for research. The GBA will identify and share information on research funding opportunities offered by multiple institutions. Most importantly, the alliance will foster international relationships among collaborators, agencies, and organizations, which can produce long-term, sustainable partnerships that withstand changes in government and organization budgets, priorities, postures, and policies.

The Trusted Agents of the alliance with play a role in operationalizing the GBA, strengthening the linkages and reducing overlap in the global research effort on high-priority diseases of bats (especially

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[1] Hayman, David T.S., "As the bat flies," *Science* 02 Dec 2016: Vol. 354, Issue 6316, pp. 1099-1100 http://science.sciencemag.org/content/354/6316/1099

[2] Schountz, Tony, "Immunology of Bats and Their Viruses; Challenges and Opportunities," *Viruses,* 2014 Dec; 6(12): 4880-4901. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4276934/

zoonoses) to maximize the efficient use of expertise and resources and accelerate the coordinated development of disease surveillance and control methods.

3. OBJECTIVES

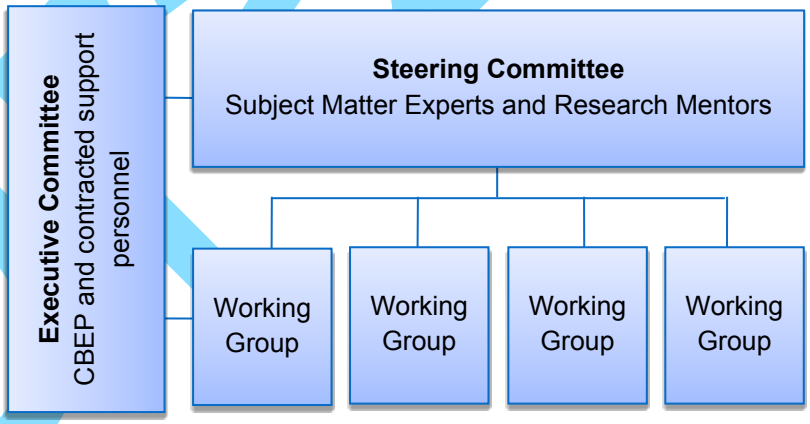
The objectives of the GBA are as follows:

- Facilitate interdisciplinary collaboration to identify research goals and needs for bat-associated disease research and disease threat reduction; and
- Unify CBEP regions to create a common action plan that yields collaborative projects that achieve the following end states: (1) better informed policy-makers; (2) better informed scientific community regarding funding targets and gaps in areas of research and development; and (3) better defined threat to global health security from bat-associated pathogens

4. APPROACH

The Terms of Reference for Trusted Agents (TORFTA) will convene subject matter experts to serve as mentors and function as independent, trusted advisors and honest brokers for research within the GBA. Trusted Agents will function within an organizational structure that consists of an Executive Committee, a Steering Committee, and four subject matter focused Working Groups.

4.1 The **Executive Committee (EC)** will be chaired by the CBEP Science Leads from Africa and Southeast Asia with organizational and administrative support from designated contractors for the program. The EC shall be responsible for developing GBA governance policies and guidelines, which includes funding decisions and approval of nominations for individuals to serve on the Steering Committee (SC) and within the Working Groups. As such, the EC shall be the sole decision-making body regarding funding while the SC shall be a separate body that makes recommendations on research priorities and targets to the EC. Since the EC will be comprised of members from the CBEP Research Program, the details regarding program requirements and processes for funding can be found in Appendix A of this document and should be used as a resource for all GBA members who wish to submit projects to CBEP.



The EC and their team shall additionally be responsible for the following tasks (at a minimum):

- Establish broad objectives and goals for the GBA
- Organize and facilitate meetings for the GBA
- Provide secretarial support for all virtual and in-person meetings for the GBA
- Prepare materials on request

- Disseminate information including (but not limited to) newsletters, website links, press releases, meetings and conferences
- Coordinate with other funding agencies and organizations

4.2 The **Steering Committee (SC)** shall include scientific experts that shall act as the scientific coordinating body for global bat research, provide research gap analysis, and priority setting to the EC, as well as considering the scientific merit of proposals from the EC and assist with their implementation as per the terms of reference. As such, the selection process for SC membership seeks to cultivate a balanced body of globally representative individuals, both geographically and across the bat research spectrum. The SC shall be responsible for the following items (at a minimum):

- Act as a scientific coordinating body for the GBA
- Consider the scientific merit of proposals from the EC
- Serve as subject matter experts and research mentors for implementation of accepted GBA-endorsed projects
- Propose research priorities
- Review and make recommendations on any matter involving an alteration in the mandate, terms of reference, membership, or structure of the GBA
- Review, discuss, and make recommendations for the logistics requirements of the GBA, sources and means of political and financial support, and its capability to function correctly in the future
- Define missions and submissions of the Working Groups (WGs), as well as identifying need for proposing establishment of new or closing-out existing WGs
- Supporting WGs in organizing gap analyses and research prioritization
- Promote interactions between WGs
- Assess and report progress of the WGs to other members of the SC and EC
- Develop and encourage exchange of protocols and best practices, and agree on standard operating procedures, good research practice, and roadmap to reach GBA goals (short and long-term)

4.2.1 Participate in semi-annual meetings. Meetings will normally take place twice annually in a place and at a time that is convenient for participants to a bat-relevant conference or meeting. The Chair (*please note: a more in-depth discussion concerning the SC "Chairman" will take place at the 29 June meeting; this document will be updated live in accordance with the outcomes of those discussions*) may convene meetings at other times when they find support of at least two thirds of the members of the Steering Committee. These meetings can be virtual or in-person. The Secretary is responsible for ensuring that the agenda of the meeting is made available to the members no later than one week before the meeting.

4.2.2 Develop recommendations. Business will be conducted by careful and considered deliberation leading to recommendations to the GBA. Recommendations shall be decided by consensus where possible. Consensus means that after deliberation all members support a particular point of view. Where consensus is not achieved, recommendations

shall be decided by simple majority vote of members voting on the question. In the case of a tied vote, the person acting as Chair shall be entitled to a second or deciding vote.

4.2.3 Attain consensus. A quorum is constituted by half of the number of individuals composing the Steering Committee rounded up when the number in the Steering Committee is uneven. The Steering Committee may decide by consensus or majority vote to ask parties who are not members of the Steering Committee to participate in a meeting so that they can provide relevant information, material, or knowledge. The Steering Committee may establish sub-committees consisting of 3 or more of its members and refer to them any matter in the Steering Committee's mandate. It may co-opt other GBA participants onto such committees.

4.3 The **Working Groups (WGs)** shall serve to divide the GBA into multi-disciplinary, multi-national focus areas to meet the research challenges associated with bat-borne diseases. Members of the SC shall serve as research mentors and subject matter experts within each WG. There will be no term limits, as WG members are encouraged to contribute and participate indefinitely. GBA members shall be nominated to participate in a WG by members of the EC or SC. The WGs will focus on the following focus areas (*please note, these focus areas are very much in draft form and will be the subject of discussion during the 29 June GBA Meeting in Fort Collins)*:

- Virus / host relationship
- Commodity chain and trade routes
- Ecological change and effects
- Bat, livestock, and wildlife interactions

5. GOVERNANCE AND MEMBERSHIP

5.1 Accountability

The overarching duty of the GBA is to develop multi-disciplinary and multi-national, hypothesis driven, research projects that meet the prioritized challenges defined by the Executive Committee under advice from the Steering Committee. Accountabilities of the GBA EC, SC, and Members include the following:

- Each member shall be familiar with the TORFTA and the mandate of the committees or WGs on which they serve
- Each member shall promote a culture of responsible practice for scientific research
- Each member shall work towards the short and long-term goals for the benefit of the GBA with a particular emphasis on the foci that fall within their WG
- Members of the SC are selected for their breadth of experience, insight and knowledge, integrity and character, and sound and independent judgment; therefore, they are expected to bring these personal qualities to their role on the SC and apply impartial judgment to help the EC make informed and independent decisions

5.2 Conflicts of Interest

This terms of reference document chooses the National Academy of Sciences (NAS) definition of Conflict of Interest: "a conflict of interest in research exists when the individual has interests in the

outcome of the research that may lead to a personal advantage and that might therefore, in actuality or appearance compromise the integrity of the research."

No member of the Steering Committee may participate in a discussion where such participation would give rise to a potential conflict of interest. As defined in section 4.1, the EC shall review all situations and decisions insofar as a financial obligation is at stake. SC members may leave their term of service on the SC if they wish to participate in a funding opportunity that would otherwise be perceived as a conflict of interest. SC members may recuse themselves if any personal advantage, not just those of financial benefit, is perceived. Any member of the SC may discuss possible conflicts of interest with the EC before stepping down from their term of service.

5.3 Selecting Committee Members

The SC and members of the WGs shall include members that reflect the multi-disciplinary and multi-national nature of the GBA. There are no term limits for members of the GBA, who are allowed to participate at will in accordance with terms of the TORFTA. However, members of the SC follow other rules for selection:

- ***5.3.1*** ***Terms of service –*** *2 years, no term limit*
- ***5.3.2*** ***Eligibility*** *– representation from each CBEP region must be maintained*
- ***5.3.3*** ***Nomination process –*** *nominated at the end of even calendar years by peers (members of the GBA) at GBA research review meetings or electronically*
- ***5.3.4*** ***Selection process –*** *reviewed by members of the EC under advisement of the SC*

(*please note: a more in-depth discussion concerning the scope of the total number of SC members will take place at the 29 June meeting; this document will be updated live in accordance with the outcomes of those discussions*)

APPENDIX A: APPLYING FOR FUNDING VIA EXECUTIVE COMMITTEE / CBEP

A.1 CBEP Research Scope

In order for CBEP to remain relevant, agile, and sustainable, research projects must be aimed at threat reduction objectives and demonstrate a clear nexus with the biosurveillance mission. The scope of CBEP research priorities include (but are not limited to):

- Understanding the ecology and epidemiology of pathogens of security concern, including HHS and USDA Biological Select Agents and Toxins and pathogens of pandemic potential, emerging, and re-emerging infectious diseases (e.g., avian influenza [low and highly pathogenic], African swine fever, Middle East Respiratory Syndrome (MERS), Ebola)
- Differentiating infectious diseases presenting clinical signs and symptoms similar to those of pathogens of security concern (e.g., influenza-like illness, acute febrile illness, fever of unknown origin)

CBEP will not support research projects that have no clear link to its threat reduction mission, are not sustainable for the partner country, or propose activities constituting Dual Use Research of Concern. These and other requirements and constraints are outlined in the figure below.

CBEP Fundamental Research Scope

In Scope	Out of Scope

Projects that demonstrate:
• Clear relationships to pathogens of security concern
  ○ U.S. Biological Select Agents *
  ○ Pathogens of pandemic potential
  ○ Emerging or re-emerging infectious diseases
  ○ Differentiating pathogens of security concern from agents with similar clinical signs and symptoms
• Links to threat reduction mission
• Support of BS&S and biosurveillance capabilities that reduce the threat of pathogens of security concern
  ○ Rapid, accurate, and safe detection, diagnoses, and reporting
• Alignment with both CBEP and partner country infectious disease priorities
• Use of sustainable techniques, procedures, and approaches in appropriate facilities
	Projects that focus on:
	• Dual-Use Research of Concern (DURC)
	• Diagnostic assay / novel technology
	• Development **
	• Medical countermeasures
	• Non-infectious diseases
	
	Projects that contain:
	• Establishment of new pathogen repositories
	• No link to pathogens of security concern
	• No clear alignment to threat reduction mission
	• Use of unsustainable techniques, procedures, or inappropriate facilities
	  ○ Requires use of supplies or resources not available in country
	• No clear research question or hypothesis

	• No potential to generate knowledge that may result in scientific publications

* Pathogens on the HHS and USDA Biological Select Agent and Toxins List

** Field or country-specific validation of new diagnostic assays, novel technologies or equipment may be in scope if meeting other in-scope criteria

A.2 Applying for DTRA CBEP Research Funding

CBEP Research Objectives and Scope

DTRA CBEP is continuously seeking new collaborators, partners and international partners to conduct cooperative biological research to inform and enhance disease surveillance and global health security. Projects that are hypothesis-driven and contain substantive engagement with and contribution by partner country institutions and scientists are appropriate for CBEP research funding. Research projects that support CBEP objectives in partner countries include those that promote One Health, improve disease surveillance, enhance understanding of endemic pathogens, explore the microbial ecology of endemic organisms, and enhance host country capabilities in support of World Health Organization International Health Regulations and World Organization for Animal Health reporting standards. Pathogens of interest include Biological Select Agents and Toxins, pathogens of pandemic potential, emerging and re-emerging infectious diseases, and pathogens that are co-syndromic with associated select agent etiologies such as Influenza-Like Illness or Acute Febrile Illness. CBEP does not support research topics that involve Dual- Use Research of Concern or focus on disease agents that are sexually transmitted, non-infectious, or do not pose a threat to global health security.

Research projects supported by CBEP must align with CBEP's overarching goals to reduce the threat to U.S. and global health security and are expected to produce results suitable for scientific publication.

Applying to the Broad Agency Announcement (BAA) and Government Call

CBEP welcomes research funding applications from domestic and foreign academic, private, and government institutions, and has multiple solicitations available for proposals.

- Academic institutions, non-governmental organizations, industry, foreign laboratory equivalents, and members of the private sector must apply through Thrust Area 6: Cooperative Counter Weapons of Mass Destruction (CWMD) Research with Global Partners of the Fundamental Research to Counter Weapons of Mass Destruction (FRCWMD) – BAA (HDTRA1-14-24- FRCWMD-BAA).
- U.S. Government partners and Federally Funded Research and Development Centers (FFRDCs) must apply through Thrust Area 6 of the FRCWMD Government Call (HDTRA1-12-17- FRCWMD-Call).

All research ideas MUST be pre-coordinated through submission of an abstract to FRCWMD-TA6@dtra.mil prior to submitting a white paper. White papers (aka Phase I proposal) must be submitted and a full proposal (aka Phase 2 Proposal) invited prior to submission of a full proposal. Phase 1 and Phase 2 proposals to the FRCWMD-BAA must be submitted through www.grants.gov. Phase 1 and Phase 2 proposals to the FRCWMD-Call must be submitted through www.dtrasubmission.net. White papers and proposals will be peer reviewed in accordance with the evaluation criteria published in the

BAA and Call and in coordination with appropriate CBEP Regional and Country Managers. To be successful, a white paper and/or proposal must align with both the DTRA/SCC-WMD CBEP mission and regional priorities.

Detailed instructions for the FRCWMD-BAA and the FRCWMD-Call can be found through the solicitation links at www.dtrasubmission.net. Please ensure that you are downloading and reviewing the latest amended full announcement for the most accurate information and instructions. Offerors may submit questions of an administrative nature to HDTRA1-FRCWMD-A@dtra.mil, and of a technical nature to FRCWMD-TA6@dtra.mil.

From: Kingston, Tigga
Sent: Thursday, March 22, 2018 2:56 PM EDT
To: Megan Hudson >; nisreen.hmoud >; joram.buza ; cryanp c demetria >; ecohealthalliance.org >; Kading,Rebekah < >; vkapur ; kityrob tamar_kutateladze ; ian.mendenhall < ecohealthalliance.org >; dreeder >; ksidamonidze >; gavin.smith ; l.urushadze ; spwa >; abelwade >
CC: Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) >; Gano Cohen, Kelsey A CTR DTRA J3-7 (US) >; Katie Leahy ; Stokes, Martha M CIV (US) ; Becker, Stephen M CTR DTRA J3-7 (US) >
Subject: RE: BOHRN Steering Committee/One Health Congress Meeting

Dear Megan et al.
Regrettably I can't attend this time, as this falls just at the start up of a field project in Sabah.

Best wishes
Tigga

From: Megan Hudson
Sent: Thursday, March 22, 2018 12:46 PM
To: nisreen.hmoud ; joram.buza ; cryanp ; c_demetria ; ecohealthalliance.org; rebekah.kading ; vkapur Kingston, Tigga < ; kityrob ; tamar_kutateladze ; ian.mendenhall .sg; ecohealthalliance.org; dreeder ; ksidamonidze ; gavin.smith l.urushadze ; spwa ; abelwade
Cc: Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) Gano Cohen, Kelsey A CTR DTRA J3-7 (US) < ; Katie Leahy Stokes, Martha M CIV (US) >; Becker, Stephen M CTR DTRA J3-7 (US)
Subject: BOHRN Steering Committee/One Health Congress Meeting

All,

You are receiving this email, as part of a save the date to attend our BOHRN Steering Committee meeting and the 5th International One Health Congress (OHC) in Saskatoon, Canada.

Our meeting will take place on 20-21 June (location TBD, though likely at the Hilton Garden Inn). The agenda and travel information for this two day event will follow shortly. The OHC will take place 22-25 June.

On behalf of Dr. Marty Stoke and Dr. Mary Lancaster, CBEP will provide funding your travel and registration to the OHC and BOHRN Planning Meeting. While the OHC is not required it would be a good opportunity for networking on behalf of BOHRN. CBEP will be paying for OHC attendance next week. **Therefore, we need you to confirm your attendance to the OHC NLT tomorrow 23 March.** However, please note if regulations for DoD travel are not met by the specified due date, funding for the conference and travel will not be provided.

Please respond with your availability to attend the meeting NLT 23 March.

v/r,

Megan

Megan Hudson
Task Lead | Global Systems Engineering
6303 Little River Turnpike #208
Alexandria, VA 22312

http://globalsyseng.com

From: Wade Abel
Sent: Thursday, March 22, 2018 3:03 PM EDT
To: Megan Hudson >
CC: Nisreen Alhmoud >; Joram Buza ; Paul Cryan ; Catalino Demetria >; Jon Epstein @ecohealthalliance.org>; Kading,Rebekah Vivek Kapur ; Tigga Kingston ; Robert Kityo ; Tamar Kutateladze ; Ian Mendenhall ; Kevin Olival ecohealthalliance.org>; DeeAnn Reeder ; Keti Sidamonidze >; Gavin James Smith Lela Urushadaze >; Supaporn Wacharapluesadee ; Lancaster, Mary J CIV DTRA J3-7 (US) >; Gano Cohen, Kelsey A CTR (US) >; Katie Leahy ; Stokes, Martha M CIV (US) ; Becker, Stephen M CTR DTRA J3-7 (US)
Subject: Re: BOHRN Steering Committee/One Health Congress Meeting

Dear Megan

Thanks for the information. I do confirm my participation to the meeting.

Kind regards

WADE

On 22 Mar 2018 9:46 pm, "Megan Hudson" > wrote:

> All,
>
> You are receiving this email, as part of a save the date to attend our BOHRN Steering Committee meeting and the 5th International One Health Congress (OHC) in Saskatoon, Canada.
>
> Our meeting will take place on 20-21 June (location TBD, though likely at the Hilton Garden Inn). The agenda and travel information for this two day event will follow shortly. The OHC will take place 22-25 June.
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>
> Please respond with your availability to attend the meeting NLT 23 March.
>
> v/r,
>
> Megan
>
> **Megan Hudson**
>
> *Task Lead* | Global Systems Engineering
>
> 6303 Little River Turnpike #208
>
> Alexandria, VA 22312
>
> http://globalsyseng.com
>
>

From: DeeAnn Reeder
Sent: Tuesday, August 22, 2017 8:26 PM EDT
To: Katie Leahy >
CC: Robert Kityo ; Ian Mendenhall ; Joram Buza ; Vivek Kapur < ; Kevin Olival <oliva >; Jon Epstein @ecohealthalliance.org>; Kading,Rebekah ; Lela Urushadaze ; Lela Urushadaze ; Tamar Kutateladze ; Supaporn Wacharapluesadee >; Abel Wade ; Catalino Demetria >; Tigga Kingston ; Paul Cryan < ; Gavin Smith ; Nisreen Alhmoud ; Lancaster, Mary J CIV (US) >; Stokes, Martha M CIV (US) >; Sander, William E CTR (US) >; Caitlin Devaney >
Subject: Re: GBA Update and Request

Thanks Katie,

Very glad to see the PENAPH meeting selected. For the record I support the first name:
Bat-associated Pathogen and Ecology Research Network (BPERN) and strongly oppose the second name - we are not an "Alliance for Pathogens" - i.e., in support of pathogens - which is how this grammatically reads.

Looking forward to seeing everyone again.

Regards - DeeAnn

On Tue, Aug 22, 2017 at 8:17 PM, Katie Leahy< wrote:

> All,
>
> On behalf of Dr. Mary Lancaster and Dr. Marty Stokes, we would like to thank everyone, for your responses over the last couple weeks! Based on your feedback, we have a few announcements and one request:
>
> Based on committee consensus, the group chose our next event to coincide with the Participatory Epidemiology Network for Animal and Public Health (PENAPH) on 10-12 January 2018, in Khon Kaen, Thailand. Details will be forthcoming, but please visit the hyperlink for further information (https://penaph.net/second-penaph-conference-participatory-approaches-in-animal-health-public-health-one-health-and-ecohealth/).
>
> We did not receive additional nominations to serve as co-chairs, so we are pleased to announce our first Steering Committee Co-chairs: Dr. Jon Epstein from EcoHealth Alliance and Dr. Vivek Kapur from Penn State University. We will be setting up coordination calls with our two co-chairs, so you can expect communication and direction from them in the future.
>
> Finally, one request; we did not have a majority vote selection for our organization's name, which leaves us with two options:
>
> Option 1 Bat-associated Pathogen and Ecology Research Network (BPERN) and
>
> Option 2 Global Alliance for Bat-borne Pathogens (GABP).
>
> Please respond to this email with your selection no later than 24 August. We will tally the votes and make an announcement thereafter.
>
> Thank you, again, for signing up to the APAN site and being so responsive to the request. We will be loading the first documents and drafts to the site (e.g., the TORFTA and community fact sheet) in the next couple weeks. You may expect email from us with information concerning our next meeting in January and planning discussions leading up to that meeting.
>
> V/r,

Katie Leahy

Program Manager | Global Systems Engineering

5881 Leesburg Pike, Suite 506

Baileys Crossroads, VA 22041

http://globalsyseng.com

--
DeeAnn M. Reeder, PhD
Presidential Professor
Department of Biology
Bucknell University
Lewisburg, PA 17837

www.facstaff.bucknell.edu/dreeder

From: Nesreen Alhmoud o>
Sent: Thursday, August 24, 2017 5:01 AM EDT
To: Katie Leahy < Robert Kityo >; Ian Mendenhall ; Joram Buza ; Vivek Kapur ; Kevin Olival ecohealthalliance.org>; Jon Epstein @ecohealthalliance.org>; Kading,Rebekah Lela Urushadaze >; Lela Urushadaze ; Tamar Kutateladze ; Supaporn Wacharapluesadee < ; Abel Wade ; Catalino Demetria >; Tigga Kingston Paul Cryan ; DeeAnn Reeder ; Gavin Smith
CC: Lancaster, Mary J CIV (US) >; Stokes, Martha M CIV (US) >; Sander, William E CTR (US) >; Caitlin Devaney >
Subject: RE: GBA Update and Request

Dear Ms. Katie,

Thank you for your e-mail.

Regarding the name of the network, I will go for Option 1 *Bat-associated Pathogen and Ecology Research Network (BPERN)*.

Best,

Nisreen

الجمعية العلمية الملكية
Royal Scientific Society

Dr. Nesreen Alhmoud

Director of Bio-Safety and Bio-Security Center

Tel:
Mob: **P.O.Box**: 1438 Amman 11941 Jordan
Email: **Website**: www.rss.jo

Our Vision at The Royal Scientific Society is to be the local and regional reference point and knowledge leader for science and technology using scientific and engineering research to power economic development and social progress.

From: Katie Leahy]
Sent: Wednesday, August 23, 2017 3:18 AM
To: Robert Kityo; Ian Mendenhall; Joram Buza; Vivek Kapur; Kevin Olival; Jon Epstein; Rebekah Kading; Lela Urushadaze; Lela Urushadaze; Tamar Kutateladze; Supaporn Wacharapluesadee; Abel Wade; Catalino Demetria; Tigga Kingston; Paul Cryan; DeeAnn Reeder; Gavin Smith; Nesreen Alhmoud
Cc: Lancaster, Mary J CIV (US); Stokes, Martha M CIV (US); Sander, William E CTR (US); Caitlin Devaney
Subject: GBA Update and Request

All,

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Finally, one request; we did not have a majority vote selection for our organization's name, which leaves us with two options:

Option 1 Bat-associated Pathogen and Ecology Research Network (BPERN) and

Option 2 Global Alliance for Bat-borne Pathogens (GABP).

Please respond to this email with your selection no later than 24 August. We will tally the votes and make an announcement thereafter.

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V/r,

Katie Leahy
Program Manager | Global Systems Engineering
5881 Leesburg Pike, Suite 506
Bailevs Crossroads. VA 22041

http://globalsyseng.com

From: Wade Abel >
Sent: Wednesday, August 23, 2017 4:33 AM EDT
To: Katie Leahy >
CC: Robert Kityo ; Ian Mendenhall >; Joram Buza Vivek Kapur >; Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Kading,Rebekah >; Lela Urushadaze ; Lela Urushadaze >; Tamar Kutateladze >; Supaporn Wacharapluesadee ; Catalino Demetria Tigga Kingston ; Paul Cryan ; DeeAnn Reeder >; Gavin Smith >; Nisreen Alhmoud ; Lancaster, Mary J CIV (US) ; Stokes, Martha M CIV (US) >; Sander, William E CTR (US) >; Caitlin Devaney < >
Subject: Re: GBA Update and Request

Dear Katie,

Happy to read that we are advancing. Good that Thailand is the next meeting venue.
For the selection, I was at the point of suggesting, if allowed, a combination of both as

Global Alliance for Bat-borne Pathogens and Ecological Research (GABPER)

However, to respond to your request, let me go forOption 2: Global Alliance for Bat-borne Pathogens (GABP)

Kind regards

2017-08-23 1:17 GMT+01:00 Katie Leahy >:

> All,
>
> On behalf of Dr. Mary Lancaster and Dr. Marty Stokes, we would like to thank everyone, for your responses over the last couple weeks! Based on your feedback, we have a few announcements and one request:
>
> Based on committee consensus, the group chose our next event to coincide with the Participatory Epidemiology Network for Animal and Public Health (PENAPH) on 10-12 January 2018, in Khon Kaen, Thailand. Details will be forthcoming, but please visit the hyperlink for further information (https://penaph.net/second-penaph-conference-participatory-approaches-in-animal-health-public-health-one-health-and-ecohealth/).
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>
> V/r,

Katie Leahy

Program Manager | Global Systems Engineering

5881 Leesburg Pike, Suite 506

Baileys Crossroads, VA 22041

http://globalsyseng.com

--

Dr Abel WADE
Director of the National Veterinary Laboratory (LANAVET) annex inYaounde
Ministry of Livestock, Fisheries and Animal Industries (MINEPIA)
Yaounde-Cameroon

www.lanavet.com; www.minepia.org.cm

From: Gavin James Smith <
Sent: Wednesday, August 23, 2017 9:56 PM EDT
To: Kading,Rebekah >
CC: Kevin Olival, PhD ecohealthalliance.org>; Katie Leahy >; Robert Kityo ; Ian Mendenhall >; Joram Buza >; Vivek Kapur >; Jon Epstein ecohealthalliance.org>; Lela Urushadaze ; Lela Urushadaze >; Tamar Kutateladze >; Supaporn Wacharapluesadee >; Abel Wade ; Catalino Demetria >; Tigga Kingston ; Paul Cryan ; DeeAnn Reeder >; Nisreen AL-Hmoud < >; Mary J. Lancaster Ph.D. ; Martha M CIV Stokes >; Sander, William E CTR (US) >; Caitlin Devaney >
Subject: Re: GBA Update and Request

Hi All. I look forward to working with this group and hopefully I am able to make it to the Thailand meeting.

Regarding the name, my preference is for Option 2 with the modification suggested by Kevin, so the Global Alliance for Bat-borne Pathogens Research".

Best Wishes,
Gavin.

Dr Gavin JD Smith | Associate Professor | Programme in Emerging Infectious Diseases, Duke-NUS Medical School | 8 College Road, Singapore 169857 | Tel +65 6601 1109 Fax +65 6221 2529 | Email gavin.smith@duke-nus.edu.sg and Associate Research Professor of Global Health | Duke Global Health Institute, Duke University | Durham NC United States

On 23 Aug 2017, at 11:43 PM, Kading,Rebekah wrote:

Hi Everyone,

Thank you Katie for sending the update! I will look forward to the next steps for our group! I vote for option #1, however I do think Kevin's suggestion for modifying option #2 is good.

Best regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kevin Olival, PhD
Sent: Wednesday, August 23, 2017 8:22:17 AM
To: Katie Leahy
Cc: Robert Kityo; Ian MENDENHALL PhD; Joram Buza; Vivek Kapur; Jon Epstein; Kading,Rebekah; Lela Urushadaze; Lela Urushadaze; Tamar Kutateladze; Supaporn Wacharapluesadee; Abel Wade; Catalino Demetria; Tigga Kingston; Paul Cryan; DeeAnn Reeder; Gavin Smith; Nisreen AL-Hmoud; Mary J. Lancaster Ph.D.; Martha M CIV Stokes; Sander, William E CTR (US); Caitlin Devaney
Subject: Re: GBA Update and Request

Dear Katie and all,

First off, congratulations to Jon and Vivek, very happy to see them both selected as our first co-chairs!

Unfortunately I have another meeting in Europe the week of Jan 10th, so will likely be unable to make Khon Kaen.

As for the name, I'll cast a vote for #1. One option to alleviate DeeAnn's valid concerns about grammar would be to add the word research to the end of option #2. e.gGlobal Alliance for Bat-borne Pathogens Research (GABPR). Just a suggestion.

Best regards,
Kevin

Kevin J. Olival, PhD
Associate Vice President for Research

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

www.ecohealthalliance.org

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

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V/r,

Katie Leahy
Program Manager | Global Systems Engineering
5881 Leesburg Pike, Suite 506
Baileys Crossroads, VA 22041

http://globalsyseng.com

From: Kevin Olival, PhD ecohealthalliance.org>
Sent: Wednesday, August 23, 2017 10:22 AM EDT
To: Katie Leahy
CC: Robert Kityo >; Ian MENDENHALL PhD >; Joram Buza ; Vivek Kapur ; Jon Epstein <epstein Kading,Rebekah >; Lela Urushadaze ; Lela Urushadaze >; Tamar Kutateladze >; Supaporn Wacharapluesadee ; Abel Wade Catalino Demetria >; Tigga Kingston ; Paul Cryan DeeAnn Reeder >; Gavin Smith >; Nisreen AL-Hmoud ; Mary J. Lancaster Ph.D. >; Martha M CIV Stokes >; Sander, William E CTR (US) >; Caitlin Devaney
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Kevin

Kevin J. Olival, PhD
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)

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>
> V/r,

Katie Leahy
Program Manager | Global Systems Engineering
5881 Leesburg Pike, Suite 506
Baileys Crossroads, VA 22041

http://globalsyseng.com

From: Lela Urushadze >
Sent: Wednesday, August 23, 2017 6:39 AM EDT
To: Katie Leahy >
CC: Robert Kityo Ian Mendenhall <i ; Joram Buza ; Vivek Kapur ; Kevin Olival ecohealthalliance.org>; Jon Epstein @ecohealthalliance.org>; Kading,Rebekah ; Lela Urushadaze >; Tamar Kutateladze ; Supaporn Wacharapluesadee ; Abel Wade >; Catalino Demetria < >; Tigga Kingston ; Paul Cryan ; DeeAnn Reeder ; Gavin Smith ; Nisreen Alhmoud ; Lancaster, Mary J CIV (US) >; Stokes, Martha M CIV (US) >; Sander, William E CTR (US) ; Caitlin Devaney >
Subject: Re: GBA Update and Request

Dear Katie

Great that next meeting will be Thailand, PENAPH
Due to Dr Reeder concern that we are not an "Alliance for Pathogens", I will change my preference and will support for BPERN

Best regards
Lela

On Wed, Aug 23, 2017 at 4:17 AM, Katie Leahy< wrote:

> All,
>
> On behalf of Dr. Mary Lancaster and Dr. Marty Stokes, we would like to thank everyone, for your responses over the last couple weeks! Based on your feedback, we have a few announcements and one request:
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Katie Leahy

Program Manager | Global Systems Engineering

5881 Leesburg Pike, Suite 506

Baileys Crossroads, VA 22041

http://globalsyseng.com

--
Lela Urushadze M.Sc.
Senior specialist
National Center for Disease Control and Public Health (NCDC) of Georgia
9M. Asatiani str. Tbilisi, 0177, Georgia

From: Tamar Kutateladze >
Sent: Thursday, August 24, 2017 2:32 AM EDT
To: Katie Leahy ; Robert Kityo < Ian Mendenhall ; Joram Buza Vivek Kapur ; Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Kading,Rebekah Lela Urushadaze ; Lela Urushadaze Supaporn Wacharapluesadee ; Abel Wade ; Catalino Demetria Tigga Kingston < Paul Cryan DeeAnn Reeder Gavin Smith ; Nisreen Alhmoud >
CC: Lancaster, Mary J CIV (US) ; Stokes, Martha M CIV (US) >; Sander, William E CTR (US) >; Caitlin Devaney >
Subject: Re: GBA Update and Request

Dear Colleagues,

Glad to see the PENAPH meeting selected.

As for the name, I vote for option #1, however Option 2 with the modification - "Global Alliance for Bat-borne Pathogens Research" is also good.

Best regards,

Tamar Kutateladze
NCDC&PH,Tbilisi,Georgia

All,

On behalf of Dr. Mary Lancaster and Dr. Marty Stokes, we would like to thank everyone, for your responses over the last couple weeks! Based on your feedback, we have a few announcements and one request:

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Baileys Crossroads, VA 22041

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From: Robert Kityo >
Sent: Tuesday, August 22, 2017 10:13 PM EDT
To: Katie Leahy
CC: Ian Mendenhall >; Joram Buza Vivek Kapur ; Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Kading,Rebekah ; Lela Urushadaze >; Lela Urushadaze ; Tamar Kutateladze ; Supaporn Wacharapluesadee ; Abel Wade ; Catalino Demetria ; Tigga Kingston ; Paul Cryan ; DeeAnn Reeder ; Gavin Smith < ; Nisreen Alhmoud ; Lancaster, Mary J CIV (US) ; Stokes, Martha M CIV (US) ; Sander, William E CTR (US) ; Caitlin Devaney
Subject: Re: GBA Update and Request

Dear Katie
Glad to receive yours and the updates. I shall be looking out for further notifications and updates
I like the name in option 1.
Best regards
Robert Kityo

Kityo Robert M (PhD)
Makerere University
College of Natural Sciences
School of BioSciences
Department of Zoology, Entomology and Fisheries Sciences
P.O. Box 7062 Kampala
Phone:
alternate email addresses:

On Wed, Aug 23, 2017 at 3:17 AM, Katie Leahy< > wrote:

> All,
>
> On behalf of Dr. Mary Lancaster and Dr. Marty Stokes, we would like to thank everyone, for your responses over the last couple weeks! Based on your feedback, we have a few announcements and one request:
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> V/r,

Katie Leahy

Program Manager | Global Systems Engineering

5881 Leesburg Pike, Suite 506

Baileys Crossroads, VA 22041

http://globalsyseng.com

From: Katie Leahy
Sent: Monday, June 12, 2017 10:46 AM EDT
To: Kevin Olival, PhD ecohealthalliance.org>
CC: Prof. Joram Buza >; Devaney, Caitlin (US) Martha M CIV Stokes ; Leahy, Catharine (US) Mary J. Lancaster Ph.D. >; Sander, William E CTR (US) Vivek Kapur Jon Epstein @ecohealthalliance.org>; gavin. Ian MENDENHALL PhD >; kityrob ; Kading,Rebekah >; Caitlin Devaney >; mary dugan >
Subject: Re: Global Bat Alliance Follow-up

Hi, Kevin. I will not speak for Marty and Mary here, but I think we are open to your suggestions. The intent is to capture a global picture of research, researchers, and networks, so we can better see where there are gaps, and where to target investments. At some point, we envision turning this into a database with a map overlay, so the more inclusive the better.

Thanks!

Katie

From: "Kevin Olival, PhD" ecohealthalliance.org>
Date: Monday, June 12, 2017 at 10:33 AM
To: Katie Leahy < >
Cc: "Prof. Joram Buza" >, "Devaney, Caitlin (US)" >, Martha M CIV Stokes , "Leahy, Catharine (US)" < , "Mary J. Lancaster Ph.D." , "Sander, William E CTR (US)" >, Vivek Kapur , Jon Epstein ecohealthalliance.org>, "gavin.smith " Ian MENDENHALL PhD >, "kityrob " < , "Rebekah.Kading < >, Caitlin Devaney , mary dugan
Subject: Re: Global Bat Alliance Follow-up

Thanks for this Katie. What are your criteria for inclusion here? We have been keeping track of a bunch of bat disease studies for various project here at EcoHealth Alliance, so would be happy to advise and contribute to this list depending on how inclusive you want to be - there will be 100s of papers!

Cheers,
Kevin

Kevin J. Olival, PhD
Associate Vice President for Research

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> On Jun 12, 2017, at 9:53 AM, Katie Leahy > wrote:
>
> All,
>
> As a follow-up to last week's GBA call, please find a very rough draft spreadsheet of the information we have collected for the GBA. Please take a look and modify or add to the list as needed.
>
> We are in the process of updating the Terms of Reference and will get a second draft of that out to the group in the next day.
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> V/r,
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> Katie Leahy
> <GBA Database[1].xlsx>

From: Kevin Olival, PhD ecohealthalliance.org>
Sent: Monday, June 12, 2017 10:33 AM EDT
To: Katie Leahy >
CC: Prof. Joram Buza >; Devaney, Caitlin (US) >; Martha M CIV Stokes < Leahy, Catharine (US) >; Mary J. Lancaster Ph.D. ; Sander, William E CTR (US) < >; Vivek Kapur >; Jon Epstein ecohealthalliance.org>; gavin.smith Ian MENDENHALL PhD ; kityrob Kading,Rebekah Caitlin Devaney >; mary dugan >
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> V/r,
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> Katie Leahy
> <GBA Database[1].xlsx>

From: Katie Leahy
Sent: Tuesday, January 30, 2018 1:14 AM EST
To: lance.r.brooks < ; Newman, Carl I CIV DTRA J3-7 (US)
Lancaster, Mary J CIV (US)
christopher.r.lewis < Kading,Rebekah
>; DeeAnn Reeder >; Cryan, Paul >; Vivek
Kapur >; Gavin James Smith ; Tigga Kingston
abelwade Ian Mendenhall
tamar_kutateladze < >; Keti Sidamonidze
>: Lela Urushadze < >; joram.buza
c_demetri ; Kevin Olival < >; Jon
Epstein >; cryan.paul
CC: Stokes, Martha M CIV (US) ; Simmi Ghai S
Wacharapluesadee >
Subject: Afternoon Session
Attachment(s): "Afternoon Session BPERNet.pptx"

All,

Here are slides to start filling out for the afternoon session.

V/r,

Katie Leahy

From: Katie Leahy >
Date: Tuesday, January 30, 2018 at 10:30 AM
To: "lance.r.brooks "Newman, Carl I CIV DTRA J3-7 (US)"
>, "Lancaster, Mary J CIV (US)" < >,
"christopher.r.lewis "Kading,Rebekah"
, DeeAnn Reeder "Cryan, Paul" Vivek
Kapur >, Gavin James Smith Tigga Kingston
, "abelwade ' >, Ian Mendenhall
"tamar_kutateladze , Keti Sidamonidze
, Lela Urushadze , "joram.buza
"c_demetria " , Kevin Olival Jon
Epstein , Jason Rao >, "cryan.paul "

Cc: "Stokes, Martha M CIV (US)" , Simmi Ghai , S
Wacharapluesadee
Subject: NEW SLIDES

Here are the working group slides that were live-edited for your use in break-out groups.

V/r,

Katie Leahy

From: Katie Leahy >
Date: Monday, January 29, 2018 at 9:01 PM
To: "lance.r.brooks " >, "Newman, Carl I CIV DTRA J3-7 (US)"
>, "Lancaster, Mary J CIV (US)" ,
"christopher.r.lewis " "Kading,Rebekah"
, DeeAnn Reeder >, "Cryan, Paul" Vivek
Kapur , Gavin James Smith Tigga Kingston
, "abelwade , Ian Mendenhall
"tamar_kutateladze " >, Keti Sidamonidze
, Lela Urushadze "joram.buza
ais "c_demetria , Kevin Olival , Jon
Epstein , "cryan.paul

Cc: "Stokes, Martha M CIV (US)" , Simmi Ghai >, S
Wacharapluesadee
Subject: Update to the BPERNet Slides

Hi, everyone! We made a couple changes to the slides for tomorrow. Nothing substantive, just our approach to conducting the brief-out discussions and the order of a couple of the initial slides.

A reminder again to please be in the lobby at 0745, the bus will depart for Chulalongkorn promptly at 0800.

V/r,

Katie Leahy

From: Katie Leahy >
Date: Monday, Januarv 29. 2018 at 10:28 AM
To: "lance.r.brooks >, "Newman, Carl I CIV DTRA J3-7 (US)" , "Lancaster, Mary J CIV (US)" , "christopher.r.lewis , "Kading,Rebekah" , DeeAnn Reeder , "Cryan, Paul" , Vivek Gavin James Smith , Tigga Kingston , "abelwade Ian Mendenhall "tamar_kutateladze Keti Sidamonidze , Lela Urushadze >, "joram.buza "c_demetria , Kevin Olival , Jon Epstein >
Cc: "Stokes, Martha M CIV (US)" , Simmi Ghai >, S Wacharapluesadee
Subject: BPERNet: Transportation Times and Other Useful Information (30 and 31 January 2017)

Hello, everyone! Welcome to Bangkok. On behalf of the Executive Committee (Dr. Martha Stokes and Dr. Mary Lancaster), we are so pleased that you are able to join us this week for our BPERNet planning meeting and other PMAC activities.

Please use this email as your resource for information regarding transportation, logistics, and other coordinating information for 30 January – 31 January.

30 January – BPERNet Meeting at Chulalongkorn Hospital

1. **The bus will depart from the Renaissance Hotel promptly at 0800** ; please be in the lobby for head count at 0745
2. We will provide coffee and light refreshment during the meeting; you will take lunch at one of the many canteen options at the hotel; please bring about 200 - 300 thai baht (~10 USD) for lunch

31 January – PMAC / BPERNet Field Trip

1. **The bus will depart from the Renaissance Hotel promptly at 0630** ; please be in the lobby for head count at 0615; please make sure that you are on time, as we are caravanning with a delegation from the Centara Hotel and will receive a police escort to move us quickly through traffic
2. We will provide a box breakfast for the bus ride
3. Please make sure that you dress appropriately for this field trip; we strongly suggest covered shoes and loose, comfortable clothing; in addition to this mode of dress we also suggest that you bring accompaniments for spending a day outdoors amongst bat roosts; such as:
    a. Hat
    b. Sunscreen
    c. Sunglasses
    d. Bug spray
    e. Water bottle

We will provide information regarding the Ambassador's reception at the close of tomorrow's meeting.

Again, we are so excited to have you all here. Please do not hesitate to reach out to me or Megan Hudson (copied) if you have any questions.

V/r,

Katie Leahy

Katie Leahy
Program Manager | Global Systems Engineering
6303 Little River Turnpike, Suite 208
Alexandria, VA 22305

http://globalsyseng.com

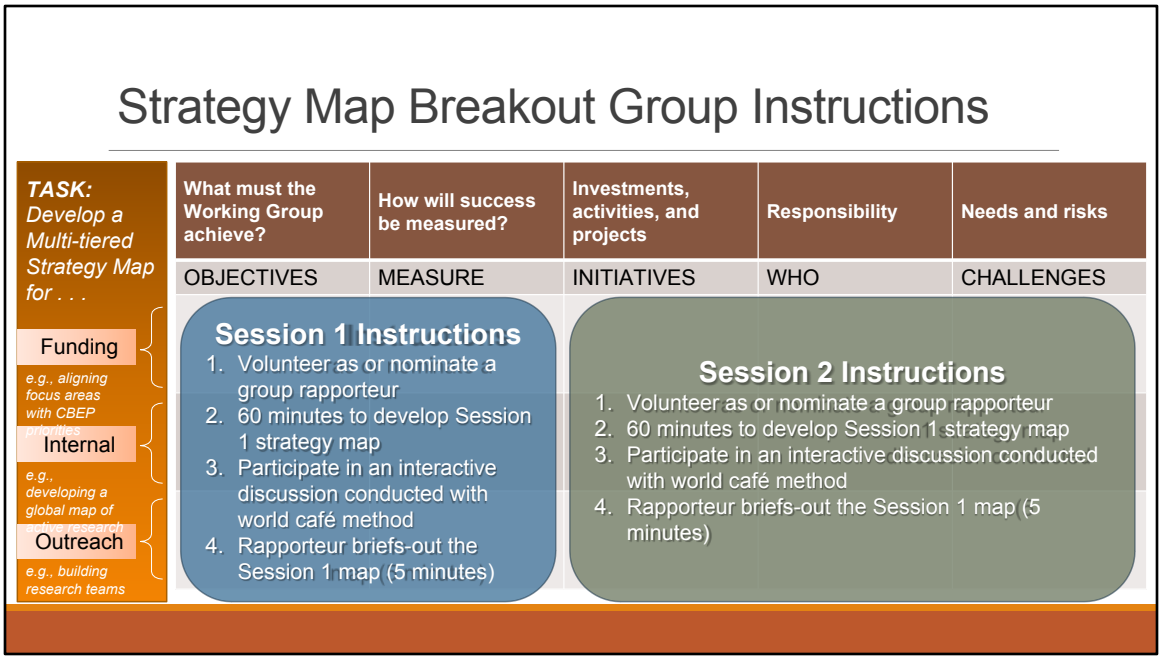
Today's Agenda

1215 – 1330	Lunch
1330 – 1430	Session 2: Focus Area Strategy Mapping
1430 – 1510	Session 2: Interactive Feedback (World Café Method)
1510 – 1530	Breakout Group Session 2 Summary (5-minutes / group)
1530 – 1545	Working Tea Break
1545 – 1615	Close-out Discussion (next steps)

Revisit: Working Groups and Research Mentors

Working Group	Research Mentors
1. Host-pathogen biology and interactions	◦ Dr. Joram Buza ◦ Dr. Vivek Kapur ◦ Dr. DeeAnn Reeder ◦ Dr. Gavin Smith
2. Pathogen surveillance, diagnostic capacity, and epidemiology	◦ Dr. Catalino Demetria ◦ Dr. Jon Epstein ◦ Dr. Tamar Kutateladze ◦ Dr. Abel Wade ◦ Dr. Keti Sidamonidze
3. Ecology setting	◦ Dr. Paul Cryan ◦ Dr. Tigga Kingston ◦ Dr. Robert Kityo ◦ Dr. Rebekah Kading ◦ Dr. Eiichi Hondo
4. Human-bat interactions	◦ Dr. Kevin Olival ◦ Dr. Ian Mendenhall ◦ Dr. Supaporn Wacharapluesadee ◦ Dr. Lela Urushadze ◦ Dr. Nesreen Alhmoud

Strategy Map Breakout Group Instructions



Session 1: Strategy Map

What must the Working Group achieve?	How will success be measured?
OBJECTIVES	MEASURE

Session 2: Strategy Map

Investments, activities, and projects	Responsibility	Needs and risks
INITIATIVES	WHO	CHALLENGES

From: Kevin Olival ecohealthalliance.org>
Sent: Monday, August 13, 2018 11:55 PM EDT
To: Kading,Rebekah <
Subject: Away from office Aug 10-17 Re: Draft Executive Summary and Website Materials

I will be on vacation from Aug 10-17th, and back in the office on Aug 20th.

I will respond to you as soon as possible after Aug 20th.

Cheers,
Kevin

From: Schountz,Tony
Sent: Thursday, June 22, 2017 3:23 PM
To:

; Kading,Rebekah;

Cc: Charles H Calisher; Kading,Rebekah; Fagre,Anna; Rovnak,Joel; Amy T Gilbert; Rosenberg,Corey; Prescott, Joseph (NIH/NIAID) [E]; Szalai,Edit; Schountz,Tony; Miles Eckley; Malmlov,Ashley; Candace Cotter
Subject: Bat ID Symposium logistics

Dear Colleagues,

The symposium is one week away and I want to provide you with some logistical information for your arrival to Fort Collins.

1. Speakers. If you can email your presentation directly to me I will get it on the computer for the presentation.**However, the file size must be less than 15 MB to accommodate our email server limit**. Otherwise, please bring your presentation on a USB drive if it is larger than 15 mb. We will have both Microsoft Power Point and Apple Keynote software for your presentations. **Bring your USB drive to the Thursday evening reception if you want to transfer it then.**

2. Poster presenters. The maximum size of the posters is 48" x 48" (120 cm x 120 cm). We will provide push pins to mount your poster on the easels. When you register, your poster will have a number assigned to it that corresponds to the easel number. Please mount your poster on that easel. **Bring your poster to the Thursday evening reception.**

3. Getting to Fort Collins. Those of you who are flying to Denver International Airport can schedule a ride with the**Green Ride Airport Shuttle** service. Please visit its web site (https://greenrideco.hudsonltd.net/) to make arrangements convenient for your flight schedules. There is a Green Ride desk in the main terminal at the airport with employees that can help you find the bus pickup. The bus ride is about 1 hour and 15 minutes. On the web site, in the box "Dropoff location" choose the appropriate destination from the pull-down menu. For those of you staying in the university dormitories it is "FC - Laurel Village", the Hilton Hotel near campus is "FC - Hilton Ft Collins", and the University Inn is "FC - Best Western University Inn". And just to make you aware, afternoon and evening flights into Denver can be rather bumpy!

4. Weather and Climate. Fort Collins has lots of sunshine and is at 5000 ft/1500 meters. If you intend to be outdoors much you should bring sunscreen. We often get afternoon thunder showers in our otherwise dry climate but they are typically not more than an hour or two and it usually clears up afterwards. You may want to bring rain gear or a small umbrella. The current forecast is for the mid to high 80sF/low 30sC.

5. Getting to the UCA. The conference venue is the **University Center for the Arts (UCA)** (attached map, blue box, lower right). Oral and poster presentations will be in this building and directions will be posted inside. After you get settled in Thursday, please come to the UCA for the opening registration and social mixer by 5:30 PM. Walking paths (routes) are noted in blue hatched lines.

A. Laurel Village Alpine Dormitory. Those who are staying in campus housing, walk south to Plum Street and turn east to Meridian Avenue. Take Meridian Avenue south to Pitkin Street and take it east to Mason Street. Cross the railroad tracks and immediately turn right (south) just before the parking garage. Follow the path to just past the parking garage and turn left (east). This path leads to a **tunnel that passes under College Avenue** and comes out at the University Test Gardens (lots of flowers). Continue on this path and it will cross Remington Street to the UCA. **Allow 15-20 minutes to walk**.

B. Hilton Hotel. Proceed from the hotel to Prospect and Centre Avenue at the northwest corner of the Hilton Hotel parking lot. Cross

Centre to the west and **take the tunnel under Prospect Avenue**. At Lake Street, turn right (east) to Mason Street. Cross the railroad tracks and immediately turn left (north). Just before the parking garage, turn right (east) and take the path that leads to a **tunnel that passes under College Avenue** and comes out at the University Test Gardens. Continue on this path and it will cross Remington Street to the UCA. **Allow 10 minutes to walk**.

C. University Inn Best Western Hotel. Take Elizabeth Street east to Remington Street (one block). Turn right (south) to Pitkin Street. Once you cross Pitkin Street, the University Center for the Arts is to your left. **Allow 5 minutes to walk.**

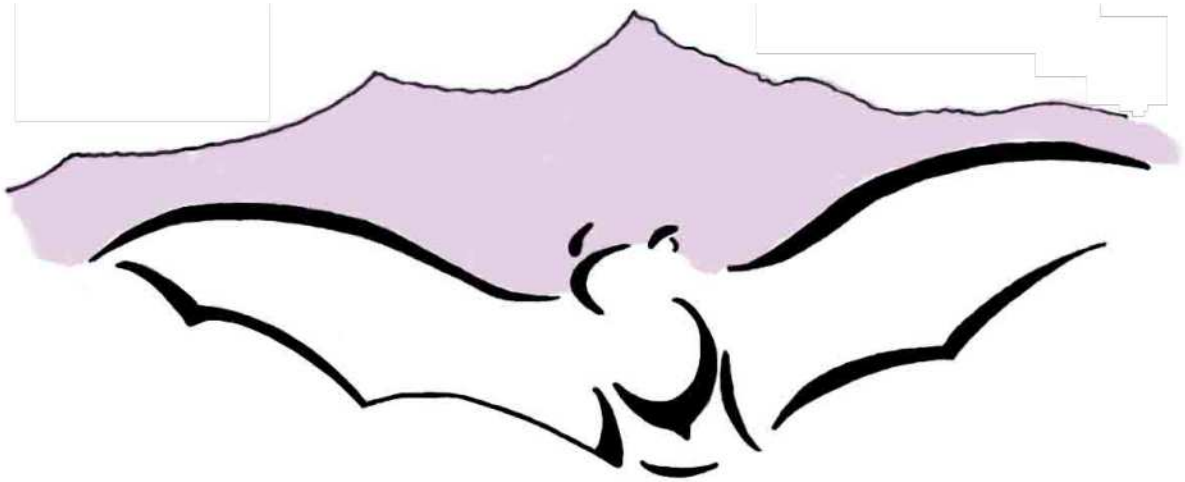
6. Registration packet. Your registration packet will include the program, name badge, water bottle and a pass for the Fort Collins MAX bus. The pass allows you to ride the bus through Saturday night. Registration also includes lunch for Friday and Saturday. If you are staying in the dorms you will also have breakfast provided at the dorm dining hall, Corbett Hall, which is just east of Alpine Hall where you are staying (please see the attached map).

If you have questions, please contact me and I will address them. Finally, I will be at the American Society for Virology meeting Saturday through Wednesday so my email access may be intermittent.

Thanks and see you next week.

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

Infectious Diseases of Bats Symposium



June 29-July 1, 2017
University Center for the Arts
1400 Remington St
Colorado State University
Fort Collins, CO 80524

Table of Contents

Program

Venue: **University Center for the Arts**, Colorado State University

Thursday, June 29

5:30 p.m. Registration, PowerPoint file transfer, lobby, **University Center for the Arts**

6:00 p.m. Reception - *Wine, beer and snacks*, **University Center for the Arts**

Friday, June 30

7:00 a.m. Registration, University Center for the Arts

8:00 a.m. Tony Schountz. Colorado State University. **Welcoming remarks**

8:10 a.m. Session I - Filoviruses (Joseph Prescott, Moderator)

8:10 a.m. **Studies of horizontal transmission of Marburg virus among experimentally infected fruit bats**
Jonathan S. Towner[1,2], Amy J. Schuh[1], Brian R. Amman[1], Megan E. B. Jones[1,2], Tara K. Sealy[1], Uebelhoer LS, Spengler JR, Stuart T. Nichol[1]

[1]Viral Special Pathogens Branch, Centers for Disease Control and Prevention, Atlanta, USA, [2]Department of Pathology, College of Veterinary Medicine, University of Georgia, Athens, USA

8:30 a.m. **Investigations of Long-term Protective Immunity against Marburg Virus Reinfection in Egyptian Rousette Bats**
Amy Schuh, Amman BR, Sealy TK, Spengler JR, Nichol ST and Towner JS

Viral Special Pathogens Branch, Division of High-Consequence Pathogens and Pathology, Centers for Disease Control and Prevention, Atlanta, GA 30333, USA

8:45 a.m. **Innate immune response to filoviruses and the role of filoviral interferon-inhibiting domains in bat and human cells**
Ivan V. Kuzmin[1,2], Toni M. Schwarz[3], Philipp A. Ilinykh[1,2], Ingo Jordan[4], Thomas G. Ksiazek[1,2,5], Ravi Sachidanandam[6], Christopher F. Basler[3, 7], and Alexander Bukreyev[1,2,5]

[1] Department of Pathology, The University of Texas Medical Branch, Galveston, Texas, USA; [2] Galveston National Laboratory, The University of Texas Medical Branch, Galveston, Texas, USA; [3] Department of Microbiology, Icahn School of Medicine at Mount Sinai, New York, New York, USA; [4] ProBioGen AG, Berlin, Germany; [5] Department Microbiology & Immunology, The University of Texas Medical Branch, Galveston, Texas, USA; [6] Department of Oncological Sciences, Icahn School of Medicine at Mount Sinai, New York, New York, USA; [7] Current Address: Center for Microbial Pathogenesis, Institute for Biomedical Sciences, Georgia Research Alliance, Eminent Scholar in Virology, Georgia State University, Atlanta, Georgia, USA

9:00 a.m. **Broad based surveillance for ebolaviruses: PREDICT in Sierra Leone, Liberia, and Guinea.**
Brian Bird[1], Goldstein T[1], Anthony S[2], Gbakima A[3], Saylors K[3], Jean Louis F[3], Wolking D[1], Epstein J[4], Karesh W[4], Kreuder-Johnson C[1], Mazet J[1]

One Health Institute UC Davis School of Veterinary Medicine[1], Center for Infection and Immunity Columbia University[2], Metabiota Inc.[3], EcoHealth Alliance[4]

9:15 a.m. **Quantifying signatures of resistance and tolerance to filoviruses in bat cell lines**
Cara E. Brook[1], Melinda Ng[2], Esther Ndungo, Rohit K. Jangra, Andrew P. Dobson, Andrea L. Graham, Bryan T. Grenfell, C. Jessica E. Metcalf[1]*, Kartik Chandran[1]*
[1]Department of Ecology and Evolutionary Biology, Princeton University;
[2]Department of Microbiology and Immunology, Albert Einstein College of Medicine
*These senior authors contributed equally to this work.

9:30 a.m. **Serologic evidence of exposure to filoviruses in fruit bats, Singapore**
Laing ED[1], Ian H Mendenhall[2], Linster M[2], Low DHW[2], Chen Y[2], Yan L[1], Sterling SL[1], Borthwick S[2], Neves ES[2], Lim JSL[2], Skiles M[2], Lee BPY[4], Wang LF[2], Broder CC[1], Smith GJD[2, 5]

Uniformed Services University, Bethesda, MD, USA[1], Duke-National University of Singapore Medical School, Singapore[2], North Carolina State University, Raleigh, NC, USA[3], National Parks Board, Singapore[4], Duke Global Health Institute, Duke University, Durham, North Carolina, USA[5]

9:45 a.m. **Predicting undiscovered filovirus reservoirs and patterns of disease emergence**
David Hayman

Molecular Epidemiology and Public Health Laboratory, Hopkirk Research Institute, Massey University, New Zealand

10:00 a.m. Break

10:30 a.m. Session II - Coronaviruses A (Joel Rovnak, Moderator)

10:30 a.m. **Bats as possible animal origin of MERS-CoV**
Susanna K. P. Lau

Department of Microbiology, The University of Hong Kong, Hong Kong, China

10:45 a.m. **Rapid detection of MERS coronavirus ancestors in bats**
Prof. Patrick CY Woo

Department of Microbiology, The University of Hong Kong, Hong Kong.

11:00 a.m. **Global patterns in coronavirus diversity**
Simon J Anthony[1,2,3]; Johnson, C.K[4]; Greig, D.J[4]; Kramer, S[1,5]; Che, X[1]; Wells, H[1]; Hicks, A.L[1]; Joly, D.O[6, 7]; Wolfe, N.D[6]; Daszak, P[3]; Karesh, W[3]; Lipkin, W.I[1,2]; Morse, S.S[2]; PREDICT Consortium[8]; Mazet, J.A.K[4]; Goldstein, T[4]

[1]Center for Infection and Immunity, Mailman School of Public Health, Columbia University, 722 West 168th Street, New York, NY, 10032 (USA); [2]Dept of Epidemiology, Mailman School of Public Health, Columbia University, 722 West 168th Street, New York, NY (USA); [3]EcoHealth Alliance, 460 West 34th Street, NY, New York (USA); [4]One Health Institute & Karen C Drayer Wildlife Health Center, School of Veterinary Medicine, University of California Davis, California (USA); [5]Dept of Environmental Health Sciences, Mailman School of Public Health, Columbia University, 722 West 168th Street, New York, NY (USA); [6]Metabiota, Inc. One Sutter, Suite 600, San Francisco, CA, 94104 (USA); [7]Wildlife Conservation Society, New York, NY, (USA)

11:15 a.m. **SARS coronavirus may have originated from frequent recombination events between SARS-like coronaviruses in a single horseshoe bat habitat**
Ben Hu[1], Lei-Ping Zeng[1], Xing-Lou Yang[1], Xing-Yi Ge[1], Wei Zhang[1], Bei Li[1], Dong-Sheng Luo[1], Yun-Zhi Zhang[2], Mei-Niang Wang[1], Peter Daszak[3], Lin-Fa Wang[4], Jie Cui[1], Zheng-Li Shi[1]

[1] CAS Key Laboratory of Special Pathogens and Biosafety, Center for Emerging Infectious Diseases, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China; [2]Yunnan Institute of Endemic Diseases Control and Prevention, Dali, China; [3]EcoHealth Alliance, New York City, New York, USA; [4]Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore.

11:30 a.m. **A metagenomic approach identifying a MERS-related coronavirus in a bat from South Africa**
Marike Geldenhuys[1], Marinda Mortlock[1], Jaqueline Weyer[2], Oliver Bezuidt[3], Ernest Seamark[4], Teresa Kearney[5,6], Cheryl Gleasner [7], Tracey Erkkila[7], Helen Cui[7] and Wanda Markotter[1]

[1] Centre for Viral Zoonosis, Department of Medical Virology, Faculty of Health sciences, University of Pretoria, Pretoria, South Africa. [2] Centre for Emerging, Zoonotic and Parasitic Diseases,

National Institute for Communicable Diseases, Sandringham, South Africa. [3] Centre for Microbial Ecology and Genomics, University of Pretoria, Pretoria, South Africa. [4] AfricanBats NPC, South Africa and Centre for Wildlife Management, University of Pretoria, Pretoria, South Africa. [5] Animal, Plant and Environmental Sciences, University of the Witwatersrand, Johannesburg, South Africa

12:00 p.m. Lunch and Poster Session

2:00 p.m. Session III - Rhabdoviruses (Ashley Malmlov, Moderator)

2:00 p.m. **New insights into the antiviral innate immune response of *Desmodus rotundus***
Sarkis Sarkis, Marie-Claude Lise, Edith Darcissac, Stéphanie Dabo, Christine Neuveut, Benoît de Thoisy, Eliane Meurs, Anne Lavergne and Vincent Lacoste

Institut Pasteur de la Guyane, French Guiana/ France

2:15 p.m. **A comparative study of the autophagy pathway during virus infection of bat (natural) and human (accidental) host cells**
Eric D. Laing[1], Spencer L. Sterling[1], Dawn L. Weir[1], Sasha E. Larsen[2], Linfa Wang[3], Brian C. Schaefer[1], and Christopher C. Broder[1]

[1]Department of Microbiology, Uniformed Services University, Bethesda, MD, USA; [2]Department of Pharmacology, Uniformed Services University, Bethesda, MD, USA; [3]Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore

2:30 p.m. **Lagos bat virus in South Africa, 2013-2017**
Jessica Coertse[1], Le Roux, K.[2], Richardson, E.[3], White, W.[3], Markotter, W.[1]

[1]Centre for Viral Zoonoses, Department of Medical Virology, Faculty of Health Sciences, University of Pretoria, South Africa; [2]Allerton Provincial Veterinary Laboratory, Pietermaritzburg, KwaZulu-Natal, South Africa; [3]KwaZulu-Natal Bat Interest Group, KwaZulu-Natal, South Africa

2:45 p.m. **Characterization of a novel Rhabdovirus isolated from insectivorous bat (*Pipistrellus kuhlii*) in Italy**
Davide Lelli[1], Alice Prosperi[1], Chiara Chiapponi[1], Paola Debenedictis[2], Anna Maria Gibellini[3], Stefania Leopardi[2], Enrica Sozzi[1], Dino Scaravelli[4], Ana Moreno[1], Antonio Lavazza[1]

[1]Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna, Via Bianchi 9 - 25124 Brescia, Italy; [2]Istituto Zooprofilattico Sperimentale delle Venezie, OIE Collaborating Centre and National Reference Centre for Research on Infectious Diseases at the Animal-Human Interface, Viale dell'Università 10 - 35020 Legnaro (PD), Italy; [3]Wildlife Rehabilitation Center WWF of Valpredina via Pioda n.1, 24060 Cenate Sopra(BG), Italy; [4]University of Bologna, Department of Veterinary Medical Sciences, via Tolara di sopra 50 - 40064 Ozzano Emilia (BO), Italy

3:00 p.m. Session IV - Paramyxoviruses (Danielle Adney, Moderator)

3:00 p.m. **Age-specific dynamics of maternally- and infection- derived immunity within African bat populations**
Alison J Peel[1], Kate S Baker[2], David TS Hayman[3], Andrew A Cunningham[4], James LN Wood[5], Romain Garnier[5] and Olivier Restif[5]
[1] Environmental Futures Research Institute, Griffith University, Nathan, QLD, Australia; [2] Institute for Integrative Biology, University of Liverpool, UK; [3] Molecular Epidemiology and Public Health Laboratory, Hopkirk Research Institute, Massey University, Palmerston North, New Zealand; [4] Institute of Zoology, Zoological Society of London, Regent's Park, London, UK; [5] Department of Veterinary Medicine, University of Cambridge, Cambridge, UK

3:15 p.m. **Detection of rubula- and related viruses in an Egyptian fruit bat (*Rousettus aegyptiacus*) colony in South Africa**
Marinda Mortlock[1], Jacqueline Weyer[2], Janusz Paweska[2] and Wanda Markotter[1]

[1]Centre for Viral Zoonoses, Department of Medical Virology, Faculty of Health Science, University of Pretoria, South Africa; [2]Centre for Emerging, Zoonotic and Parasitic Diseases, National Institute for Communicable Diseases, Sandringham, Johannesburg, South Africa

3:30 p.m. Break

4:00 p.m. **Influenza-like virus and paramyxovirus screening in Brazilian bats**

Angélica Cristine Campos[1]; Luiz Gustavo Góes[1]; Cristiano Carvalho[2]; Guilherme Ambar[5]; Luciano M. Thomazelli[1]; Jhiovana Cristielly Costa[1]; Mariana Cristine de Souza[1]; Adriana Ruckert[3]; Débora C. Oliveira[3]; Luzia F. Martorelli[3]; Ana Paula Kataoka[3]; Marcelo S. Nardi[4]; Juliana L. Summa[4]; Roberta Marcatti de Azevedo[4]; Wagner A. Pedro[2]; Luzia H. Queiroz[2]; Ariovaldo P. Cruz-Neto[5] and Edison Durigon[1]

[1] Departamento de Microbiologia, Instituto de Ciências Biomédicas (ICB), Universidade de São Paulo (USP), São Paulo-SP; [2] Faculdade de Medicina Veterinária de Araçatuba, Universidade Estadual Paulista (UNESP), Araçatuba- SP; [3] Centro de Controle de Zoonozes (CCZ) do Município de São Paulo-SP; [4] Divisão Técnica de Medicina Veterinária e Manejo da Fauna Silvestre (DEPAVE-3), Secretaria do Verde e Meio Ambiente, Prefeitura do Município de São Paulo, São Paulo-SP; [5] Departamento de Zoologia, Instituto de Biociências, Universidade Estadual Paulista (UNESP), Rio Claro-SP

4:15 p.m. **Hendra virus dynamics and spillover**

Raina Plowright[1], Maureen Kessler[1], Alison Peel[2], Hamish McCallum[2], Peggy Eby[3]

[1]Department of Microbiology and Immunology, Montana State University; [2]Environmental Futures Research Institute, Griffith University, Queensland, Australia; [3]University of New South Wales, Australia.

4:30 p.m. Session V - Methodology in Bat-borne Viruses (Danielle Adney, Moderator)

4:30 p.m. **Using serology to understand the dynamics of concurrent viral infections in pteropid bats**

Jonathan H. Epstein[1], Noam Ross[1], Ariful Islam[1], Dan Crowley[1,2], Gary Crameri[3], Christopher Broder[4], Linfa Wang[5], and Peter Daszak[1].

[1]EcoHealth Alliance, NY USA; [2]Columbia University Mailman School of Public Health, NY USA; [3]CSIRO Australian Animal Health Laboratory, Geelong, VIC, AUS; [4]Uniformed Services University, MD USA; [5]Duke-NUS, Singapore

4:45 p.m. **Estimating viral richness and viral sharing in bats: integrating previously-published and newly-acquired field data**

Kevin J. Olival[1], Noam Ross[1], Evan A. Eskew[1], Anna R. Willoughby[1], Carlos Zambrana-Torrelio[1], Peter Daszak[1], and PREDICT Consortium[2]

[1] EcoHealth Alliance, New York, NY 10001, USA; [2] http://www.vetmed.ucdavis.edu/ohi/predict/publications/Authorship.cfm

5:00 p.m. **Open Discussion**

6:00 p.m. Recess

Saturday, July 1

7:30 a.m. Registration, North Ballroom, University Center for the Arts

8:00 a.m. Session II - Coronaviruses B (Rebekah Kading, Moderator)

8:00 a.m. **Optimised sampling efforts and screening assays identify several MERS-related coronaviruses in South African bats**

Wolfgang Preiser[1,2], Ndapewa L. Ithete[1], Nadine Cronjé[1], Tasnim Suliman[1]

[1]Division of Medical Virology, Faculty of Medicine & Health Sciences, University of Stellenbosch, South Africa; [2]National Health Laboratory Service (NHLS) Tygerberg, Cape Town, South Africa

8:15 a.m. **Coronavirus diversity in bats from urban, rural and forest areas of Atlantic and Amazon Forest biomes, Brazil.**
Luiz Gustavo Góes[1]; Angélica Cristine Campos[1]; Cristiano Carvalho[2]; Guilherme Ambar[5]; Douglas Oliveira[1]; Caroline Alvarenga[1]; Jhiovana Cristielly Costa[1]; Adriana Ruckert[3]; Débora C. Oliveira[3]; Luzia F. Martorelli[3]; Ana Paula Kataoka[3]; Marcelo S. Nardi[4]; Juliana L. Summa[4]; Roberta Marcatti de Azevedo[4]; Luzia H. Queiroz[2]; Ariovaldo P. Cruz-Neto[5] and Edison Durigon[1]

[1]Departamento de Microbiologia, Instituto de Ciências Biomédicas (ICB), Universidade de São Paulo (USP), São Paulo-SP; [2] Faculdade de Medicina Veterinária de Araçatuba, Universidade Estadual Paulista (UNESP), Araçatuba- SP; [3] Centro de Controle de Zoonozes (CCZ) do Município de São Paulo-SP; [4] Divisão Técnica de Medicina Veterinária e Manejo da Fauna Silvestre (DEPAVE-3), Secretaria do Verde e Meio Ambiente, Prefeitura do Município de São Paulo, São Paulo-SP; [5] Departamento de Zoologia, Instituto de Biociências, Universidade Estadual Paulista (UNESP), Rio Claro-SP

8:30 a.m. **Preliminary Evidence of a Novel Alphacoronavirus and Secondary Acquisition of Tymoviridae and Partitiviridae in Little Brown Bats (*Myotis lucifugus*) in Southcentral Alaska.**
Douglas Causey[1], Jonathan C. Rupp*[1], Maegan Lange[1], Megan Howard[2], Anitha Sundarajan[3], Jonny Sena[3], Faye D. Schilkey[3], Molly Murphy[4], Sarah Cooperman[1], Eric Bortz[1]

[1]Dept. of Biological Sciences, University of Alaska Anchorage; [2]Battelle Memorial Institute; [3]National Center for Genome Resources, Santa Fe NM; [4]Dept. of Veterinary Medicine, University of Alaska Fairbanks

8:45 a.m. **Are big brown bat cells different than human cells in their innate immune response to coronavirus and viral ligands?**
Arinjay Banerjee[1], Robert Brownlie[3], Noreen Rapin[1], Trent Bollinger[2], Darryl Falzarano[1,3] and Vikram Misra[1]

[1]Department of Microbiology, Western College of Veterinary Medicine, University of Saskatchewan, Canada. [2]Department of Pathology, Western College of Veterinary Medicine, University of Saskatchewan, Canada. [3]VIDO-InterVac, University of Saskatchewan, Canada.

9:00 a.m. **Session V - Influenza** (Corey Campbell, Moderator)

9:00 a.m. **Reverse genetic analysis of bat influenza viruses: A journey full of surprises.**
Martin Schwemmle

Institute of Virology, University of Freiburg Medical Center

9:30 a.m. **Towards understanding bat influenza A-like viruses**
Wenjun Ma[1], Bin Zhou[2], Jingjiao Ma[1], Qingfang Liu[1], Jinhwa Lee[1], Michael Duff[1], Juergen A. Richt[1], David E. Wentworth[2]
[1]Department of Diagnostic Medicine/Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan, Kansas, United States of America.
[2]Virology, J. Craig Venter Institute, Rockville, Maryland, United States of America.

9:45 a.m. **Experimental Infection of Jamaican Fruit Bats (*Artibeus jamaicensis*) with a Rescued Bat HL18NL11 Influenza A-like Virus**
Tony Schountz[1], Ashley Malmlov[1], Jingjiao Ma[2], Jinhwa Lee[2], Corey Campbell[1], Tawfik Aboellail[1], Ann Hawkinson[3] and Wenjun Ma[2]

[1]Department of Microbiology, Immunology and Pathology, College of Veterinary Medicine and Biomedical Sciences, Colorado State University; [2]Department of Diagnostic Medicine and Pathobiology, College of Veterinary Medicine, Kansas State University; [3]School of Biological Sciences, University of Northern Colorado

10:00 a.m. Break

10:00 a.m. Session VI - Ecology (Paul Cryan, Moderator)

10:30 a.m. **Seroprevalence of alphaviruses, flaviviruses and Rift Valley fever virus in Ugandan bats**
Rebekah C Kading[1,2], Kityo R[3], Mossel E[1], Borland E[1], Nakayiki T[4], Nalikka B[3], Nyakarahuka L[4], Ledermann J[1], Panella N[1], Gilbert A[5,6], Crabtree M[1], Kerbis Peterhans J[7], Towner J[8], Amman B[8], Sealy T[8], Nichol S[8], Powers A[1], Lutwama J[4], Miller B[1]

[1] Centers for Disease Control and Prevention, Division of Vector-borne Diseases, Arbovirus Diseases Branch, Fort Collins, CO. [2]Current Affiliation: Colorado State University, Department of Microbiology, Immunology and Pathology, Fort Collins, CO. [3]Makerere University, Department of Biological Sciences, Kampala, Uganda. [4]Uganda Virus Research Institute, Entebbe, Uganda. [5]Centers for Disease Control and Prevention, Division of High Consequence Pathogens, Rabies and Poxvirus Branch, Atlanta, GA. [6]Current Affiliation: United States Department of Agriculture, Animal and Plant Health Inspection Service, Fort Collins, CO. [7]College of Professional Studies, Roosevelt University &Collections & Research, The Field Museum of Natural History, Chicago, IL. [8]Centers for Disease Control and Prevention, Division of High Consequence Pathogens, Viral Special Pathogens Branch

10:45 a.m. **Presence of zoonotic bat pathogens correlate with reproductive seasons in South African bat populations**
Wanda Markotter[1], Muriel Dietrich[1], Teresa Kearney[2,3], Stewart McCulloch[1], Marinda Mortlock[1], Ernest Seamark[4,5] and Janusz Paweska[6]

[1] Centre for Viral Zoonoses, Department of Medical Virology, Faculty of Health Sciences, University of Pretoria, South Africa. [2] Ditsong National Museum of Natural History, Pretoria, South Africa. [3] Plant and Environmental Sciences, University of the Witwatersrand, Johannesburg, South Africa. [4] AfricanBats, Kloofsig, South Africa. [5] Centre for Wildlife Management, Faculty of Natural and Agricultural Sciences, University of Pretoria, Pretoria, South Africa. [6] Centre for Emerging, Zoonotic and Parasitic Diseases, National Institute for Communicable Diseases, Sandringham, South Africa.

11:00 a.m. **Body mass index of the Egyptian fruit bat, *Rousettus aegyptiacus*: An indicator of infection status**
Low J. de Vries[1], Stewart McCulloch[1], Janusz Paweska[2] and Wanda Markotter[1]

[1]Centre for Viral Zoonoses, Department of Medical Virology, Faculty for Health Science, University of Pretoria, South Africa; [2]Center for Emerging, Zoonotic and Parasitic Diseases, National Institute for Communicable Diseases, Sandringham, Johannesburg, South Africa

11:15 a.m. **Environmental constraints drive the viral diversity of two sympatric Amazonian bat species**
Arielle Salmier, Sourakhata Tirera, Benoit de Thoisy, Alain Franc, Edith Darcissac, Damien Donato, Christiane Bouchier, Vincent Lacoste and Anne Lavergne

Institut Pasteur de la Guyane, French Guiana/ France

11:30 a.m. **Seasonal and individual predictors of grey-headed flying fox (*Pteropus poliocephalus*) foraging movements in Adelaide, South Australia**
Cecilia A. Sánchez[1,2], Terry B. Reardon[3], Wayne S.J. Boardman[4] and Sonia Altizer[1,2]

[1]Odum School of Ecology, University of Georgia, Athens, GA, USA; [2]Center for the Ecology of Infectious Diseases, University of Georgia, Athens, GA, USA; [3]South Australian Museum, Adelaide, South Australia, Australia; [4]University of Adelaide, Adelaide, South Australia, Australia

11:45 a.m. **Uganda Bat calls library-developing a tool to survey arthropod-borne viruses associated with Chiroptera**
Robert Martin Kityo[1], Rebekah Kading[2], Betty Nalikka[1], Julius Lutwama[3]

[1]Makerere University, College of Natural Science – Department of Zoology, Entomology and Fisheries Science Kampala Uganda; [2]Colorado State University; [3]Uganda Virus research institute

12:00 p.m. Lunch

1:00 p.m. Session V - Immunology of Bats (Tony Schountz, Moderator)

1:00 p.m. **Dampening of STING-dependent IFN production: an implication of virus tolerance in bats?**
Jiazhen Xie[1], Chenxi Ma [1], Yang Li[1], Jie Cui[1], Linfa Wang [2], Zhengli Shi [1] and Peng Zhou[1*]

[1]Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan 430071, China; [2]Emerging Infectious programme, Singapore Duke-NUD Medical School, Singapore 169857, Singapore

1:15 p.m. **Regulation of immune activation and dampened inflammation in Pteropid bats**
Aaron T. Irving[1], Katarina Luko[1], Matae Ahn[1], Kong Pui San[1], & Lin-Fa Wang[1]

[1]Duke-NUS Medical School, Singapore

1:30 p.m. **Delineating the phenotype and function of the B cell population in the fruit-eating bat, *Pteropus Alecto.***
Pravin Periasamy[1,2], Martínez Gómez JM[1,2], Wang LF[3] , and Alonso S[1,2]

[1]Department of Microbiology and Immunology, [2]Immunology Programme, Yong Loo Lin School of Medicine, Life Sciences Institute, National University of Singapore, Singapore. [3]DUKE-NUS, Singapore.

1:45 p.m. **Integrative measures for assessing "health" in free-ranging bats – zoonotic and conservation implications from a One Health perspective**
DeeAnn M. Reeder, Kenneth A. Field

Department of Biology, Bucknell University

2:00 p.m. Session VI - White Nose Syndrome (Joel Rovnak, Moderator)

2:00 p.m. **Host-pathogen interactions during white-nose syndrome**
Ken Field[1], Sophia M Reeder[1], Jonathan M Palmer[2], Brent J Sewall[3], Jenni M Prokkola[4], Greg Turner[5], Thomas M Lilley[6], Marianne Gagnon[3], J Paul White[7], Joseph Johnson[8], Christopher Hauer[3], and DeeAnn M Reeder[2]

[1]Department of Biology, Bucknell University, Lewisburg, PA; [2]Center for Forest Mycology Research, Northern Research Station, US Forest Service, Madison, WI; [3]Department of Biology, Temple University, Philadelphia, PA; [4]University of Eastern Finland, Joensuu, Finland; [5]Wildlife Diversity Division, Pennsylvania Game Commission, Harrisburg, PA; [6]Institute of Integrative Biology, University of Liverpool, Liverpool L69 3BX, UK; [7]Wisconsin Department of Natural Resources, Madison, WI; [8]Biological Sciences, Ohio University, Athens, OH

2:15 p.m. **Resistance or Tolerance – How do European bats cope with *Pseudogymnoascus destructans*?**
Marcus Fritze[1,2],Voight CC[2], Czirjak GA[2], Puechmaille SJ[1,3]

[1] Zoology Institute,University of Greifswald,Soldmann-Str. 14, D - 17487 Greifswald, Germany; [2] Leibniz institute for Zoo and Wildlife Research, Alfred-Kowalke-Str. 17, 10315 Berlin, Germany and [3]School of Biology and Environmental Sciences, University College Dublin, Belfield, D4 Dublin Ireland

2:30 p.m. **Modeling the impact of White-nose syndrome on two western bat species**
C. Reed Hranac[1], Brandon J. Klüg-Baerwald[2], Yvonne A. Dzal[3], Cori Lausen[4], Jonathan C. Marshall[1,5], Sarah H. Olson[6] , David T. S. Hayman[1]

[1]Hopkirk Research Institute, Massey University, Private Bag, 11 222, Palmerston North 4442, New Zealand; [2] Department of Biology University of Regina, Regina, SK, Canada, 3737 Wascana Parkway, Regina, SK S4S 1T8; [3] Department of Zoology, University of British Columbia, Vancouver, BC, Canada #4200-6270 University Boulevard, Vancouver, BC V6T 1Z6, [4] Wildlife Conservation Society Canada, Kaslo, BC, Canada, P.O. Box 606, 202 B Ave, Kaslo, BC V0G 1M0; [5] Institute of Fundamental Sciences Massey University, Private Bag 11 222, Palmerston North 4442, New Zealand; [6] Wildlife Conservation Society, Wildlife Health Program 212 South Wallace Avenue, Suite 101, Bozeman, MT, 59715, USA

2:45 p.m. **Variable behaviors influence species susceptibility to disease – surviving white-nose syndrome.**
Paul M. Cryan

U.S. Geological Survey (USGS), USGS Fort Collins Science Center, 2150 Centre Ave., Bldg. C, Fort Collins, Colorado

3:00 p.m. Break

3:30 p.m. Session VI - Other Infectious Agents of Bats (Anna Fagre, Moderator)

3:00 p.m. **Emerging Insights into the Geographic Distribution, Genetic Diversity and Evolutionary Origin of Bat-borne Hantaviruses**
Satoru Arai[1], Se Hun Gu[2], Son Truong Nguyen[3], Vuong Tan Tu[3], Blaise Kadjo[4], Burton K. Lim[5], Joseph S. Masangkay[6], Saw Bawm[7], Joseph A. Cook[8], Shigeru Kyuwa[9], Keiko Tanaka-Taya[1], Shigeru Morikawa[1] and Richard Yanagihara[2]

[1]National Institute of Infectious Diseases, Tokyo, Japan; [2]University of Hawaii at Manoa, Honolulu, HI, USA; [3]Institute of Ecology and Biological Resources, Vietnam Academy of Science and Technology, Hanoi, Vietnam; [4]University of Félix Houphouët-Boigny, Abidjan, Côte d'Ivoire; [5]Royal Ontario Museum, Toronto, Canada; [6]University of the Philippines Los Baños, Laguna, Philippines; [7]University of Veterinary Science, Nay Pyi Taw, Myanmar; [8]University of New Mexico, Albuquerque, New Mexico, U.S.A.; [9]University of Tokyo, Tokyo, Japan;

3:15 p.m. **Neotropical Bats that Co-habit with Humans Function as Dead-End Hosts for Dengue Virus**
Amanda Vicente-Santos[1,2], Andres Moreira-Soto[1,4], Claudio Soto-Garita[1], Luis Guillermo Chaverri[3], Andrea Chaves[2], Jan Felix Drexler[4,5], Juan Alberto Morales[6], Alejandro Alfaro-Alarcón[6], Bernal Rodríguez-Herrera [2] and Eugenia Corrales-Aguilar [1*]

[1]Virology-CIET (Research Center for Tropical Diseases), Microbiology, University of Costa Rica, San José, Costa Rica. [2]Biology, University of Costa Rica, San José, Costa Rica. [3]Exact and Natural Sciences School, National Distance Education University, San José, Costa Rica. [4]Institute of Virology, University of Bonn Medical Centre, 53127 Bonn, Germany.[5]German Centre for Infection Research, Bonn-Cologne, Germany.[6] Department of Pathology, School of Veterinary Medicine, National University, Costa Rica

3:30 p.m. **Novel Gammaherpesvirus in Bats: discerning the secrets of these oncogenic viruses**
Sonu Subudhi, Noreen Rapin, Janet Hill[1] and Vikram Misra

Department of Veterinary Microbiology, University of Saskatchewan, Saskatoon, Canada

3:45 p.m. **Experimental Infection of Jamaican Fruit Bats (*Artibeus jamaicensis)* with Zika Virus**
Ashley Malmlov[1], Kaitlyn Miedema[1], Tawfik Aboellail[2], Corey L Campbell[1], Miles Eckley[1], Nunya Chotiwan[1], Rebekah C. Gullberg[1], Rushika Perera[1] and Tony Schountz[1]

[1]Arthropod-Borne and Infectious Diseases Laboratory, Department of Microbiology, Immunology and Pathology, College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, Colorado, USA and [2]Veterinary Diagnostic Laboratories, Department of Microbiology, Immunology and Pathology, College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, Colorado, USA

4:00 p.m. **Long-term monitoring of *Bartonella* bacteria in a captive colony of fruit bats and experimental evidence of bat flies as vectors of bartonella**

Clifton McKee[1,2], Colleen Webb[1], Michael Kosoy[2], Ying Bai[2], Lynn Osikowicz[2], Richard Suu-Ire[3], Yaa Ntiamoa-Baidu[4], Andrew Cunningham[5], James Wood[6], David Hayman[7]

[1]Department of Biology, Colorado State University; [2]Division of Vector-Borne Diseases, Centers for Disease Control and Prevention; [3]Wildlife Division, Forestry Commission of Ghana; [4]Department of Animal Biology and Conservation Science, University of Ghana; [5]Institute of Zoology, Zoological Society of London; [6]Department of Veterinary Medicine, University of Cambridge; [7]Institute of Veterinary, Animal and Biomedical Sciences, Massey University

4:15 p.m. **Open Discussion**

5:00 p.m. Adjourn

POSTER PRESENTATIONS

1. James N. Aegerter, Ashley C. Banyard, Anthony R. Fooks, Graham C. Smith·
Predicting the epizootiology of temperate bat disease: Is it all about the bats?

2. Danielle E. Anderson, Kristmundur Sigmundsson, So Young Kim, Brian Ho Wenkae, Jasmine Tan[1] and Lin-Fa Wang. **Comparative loss of function screens highlight common cellular pathways required by mumps virus for replication in bats and humans**

3. Victoria Avanzato, Neeltje van Doremalen, Christine Carrington, Janine Seetahal, Tony Schountz, Vincent Munster
Development Implementation of a RT-PCR Assay to Detect Henipaviruses in Trinidad Bats

4. Jonathan C. Rupp, Maegan Lange, Megan Howard, Anitha Sundarajan, Jonny Sena[3], Faye D. Schilkey, Molly Murphy, Douglas Causey, Eric Bortz.
Genomic characterization and pathogenic potential of a novel evolutionarily-divergent alphacoronavirus isolated from *M. lucifigus* bats in Alaska.

5. Douglas Causey, Jonathan C. Rupp, Maegan Lange, Megan Howard, Anitha Sundarajan, Jonny Sena, Faye D. Schilkey, Molly Murphy, Eric Bortz
Preliminary Evidence of Secondary Acquisition of Tymoviridae and Partitiviridae in Little Brown Bats (*Myotis lucifugus*) in Southcentral Alaska.

6. Marcy Kanuka, Ashley Malmlov, Christine Cornish, Kathleen Parker, Cassandra Tang Wing, Diana Stone, Tony Schountz and Sonia Cheetham
Molecular Screening of Zika and Dengue Viruses in Bats (*Artibeus jamaicensis, Glossophaga longirostris and Molossus molossus*) from Grenada, West Indies.

7. Diana Stone, Christine Cornish, Amy C. Lyons, Yan-Jang S. Huang, Dana L. Vanlandingham, Stephen Higgs, Bradley Blitvich, Abiodun A. Adesiyun, Sharlene Santana, Leith Leiser-Miller, Sonia Cheetham.
Serologic evaluation of Alphavirus and Flavivirus exposure in bats in Grenada

8. Fagre AC, Kityo R, Lee J, Mossel E, Crabtree, M, Nalikka B, Nakayiki T, Kerbis J, Gilbert, A, Bergren, N, Nyakarahuka L, Lutwama J, Stenglein M, Byas A, Malmlov A, Bergren N, Rice L, Miller B, Schountz T & Kading, RC.
Isolation and molecular characterization of Bukakata orbivirus, a novel virus from a Ugandan bat, and associated pathology in experimentally infected Jamaican fruit bats (*Artibeus jamaicensis*)

9. Robert J. Fischer, Seth D. Judson, Sarah H. Olson, Vincent J. Munster
Using GIS to Guide Ebola Virus Disease Ecology Field Investigations

10. Hannah Frank, David Enard, Chase Mendenhall, Ji-Yeun Lee, Ellie Armstrong, Stefan Prost, Seth Judson, Jamieson O'Marr, Gretchen Daily, Dmitri Petrov, Scott Boyd and Elizabeth Hadly[1,6,7]
Bat - infection interactions: Signals of evolution, ecology, immunity and deforestation

11. Yupadee Hengjan, Didik Pramono, Hitoshi Takemae, Ryosuke Kobayashi, Karla Cristine Doysabas, Keisuke Iida, Takeshi Ando, Supratikno, Chaerul Basri Yuli Sulistya Fitriana, Eko M.Z. Arifin, Yasushige Ohmori, Ken Maeda, Srihadi Agungpriyono and Eiichi Hondo
Daytime behavior of *Pteropus vampyrus* and *Acerodon jubatus* in the natural habitats: a cue of viral transmission

12. Yutthana Joyjinda, Supaporn Wacharapluesadee, Prateep Duengkae, Apaporn Rodpan, Teerada ponpinit, Thongchai Kaewpom, Sangchai Yingsakmongkol, Kevin J Olival, Thiravat Hemachudha
The study of whole spike gene of bat coronavirus from Thailand using Next Generation Sequencing

13. Jun Li & Vincent Munster
Assessment of the cross-species potential of two emerging coronaviruses, SARS-CoV and MERS-CoV, by Protein-Protein Molecular Docking analyses

14. Kessler MK, Kamath PL, Smith CS, Goldspink LK, Plowright RK
Hendra virus phylogeography in eastern Australia

15. Tamar Kutateladze, Lela Urushadze, Davit Putkaradze, Magda Dgebuadze, Giorgi Babuadze, Ioseb Natradze, Lillian Orciari, and AndresVelasco-Villa
Viral Zoonosis in Georgian Bats

16. Aiah Lebbie, Jonathan Towner, Ibrahim Bakarr Brian Amman, Amy Schuh, Jonathan Johnny, Tara Sealy, James Graziano, Celine Taboy, John Klena, Immah Conteh, Stuart Nichol, Alusine Koroma, Ibrahim Foday and Richard Wadsworth
Forestalling Future Outbreaks: Enhancing Capacity for Surveillance of Viral Hemorrhagic Fever Viruses in Sierra Leone

17. Matovu Benard, Nalikka Betty and Kityo Robert
Ecological aspects of bats in a cave frequented by members of the local community in Kaptum Cave in eastern Uganda.

18. Rebekah McMinn, Michael Letko, Neeltje van Doremalen, Kerri Miazgowicz, Vincent Munster[1]
Middle East respiratory syndrome coronavirus spike plasticity in the context of the common vampire bat (*Desmodus rotundus***) DPP4 receptor.**

19. Alison J. Peel, Victoria Boyd, Raina K. Plowright, Olivier Restif, Gary Crameri, John Giles, Hamish McCallum, Konstans Wells
Viral community dynamics of Australian Flying foxes

20. Ponpinit T, Wacharapluesadee S, Duengkae P, Kaewpom T, Yinsakmongkon S, Rodpan A, Hemachudha T
The glycoprotein of Nipah virus in Thai bats associated with Nipah virus in Bangladesh

21. Jonathan C. Rupp, Maegan Lange, Megan Howard, Anitha Sundarajan, Jonny Sena, Faye D. Schilkey, Molly Murphy, Douglas Causey, Eric Bortz.
Genomic characterization and pathogenic potential of a novel evolutionarily-divergent alphacoronavirus isolated from *M. lucifigus* **bats in Alaska.**

22. Salmier A., de Thoisy B., Crouau-Roy B., Lacoste V. and Lavergne A.
Spatial pattern of genetic diversity and selection in the MHC class II DRB of three Neotropical bat species

23. Ken Cameron, Stephanie Seifert, Shauna Milne-Price, Alain Ondzie, Trent Bushmaker, Jean-Vivien Mombouli, Sarah Olson and Vincent J. Munster
Establishing a field collection scheme to investigate the role of African fruit bats as the natural reservoir of ebolaviruses

24. Lela Urushadze, Ying Bai, Lynn Osikowicz, Ioseb Natradze, Ketevan Sidamonidze, Davit Putkaradze, and Michael Kosoy
Co-infection in Georgian Bats

25. Megan E. Vodzak, MS, MPH, Ohnmar Aung, MBBS, MA , Marc T. Valitutto, VMD, Kyaw Y. N. Tun, BVSc, MSc, PhD , Heather S. Davies, MS , Michael E. von Fricken, PhD, MPH Suzan Murray, DVM, DACZM, and Dawn M. Zimmerman, DVM, MS
Caves of Myanmar: a high-risk human-wildlife interface for zoonotic disease

26. Supaporn Wacharapluesadee, Prateep Duengkae, Aingorn Chaiyes, Sangchai Yinsakmongkon[3] Pattarapol Maneeorn[4], Patcharakiti Phengsakul, Wachirapon Khumbucha, Thongchai Kaewpom, Apaporn Rodpan, Thiravat Hemachudha
Prevalence Patterns of Coronaviruses in Lyle's flying fox (*Pteropus lylei*) in Thailand

27. Xing-Lou Yang, Yun-Zhi Zhang, Ren-Di Jiang, Hua Guo, Wei Zhang, Bei-Li, Ning Wang, Li-Wang, Cecilia Waruhiu, Ji-Hua Zhou, Shi-Yue Li, Peter Daszak, Lin-Fa Wang, Zheng-Li Shi
Genetically Diverse Filoviruses in *Rousettus* and *Eonycteris* spp. Bats, China, 2009 and 2015

28. Miles Eckley, Ann Hawkinson, Tyler Sherman, Tony Schountz, Corey L Campbell
Development of a monoclonal antibody to Jamaican fruit bat CD3γ.

29. Candace Cotter, Tony Schountz, Corey L Campbell.
Bats and Immunity: Anti-Viral IFNγ Responses Differ Among Hosts.

30. Janine F.R. Seetahal, Orchid M. Allicock, Stephen C. Sameroff, Christopher Oura, Vernie Ramkissoon, W. Ian Lipkin, Christine V.F. Carrington
Virome analysis of neotropical bats on the Caribbean island of Trinidad

31. Periasamy P, Martínez Gómez JM, Wang LF, and Alonso S.
Delineating the phenotype and function of major lymphocyte populations in the fruit-eating bat, Pteropus Alecto.

32. Cara E. Brook, Hafaliana C. Ranaivoson, Christopher C. Broder, Andrew A. Cunningham, Andrea L. Graham, Jean-Michel Héraud, Louise Wong, James L.N. Wood, Andrew P. Dobson, C. Jessica E. Metcalf
Seasonal serological signals in viral infections for Madagascar fruit bats

Oral Presentation Abstracts

Studies of horizontal transmission of Marburg virus among experimentally infected fruit bats
Jonathan S. Towner[1,2], Amy J. Schuh[1], Brian R. Amman[1], Megan E. B. Jones[1,2], Tara K. Sealy[1], Uebelhoer LS, Spengler JR, Stuart T. Nichol[1]

[1]Viral Special Pathogens Branch, Centers for Disease Control and Prevention, Atlanta, USA, [2]Department of Pathology, College of Veterinary Medicine, University of Georgia, Athens, USA

Objectives: To investigate under experimental conditions the dynamics of Marburg virus replication in a known reservoir host and determine if 1) the virus can be transmitted from infected bats to immunologically naïve bats in the absence of arthropod vectors, and 2) identify the route(s) of virus shedding and therefore likely exposure. **Methods**: Using age-matched captive borne juvenile bats, we inoculated a total of 12 animals with Marburg virus 371 bat isolate and co-housed these animals with 24 naïve contact bats for 9 months under BSL-4 conditions and tested for evidence of virus shedding and transmission. **Results**: Marburg virus shedding was detected in oral, rectal and urine specimens from the inoculated bats through 19 days post infection. During the same time frame, Marburg virus was detected in oral specimens from contact bats, indicating that they were orally exposed to the virus from the inoculated animals. In the late study phase, we found that Marburg virus was horizontally transmitted from the donor bats to naïve contact bats by finding Marburg virus RNA in blood and oral specimens from contact bats, followed by the detection of Marburg virus IgG antibodies in these same animals. **Conclusions**: This study demonstrates, in the absence of any arthropod vectors, 1) direct filovirus transmission from a natural reservoir to another animal, 2) Marburg virus is shed primarily in saliva and urine, and perhaps feces, with some bats acting as super-shedders accounting for more than 80% of the cumulative virus shed, and 3) that this virus/reservoir host system can serve as an bona-fide experimental model for investigating how filoviruses are maintained long-term in nature and what drivers might influence occasional spillover to humans and other animals.

Investigations of Long-term Protective Immunity against Marburg Virus Reinfection in Egyptian Rousette Bats
Schuh AJ, Amman BR, Sealy TK, Spengler JR, Nichol ST and Towner JS

Viral Special Pathogens Branch, Division of High-Consequence Pathogens and Pathology, Centers for Disease Control and Prevention, Atlanta, GA 30333, USA

Objectives: The Egyptian rousette bat (ERB; *Rousettus aegyptiacus*) is as a known natural reservoir host for Marburg virus (MARV). Following infection of ERBs with MARV, virus-specific IgG antibodies rapidly decline and by 3 months post infection the bats are MARV seronegative. Therefore, it is unclear whether reinfection plays a role in MARV maintenance. **Methods:** To address this question, ERBs that had been “naturally” or experimentally infected with MARV 17 to 24 months prior were challenged with homologous virus. Following challenge, evidence of MARV replication in the blood and viral shedding from the oral mucosa was monitored for 14 days, MARV IgG antibody responses were monitored for 21 days and tissues obtained at necropsy at 21 days were tested for the presence of MARV RNA. **Results:** No evidence of MARV replication in the blood or shedding from the oral mucosa was detected in either group of bats through 14 days post inoculation. A robust MARV IgG antibody response occurred by seven days post inoculation in all bats, indicating the occurrence of a secondary immune response. **Conclusions:** This study demonstrates that both “natural” and experimental infection of ERBs with MARV induces long-term protective immunity against reinfection and suggests that other factors such as the twice-yearly influx of susceptible juveniles, large colony sizes and population connectivity, drive MARV transmission dynamics in wild populations of ERBs.

Innate immune response to filoviruses and the role of filoviral interferon-inhibiting domains in bat and human cells
Ivan V. Kuzmin[1,2], Toni M. Schwarz[3], Philipp A. Ilinykh[1,2], Ingo Jordan[4], Thomas G. Ksiazek[1,2,5], Ravi Sachidanandam[6], Christopher F. Basler[3, 7], and Alexander Bukreyev[1,2,5]

[1] Department of Pathology, The University of Texas Medical Branch, Galveston, Texas, USA, [2] Galveston National Laboratory, The University of Texas Medical Branch, Galveston, Texas, USA; [3] Department of Microbiology, Icahn School of Medicine at Mount Sinai, New York, New York, USA; [4] ProBioGen AG, Berlin, Germany; [5] Department Microbiology & Immunology, The University of Texas Medical Branch, Galveston, Texas, USA; [6] Department of Oncological Sciences, Icahn School of Medicine at Mount Sinai, New York, New York, USA; [7] Current Address: Center for Microbial Pathogenesis, Institute for Biomedical Sciences, Georgia Research Alliance, Eminent Scholar in Virology, Georgia State University, Atlanta, Georgia, USA

Objectives: Innate immune responses in bat (Rousettus aegyptiacus) and human cells to the filoviruses Marburg (MARV) and Ebola (EBOV) were investigated to determine the ability of these viruses to subvert antiviral insults from different host species.
Methods: The innate immune response to filoviruses in bat and humans cells was profiled by deep sequencing and also analyzed by qRT-PCR. Bat mRNAs encoding IFNalpha, beta, gamma, lambda, and interferon stimulated genes (ISG) 54 and 56, were cloned and examined for their antiviral effect in response to MARV and EBOV infection in bat and human cells. Rates of infection and the effects of the major filoviral IFN-inhibiting domains (IID), VP35 and VP24, were analyzed in cells from both host species.
Results: We demonstrated that EBOV and MARV replicate to similar levels in all tested cell lines, indicating that permissiveness for EBOV at cell and organism levels do not necessarily correlate. Filoviruses, particularly MARV, induced a potent innate immune response in rousette cells that was generally stronger than in human cells. Both EBOV VP35 and VP24 IID were found to suppress the innate immune response in rousette cells, but only VP35 IID appeared to promote virus replication. Along with IFN-alpha and IFN-beta, IFN-gamma was demonstrated to control filovirus infection in bat cells but not in human cells suggesting host species specificity of the antiviral effect. The antiviral effects of bat IFNs appeared not to correlate with induction of bat ISG54 and ISG56, which were detected in human cells expressing bat IFN-alpha and IFN-beta.
Conclusions: Rousettus aegyptiacus cells mount robust innate immune responses to filovirus infection. Filovirus IIDs are active in both rousette and human cells; however, the VP35 IID plays a greater role in promotion of viral replication in rousette cells than in human cells. IFN-gamma plays a greater role in control of filovirus infections in rousette non-immune cells than in human cells. At least in part, the antiviral effect of IFN-gamma results from 'cross talk' leading to activation of the type I IFN response. The data are useful for understanding the interactions of filoviruses with natural (Rousettus aegyptiacus) and accidental hosts (humans).

Broad based surveillance for ebolaviruses: PREDICT in Sierra Leone, Liberia, and Guinea
Bird B[1], Goldstein T[1], Anthony S[2], Gbakima A[3], Saylors K[3], Jean Louis F[3], Wolking D[1], Epstein J[4], Karesh W[4], Kreuder-Johnson C[1], Mazet J[1]

One Health Institute UC Davis School of Veterinary Medicine[1], Center for Infection and Immunity Columbia University[2], Metabiota Inc.[3], EcoHealth Alliance[4]

Objectives: Developing and operationalizing strategies to reduce zoonotic pathogen spillover, amplification, and spread are nowhere more relevant than in Sierra Leone, Guinea, and Liberia. The devastating loss of lives associated with the Ebola virus outbreak revealed the urgent need for increased animal and public health sector capacity strengthening. Put into historical context, this epidemic was more than 60 times larger than any previous Ebola outbreak, spread to 7 additional countries, and stretched emergency response efforts to the utmost limits of capacity. **Methods**: PREDICT is working to improve understanding of wildlife reservoirs, spillover hosts, and origins of these viruses; ascertain the potential of virus-spillover into other non-typical hosts, such as livestock or companion animals; gain a greater understanding of high-risk human behavioral activities; and improve disease surveillance and laboratory capacities through workforce development in line with Global Health Security Agenda priorities. **Results**: Due to the impact on these three countries, USAID's PREDICT Project developed a focused effort to better address the threat of ebolaviruses by investigating the virus' animal origins, while strengthening in-country capacity to build and reinforce emerging disease surveillance and detection systems. In each country, teams are conducting concurrent sampling of from multiple animal taxa (dogs, cats, livestock, wildlife) and applying broad based molecular approaches to detect all known and other potential novel ebolaviruses. As of April 2017, over 6,500 animals have been sampled including over 3,500 bats in the three countries, with laboratory testing underway. Without identifying reservoirs of infection and how widely they are distributed across the region, prevention programs to reduce transmission from animals to people will have limited impact, and it is likely that future spillover of ebolaviruses from animals into humans will continue to occur. **Conclusions**: As we have seen over the years in Central and Eastern Africa where filovirus outbreaks have repeatedly occurred, effective control of these rare "spillover" events is possible and, when the right technical capacities are in place, these outbreaks can even be limited to a small number of human cases.

Quantifying signatures of resistance and tolerance to filoviruses in bat cell lines
Cara E. Brook[1], Melinda Ng[2], Esther Ndungo, Rohit K. Jangra, Andrew P. Dobson, Andrea L. Graham, Bryan T. Grenfell, C. Jessica E. Metcalf[1]*, Kartik Chandran[1]*

[1]Department of Ecology and Evolutionary Biology, Princeton University;
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Objectives: Previous work has demonstrated that a single amino acid change in the filovirus receptor, NPC1, in *Eidolon helvum* cells make them refractory to Ebola virus infection, hinting at a possible coevolutionary history between virus and bat host. We sought to expand on this nascent evidence of the evolution of pathogen resistance. **Methods:** We carried out a series of plaque assays, in which we challenged bat (EidNi/41.3, RoNi/7.1, PaKiT01), U2OS, and Vero cell lines with multicycle replicating pseudotype Ebola and Marburg filoviruses. Because of the agar overlay inherent to the plaque assay, viral transmission was restricted to neighboring cells. We visualized this transmission by photographing the timecourse of infection spread across the cell monolayer, and processing the images to quantify the proportion infected at a given time point as the proportion of photograph illuminated by GFP-tagged virus. We then fit spatially-structured traditional epidemiological models to the resulting data, in order to disentangle the mechanisms underpinning diverse trajectories of tolerance and resistance in different virus-cell line relationships. **Results:** Our modeling highlights diverse, species-specific evolutionary relationships between particular bat cell lines and particular filoviruses, which necessitate mechanisms of pathogen resistance in order to recapture data trajectories in some cases (chiefly *E. helvum* and Ebola and *P. alecto* and Marburg) and mechanisms of tolerance in others. **Conclusions:** Our work highlights the power of interdisciplinary approaches, combining quantitative epidemiology with cell biology and adds to growing evidence suggestive of unique species-specific coevolution between bats and filoviruses.

Serologic evidence of exposure to filoviruses in fruit bats, Singapore
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Objectives: Bats are known natural hosts of Nipah virus and Maburg virus, and the collective evidence suggests that bats are also the natural hosts of ebolaviruses. Reston virus, an *Ebolavirus* species, is known to circulate in species of bats in the Philippines. To examine whether ebolaviruses and marburgviruses are more broadly present in Southeast Asia, we tested sera from three fruit bat species endemic in Singapore and widely distributed throughout Southeast Asia for evidence of past exposure to known species of ebolaviruses and marburgviruses. **Methods:** Sera were collected from the above-mentioned bat species from 2011 to 2016 in Singapore to screen for evidence of exposure to filoviruses. Venous blood was diluted 1:10 in 1×PBS and tested using a Bio-Plex® bead-based multiplex assay that simultaneously probes sera for immunoglobulins specific to the viral envelope glycoprotein from representative strains of all previously described *Ebolavirus* and *Marburgvirus* spp. We employed methods developed by Peel AJ *et al.* to establish a median fluorescence intensity (MFI) cutoff value. We screened 409 samples with this *Ebolavirus/Marburgvirus* spp. Bio-Plex® assay. **Results:** Positive results indicated that bats were previously infected with viruses related to the ebolaviruses from which the virus surface proteins were derived. Of the species tested, 10% of *Eoncyteris spelaea*, 8% of *Cynopterus brachyotis*, and 4% of *Penthetor lucasi* had positive sera results for antibodies specific to ebolaviruses.
Conclusion: These serological results demonstrated that viruses related to ebolaviruses have previously infected all three species of fruit bats, and may circulate in the populations, but we have not detected the virus in any samples. We conducted next generation sequencing on urine and feces, bat cell lines and screened numerous samples from bats in Singapore and have detected no evidence of the virus. As there is no evidence of Ebola virus disease in humans in Singapore or Southeast Asia, we think that these serological findings are evidence of novel, yet undescribed viruses related to known ebolaviruses.

Predicting undiscovered filovirus reservoirs and patterns of disease emergence
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Objectives: How can we discover unidentified filovirus hosts and where should we be searching for the viruses? Filoviruses *Ebolavirus* (EBOV) and *Marburgvirus* cause hemorrhagic fevers with high mortality rates, posing significant threats to public health and wildlife conservation. The viruses have sporadically emerged over the last 40 years at least, and yet the hosts of EBOV in particular remain poorly known and characterized. Here different studies help inform field surveillance through the identification of bat traits that predict filovirus reservoirs and ecological processes that facilitate emergence. **Methods:** Different modeling approaches were used. A mathematical model with seasonal birthing synthesized filovirus and bat data to determine if biannual birthing

might facilitate pathogen persistence. Regression analyses on serological data tested the model predictions. A machine learning approach provided additional information on bats, integrating multiple host trait data. Fragmentation analyses using satellite land cover data and Ebola virus disease outbreak index cases in humans (i.e. spillover from wildlife reservoirs) tested the hypothesis that forest fragmentation was correlated with emergence. **Results:** Synthesis of filovirus and bat data through models suggests bi-annual breeding and longer incubation periods, such as reported for Egyptian fruit bats and EBOV in experimental studies, allow viral persistence in bat colony sizes often found in nature. Serological data and machine learning approaches support the findings, with bats from species with two annual birth pulses more likely to be seropositive (odds ratio 4.4, 95% confidence interval 2.5-8.7) than those with one, suggesting biannual birthing may allow filovirus persistence. Machine learning algorithms suggest species' geographic range overlap may facilitate filovirus persistence. Finally, fragmentation analyses suggest Ebola virus disease outbreaks occurred mostly in hotspots of forest fragmentation. **Discussion:** These analyses suggest surveillance for filoviruses, especially ebolaviruses, might be targeted to young bats from species with biannual birthing in areas of fragmented forested habitat. The link between forest fragmentation and EBOV outbreaks suggests there is common ground between biodiversity conservation and disease risk mitigation. Together these results will help the research community identify where, when and in which species to continue the search for filovirus hosts.

Bats as possible animal origin of MERS-CoV

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Objectives: Bats are important reservoir for emerging viruses including coronaviruses. Although dromedary camels are believed to be the immediate animal source of the recent MERS epidemic, the evolutionary origin of MERS-CoV remains obscure. While horseshoe bats are the primary reservoir of ancestors of SARS-CoV, the possible role of bats in the emergence of MERS-CoV is less clear. When MERS-CoV was first discovered, it was found to be most closely related to *Tylonycteris* bat CoV HKU4 (Ty-BatCoV HKU4) and *Pipistrellus* bat CoV HKU5 (Pi-BatCoV HKU5) previously discovered in lesser bamboo bat (*Tylonycteris pachypus*) and Japanese pipistrelle (*Pipistrellus abramus*) respectively in Hong Kong. Subsequently, two other lineage C betacoronaviruses, BtVs-BetaCoV/SC2013 and Coronavirus Neoromicia/PML-PHE1/RSA/2011 (NeoCoV) were also detected in bats from China and Africa respectively. Interestingly, a lineage C betacoronavirus, Erinaceus CoV VMC/DEU, has also been found in European hedgehogs, which are phylogenetically closely related to bats, in Europe. Although NeoCoV represents the closest bat counterpart of MERS-CoV in most genome regions, the spike (S) protein, important for host receptor binding, is genetically divergent from that of MERS-CoV. On the other hand, Ty-BatCoV HKU4 possessed an S protein being most closely related to MERS-CoV. The spike of Ty-BatCoV HKU4, but not that of Pi-BatCoV HKU5, was able to utilize the MERS-CoV receptor, human dipeptidyl peptidase 4 (hDPP4) or CD26, for cell entry. These findings suggested that bats may be the primary host of the ancestor of MERS-CoV. **Methods**:To better understand the evolutionary path of MERS-CoV, we collected bat samples from various regions in China. **Results**: Diverse CoVs were detected, including a potentially novel lineage C betacoronavirus. Compared to Ty-BatCoV HKU4 and Pi-BatCoV HKU5, the virus was even more closely related to MERS-CoV and NeoCoV in most regions of its genome. In contrast, the S1 region was less closely related MERS-CoV than Ty-BatCoV HKU4 but more closely related to MERS-CoV than Pi-BatCoV HKU5. To determine if this virus can utilize hDPP4 as receptor, binding experiments using S1-receptor-binding domain (RBD), cell entry studies using pseudovirus assays and structural modelling of the RBD-hDPP4 interphase were performed. **Conclusions**: The results suggested a stepwise evolutionary process among lineage C betacoronaviruses in gaining the ability to bind hDPP4, and support a bat origin of MERS-CoV.

Rapid detection of MERS coronavirus ancestors in bats

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Objectives: Since its first appearance in 2012, the Middle East Respiratory Syndrome (MERS) has affected more than 25 countries in four continents with more than 1,300 cases and a high fatality rate of more than 30%. A novel lineage C betacoronavirus (betaCoV), MERS-CoV, has been confirmed to be the etiological agent. Human dipeptidyl peptidase 4 (hDPP4) was found to be the cellular receptor for MERS-CoV. Subsequent detection of MERS-CoV and its antibodies in dromedaries in various countries in the Middle East and North Africa have implied that these animals are probably the reservoir for MERS-CoV. Other lineage C betaCoVs in bats [e.g. *Tylonycteris* bat CoV HKU4 (Ty-BatCoV-HKU4), *Pipistrellus* bat CoV HKU5 (Pi-BatCoV-HKU5)] and hedgehogs were found to be closely related to MERS-CoV. So far, detection of MERS-CoV and discoveries of its closely related CoVs are most efficiently achieved through RT-PCR. Although RT-PCR is highly sensitive, its turn-around-time is about four hours and the test requires expensive equipment, stringent laboratory set-up and personal attention to prevent laboratory PCR product cross contamination which may lead to false-positive results.

Methods: Recently, we have developed a monoclonal antibody-based rapid nucleocapsid protein (NP) detection assay for on-site diagnosis of MERS-CoV, which can be finished in 30 minutes. **Results and Conclusions**: This rapid test is highly specific for MERS-CoV for human and dromedary samples, as samples containing other human CoVs (HCoV-OC43, HCoV-229E, HCoV-NL63 and HCoV-HKU1) or dromedary CoV UAE-HKU23 all showed negative results. However, we hypothesize that the rapid test can pick up betaCoVs closely related to MERS-CoV; and hence would be useful for the discovery of MERS-CoV ancestors. To test this hypothesis, we examine the usefulness of this rapid test to detect four alphaCoVs and four lineage B, C and D betaCoVs in fecal samples of bats.

Global patterns in coronavirus diversity

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Objectives: Since the emergence of SARS-CoV and MERS-CoV it has become clear that bats are important reservoirs of coronaviruses (CoVs). Despite this, only 16% of all CoV sequences in Genbank come from bats. The remaining 84% largely consist of known pathogens of public health or agricultural significance, indicating that current research effort is heavily biased towards describing known diseases rather than the 'pre-emergent' CoV diversity circulating in bats. Our study addresses this critical gap, and focuses on the evolutionary and ecological drivers of CoV diversity in resource poor countries, where the risk of zoonotic emergence is believed to be highest. **Methods**: We surveyed the diversity of CoVs in multiple host taxa from 20 countries in Africa, Asia and Latin America to explore the factors driving viral diversity at a 'global' scale. Partial CoV sequences were identified using consensus PCR, which was chosen in part because it could be easily implemented in resource poor settings. Sequences were then parsed into phylogenetic clusters (operational taxonomic units) and analyzed using ecological and epidemiologic approaches. **Results**: In total we identified sequences representing 100 discrete clusters, 91 of which were found in bats, and showed that patterns of CoV diversity correlate with those of bat diversity. This cements bats as the major evolutionary reservoirs and ecological drivers of CoV diversity. Preliminary co-phylogenetic reconciliation analysis indicated that frequent host switching has contributed to CoV evolution, and that regional variation exists in the dynamics of this process. **Conclusions**: Overall our study represents a model for exploring global viral diversity and advances our fundamental understanding of CoV biodiversity and the potential risk factors associated with zoonotic emergence.

SARS coronavirus may have originated from frequent recombination events between SARS-like coronaviruses in a single horseshoe bat habitat

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Objectives: Horseshoe bats are recognized as the natural reservoirs of Severe Acute Respiratory Syndrome coronavirus (SARS-CoV), as an increasing number of SARS-like coronaviruses (SL-CoV) have been detected in this bat family since 2005. However, knowledge gaps remain between currently known bat SL-CoVs and the direct progenitor of SARS-CoV. Further information is needed to better understand where and how SARS-CoV originated from bat reservoirs. **Methods:** We have conducted a 5-year surveillance of SL-CoV in a cave inhabited by horseshoe bats in Yunnan, China. Full-length genome sequencing of 11 novel bat SL-CoVs discovered in this single location was performed and genomic characterization, phylogenetic analysis and recombination analysis were conducted. Efficiency of human ACE2 usage was also evaluated in HeLa cells for several newly identified strains. **Results:** Our findings revealed that genetically diverse bat SL-CoVs were circulating in this single location, including different strains with high sequence similarity to SARS-CoV in the highly variable N-terminal

domain (NTD) and receptor-binding domain (RBD) of S protein and the ORF8 region, respectively. Meanwhile, compared with other SL-CoVs, strains identified from this cave exhibited higher sequence similarity to SARS-CoV in the non-structural proteins. Evidence supported that frequent recombination events have occurred within the S gene and around ORF8 between bat SL-CoVs in this cave and may have promoted the generation of the pandemic SARS-CoV. Cell entry studies demonstrated that different newly identified SL-CoVs with variants of S protein are all able to use human ACE2 as the receptor, which represent a potential risk of emergence if given the opportunity to spillover. **Conclusions:** We have identified an epicenter of SL-CoVs where the director progenitor of SARS-CoV likely originated via sequential recombination events. These findings offered important new insight into understanding the geographical and evolution origin of SARS-CoV and highlights the need to pursue the surveillance of bat SL-CoVs to make better preparation for future emergence of SARS-like disease in humans.

A metagenomic approach identifying a MERS-related coronavirus in a bat from South Africa

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A Middle East Respiratory Syndrome (MERS) related coronavirus was previously detected in a Cape serotine bat (*Neoromicia capensis*) from the KwaZulu Natal Province in South Africa. Though the virus showed significant similarity to human MERS coronavirus (MERS-CoV), it was too divergent to be considered the direct progenitor of the virus causing human MERS-CoV outbreaks. **Objectives:** As part of a broader viral discovery surveillance program investigating excreted zoonotic viruses from bats, we implemented metagenomic techniques to collectively screen the virome of 60 *Neoromicia* bats constituting 6 species from 4 South African provinces sampled from 2007-2015. **Methods:** Using a viral particle enrichment methodology, total nucleic acids from faecal and rectal specimens were sequenced on Illumina's MiSeq and NextSeq500. Coding complete genome sequencing was performed with further amplicon sequencing on Illumina's MiSeq. Bayesian (BEAST) phylogenetic comparisons and pairwise estimations were performed with full genome representatives of all 4 betacoronavirus lineages. **Results:** We detected a MERS-related betacoronavirus from the same *Neoromicia* species. The virus shared a 97.2% overall nucleotide identity to another *Neoromicia* MERS-related virus identified in South Africa, and 85.5-85.6% nucleotide identity to human and camel (alternative hosts) strains of MERS-CoV. Significant discrepancies between bat-borne and human/camel MERS-CoV genomes were attributed to the low (63.7-64.3%) amino acid similarities of the spike genes, which is responsible for receptor attachment. Genome comparisons between betacoronavirus lineages of emerging viruses, namely MERS-CoV and the equivalent Severe Acute Respiratory Syndrome (SARS) coronaviruses, indicate that the relative phylogenetic distances between *Neoromicia* MERS-related strains and human/camel MERS-CoV are far greater than the distances between SARS-related bat viruses and human SARS viruses. **Conclusions:** Continued surveillance within the *Neoromicia* genus may yield additional MERS-related viruses sharing greater similarity to the human and camel MERS strains (as was shown with detected SARS-related bat viruses). Alternatively, if the progenitor of MERS-CoV originated from the *Neoromicia* genus, the currently identified diversity would suggest that significant receptor adaptation was required within dromedary camels (or unknown intermediate hosts) prior to being transmitted to humans. Continued viral surveillance in regions inhabited by both these hosts may aid in understanding the emergence of MERS.

New insights into the antiviral innate immune response of *Desmodus rotundus*

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The common vampire bat, *Desmodus rotundus*, is the main reservoir of rabies virus in South America. Mechanisms that allow persistence of viruses in bats are not well-defined. During the last decade, innate immunity has emerged as one of the implicated mechanisms. As a non-model organism, no tools were available regarding *D. rotundus*, there was therefore a crying need for characterizing their immune system. Given that the interferon (IFN) system provides the first line of defense upon viral recognition, we investigated the IFN-I response in an immortalized cell line, established from a *D. rotundus* embryonic lung, stimulated with synthetic

dsRNA (poly I:C). We observed that stimulation induced high levels of expression of all PRRs involved in dsRNA recognition, as well as a rapid up-regulation of both IFN-α1 and β. Furthermore, in characterizing some of the ISGs such as OAS1, PKR and ADAR, we identified two OAS1 genes, tentatively named *OAS1a* and *OAS1b*. Upon stimulation, *OAS1b* appeared to be the most inducible ISG tested. These results not only provide evidence of the intact signaling pathway of the IFN-I in our cellular model, but also that *OAS1b* may be a major player in antiviral activity in *D. rotundus*. In the frame of the present work, we generated a sum of insightful tools specific of the common vampire bat useable to the study of a number of different viruses, the first of which is the rabies virus.

A comparative study of the autophagy pathway during virus infection of bat (natural) and human (accidental) host cells

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Objectives: In contrast to other terrestrial animals, infection of bats with ebolaviruses and henipaviruses does not cause symptomatic disease. Whether bats have antiviral mechanisms to control these infections or how these viruses persist at a cellular level is largely unknown. Autophagy is a cellular protein homeostatic process, which has been implicated as a cell-autonomous innate defense mechanism against a broad array of intracellular infections. Bats are longer lived compared to other similarly sized mammals and increased proteostatic processes have been observed in long-lived mammalian species. **Methods:** In this study, we performed an investigation of autophagy in cell lines from the black flying fox (*Pteropus alecto*), a natural host of Hendra virus and Australian bat lyssavirus (ABLV), and human cells. ABLV, a neurotropic virus, was used as a model bat-borne virus to examine the interactions between an intracellular virus infection and autophagy in host cells. **Results:** Autophagy activation was observed in *P. alecto* brain tissue-derived primary and secondary cells infected with replication competent ABLV 1 and 2 days post infection. Compared to a human neuroblastoma cell line, *P. alecto* kidney and brain cells exhibited a higher level of basal autophagy. Treatment of bat and human cell lines with pharmacological activators of autophagy reduced ABLV replication. Quantification of ABLV titers and protein levels after infection of bat and human cells lines demonstrated that bat cells were less permissive to ABLV infection. Lentiviral knockdown of autophagy-related gene-5 (ATG-5) in bat and human cell lines did not result in a significant silencing of the autophagy pathway, however, a trending increase of ABLV replication levels was observed in the ATG-5 knockdown cells. Pre- and post-infection treatment of human neuroblastoma cells with BEZ235, an mTOR- and PI3K-inhibitor, significantly decreased virus replication in a dose-dependent manner. **Conclusions:** To our knowledge this is the first study to explore whether the autophagy pathway has a role as an antiviral defense mechanism during virus infection in bats. Ongoing experiments aimed at the interplay between autophagy and apoptosis will be critical to supporting our hypothesis that autophagy is an antiviral defense mechanism in bats.

Development of a minimally invasive individual identification technique for continuous monitoring of African bat species

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Objectives; An ever increasing number of potentially zoonotic diseases are associated with bat populations throughout the world, and as such the continuous monitoring and surveillance of these populations has become essential, not only for disease epidemiology but also in order to address the lack of knowledge available for biology, ecology and life histories of the majority of bat species. This requires the development of an ethically acceptable, cost effective, durable and reliable marking system to facilitate monitoring of individual bats. In order to address annual population structure, potential movement patterns and individuals' infection or exposure status we tested the ability to uniquely mark 11 bat species from six families, ranging in mass from 4g to 120g, using wing tattoos. Specific serological monitoring of Lagos bat virus exposure in *Rousettus aegyptiacus,* focussing on the presence and duration of neutralising antibodies has been undertaken since 2012. **Methods;** Non-toxic black ink was applied into the interdermal layers of the propatagial membrane of the bat by means of a tattoo system with nine-pronged needles. The tattooing procedure was performed on individual bats from a captive colony of *R.*

aegyptiacus (n=287) and free-flying, wild populations of the aforementioned species (n=2559). The robustness and longevity of this system was assessed from recaptures of tattooed individuals representing four of the above species in the wild, and observations of the captive colony of *R. aegyptiacus*. **Results;** This technique provides a simple, durable and cost effective marking system for both immediate and medium term monitoring, with no observed detrimental effects to the individuals to date. The longest periods between application and observation of tattoos has been; 927 days for *R. aegyptiacus*, 292 days for *N. thebaica*, 126 days for *M. natalensis* and 89 days for *Rh. smithersii.* Over 100 *R. aegyptiacus* recapture events have demonstrated individuals' seroconversion, antibody maintenance and loss against LBV. **Conclusion;** This technique has shown potential to facilitate monitoring individual bats' infection or exposure status in both captive and wild settings, with individual seroconversion and titer loss against LBV being observed, as well as providing an effective mark-recapture identification for population and movement studies.

Characterization of a novel Rhabdovirus isolated from insectivorous bat (*Pipistrellus kuhlii*) in Italy
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Objectives: *Rhabdoviridae* is one of the most ecologically diverse families of RNA viruses with clinical importance. Herein we report the isolation and the genome characterization of a novel rhabdovirus detected from a bat collected within a survey implemented in Italy on emerging viruses of bats. **Methods:** A fresh carcass of an adult female of *Pipistrellus kuhlii* spontaneously dead in a wildlife rehabilitation center in Northern Italy was fully necropsied. Tissue samples from different organs (lung, hearth, intestine) were subjected to viral isolation on cell culture. Virus identification was performed using negative staining electron microscopy (nsEM) and NGS sequencing. Molecular and phylogenetic analyses were performed. **Results:** Anamnesis reported sensory depression, inappetence, normal body mass and injuries of patagium consistent with a cat bitten. The death occurred three days after the admission to the rehabilitation center and no pathological lesions indicative of infectious diseases were observed at necropsy. CPE was observed on VERO cells inoculated with a pool of organs and nsME performed on cells supernatants revealed characteristic bullet-shaped viral particles referable to rhabdovirus. Tests aimed to exclude rabies and related lyssaviruses resulted negative. The complete genome size was 11,780 nt comprised 5 genes encoding the canonical rhabdovirus structural proteins and an additional transcriptional unit (U1) encoding a small protein (157 aa) located between the G and L genes (3'-N-P-M-G-U1-L-5'). BLAST analysis showed the highest nucleotide identity (65%) to Le Dantec virus (LDV) (human, 1965 Senegal) the prototype strain of the putative genus Ledantevirus. The most highly conserved protein L shared 70% and 69% of aa identity with LDV and Keuraliba virus (KEUV) (gerbil, 1968 Senegal) respectively. Phylogenetic tree based on full-genome sequence confirm the belonging of the new isolate to the ledantevirus group. **Conclusions:** A novel rhabdovirus was identified from *Pipistrellus kuhlii*, the most common species in urban areas in Italy. This finding represents (beside lyssaviruses) the only bat-borne rhabdovirus isolated in Europe. Specific diagnostic tools for viral detection will be set up for epizootiological investigations aimed to define the viral ecology and diffusion in bats population in Italy, in order also to further characterize and clarify its zoonotic potential.

Age-specific dynamics of maternally- and infection- derived immunity within African bat populations
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Objectives: Predicting and managing spillover of emerging infectious diseases to domestic animals and humans depend on data on reservoir host distribution, ecology and immunology as well as the mechanisms governing pathogen transmission among its populations. However, such data are generally sparse. This is exemplified by old-world fruit bats, which have been linked to an increasing number of zoonotic viruses, but whose ecology is

challenging to study and immunology has only recently begun to be elucidated. Even where appropriate data are available, fission-fusion population structures make it challenging to separate out the dynamical effect of pathogen reintroduction into the study population through movement from the transmission dynamics expected within a closed population. Island populations provide ideal natural experiments and involve simplifications analogous to the assumptions often made in modelling studies (e.g. single, closed population of a single species), allowing exploration of underlying processes. Here, building on an extensive body of work on straw-coloured fruit bats (*Eidolon helvum*), we aim to further elucidate fundamental processes governing viral dynamics, including the role of maternally-derived antibodies (MatAb). **Methods:** We focus on two viruses for which *E. helvum* is a reservoir (Lagos bat virus (LBV) and African henipavirus) and look for evidence of the presence of MatAb in wild *E. helvum* from continental and island populations. We use rare age-specific data to model waning rates of maternally- and infection- derived antibodies. These results then informed the parameterisation of a stochastic seasonal birth model to explore population-level persistence in the presence of MatAb, in both naive and non-naive populations. **Results:** Statistical modelling supported age as the strongest determinant of seroprevalence for both henipavirus and LBV, in addition to highly significant correlations between mother-offspring pairs. Age-specific seroprevalences predicted rapid loss of maternal immunity and effectively lifelong infection-induced immunity (particularly for LBV). The inclusion of MatAb had considerable implications on viral persistence within populations in a dynamic birth pulse model. **Conclusions:** This study helps to better understand endemic viral dynamics in bat populations, and the implications of considering the presence of MatAb in broader wildlife disease systems.

Detection of rubula- and related viruses in an Egyptian fruit bat (*Rousettus aegyptiacus*) colony in South Africa

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Objectives: More than 22 viral families have been associated with bats globally, eight of which with the Egyptian fruit bat (*Rousettus aegyptiacus*) occurring across sub-Saharan Africa and parts of the Middle East. Among numerous other zoonotic viruses, this species has also been associated with zoonotic henipaviruses (family *Paramyxoviridae*). More recently, a newly described zoonotic rubulavirus, Sosuga virus, was detected in this species from Uganda. The occurrence and diversity of these viruses remain unknown in Southern Africa. **Methods:** A broadly reactive hemi-nested RT-PCR assay targeting the *Avula-Rubulavirus* genera within the *Paramyxoviridae* family was used for nucleic acid detection. Spleen and kidney samples from bats collected during 2012-2016 from a cave in the Limpopo Province of South Africa, were retrospectively screened for the presence of rubulavirus RNA. Virus isolation, next-generation Illumina sequencing and amplicon sequencing were used to obtain full gene or genome sequences for comparison. **Results:** A total number of 137 bats were screened of which 5.84% of spleen samples tested positive. We detected several rubulavirus-related viruses grouping in a sister clade to the *Rubulavirus* genus. This clade contains other bat-associated rubulaviruses including the zoonotic Sosuga virus. Additionally, a co-infection with a virus closely related to human mumps virus was detected in one of the bats sampled. Preliminary results also suggest seasonality of these viruses in the colony, as positive individuals were predominantly detected in winter months. This phenomenon coincides with the loss of maternal antibodies i.e. an influx of susceptible individuals into the colony. **Conclusion:** The first evidence of bat-associated rubulaviruses from *R. aegyptiacus* in South Africa, some of which are related to know human pathogens, are reported. Additionally, a considerable diversity was detected from a small sample size. Enhanced surveillance might shed light on the prevalence of these viruses within the targeted colony. Considering the potential excretion of these viruses during the winter months might be the next step in determining their transmission potential. This is of importance as the specific cave is situated within a rural settlement surrounded by free-roaming livestock and is frequented by humans for religious practices.

Influenza-like virus and paramyxovirus screening in Brazilian bats

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Objectives: Bats are recognized as natural reservoirs of emergent viruses related to severe human disease outbreaks including Rabies, Nipah, Hendra and SARS coronavirus. Since the discovery of Hendra and Nipah emergent paramyxovirus in late 1990s in flying foxes bats from Australia and Asia, others bat-borne paramyxovirus have been identified in bats across the globe including bats species from Australia, Asia, Africa and America. Recently, new members of the influenza A virus where detected in bats from Guatemala and Peru, amplifying the host variety of Influenza virus A group. Despite the recent detection of Influenza-A and Paramyxovirus in South American bats and the spill-over events of paramyxovirus from bats to humans only few studies had analyzed the occurrence of influenza-like virus and paramyxovirus in Brazilian's bats. These study aims to analyze the occurrence and diversity of influenza-like virus and paramyxovirus in Brazilian bats. **Methods:** A total of 1071 samples including distinct tissues (intestine, lung, kidney and spleen), rectal and oral swabs, and serum (821 individuals/47 species) from urban area and Atlantic Forest biome were analyzed. The Total Nucleic Acid was extracted and cDNA synthesis was performed. Samples were screened by Pan-Flu PCR assay targeting the Influenza PB1 gene and by a Semi-Nested Pan-paramyxovirinae PCR assay targeting the L gene. **Results:** PCR fragments for both assays were observed in electrophoresis analysis. The amplicons were purified and sequenced by Sanger method. Sequencing confirmed the presence of 3 distinct Paramyxovirus lineages in eight bats. Morbillivirus-like was detected in insectivorous bat's *Molossus rufus* (intestine) and *Myotis nigricans* (lung)*;* Unclassified Paramyxovirus and one possible Henipa-like virus was found in hematophagous bats *Desmodus rotundus* in kidney samples*.* **Conclusions:** This study report the lack of detection of influenza-like in a high number of bat samples and may indicate the absence or the lower prevalence of these virus group in bats from Brazil. Our results also suggest the presence of paramyxovirus genotypes in bats commonly found in rural and urban area, including a probably Henipa-like virus in hematophagous bats, species that already had been described as vectors of rabies and others paramyxovirus with unknown zoonotic potential.

Hendra virus dynamics and spillover

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Hendra virus provides a model system for understanding the dynamics of emerging bat viruses and spillover. One factor constraining our ability to study Hendra virus spillover is the limited knowledge of the biology of the virus within its reservoir hosts. We present three different hypotheses for how within-host pathogen dynamics in bats may interact with among host factors to drive dynamics of emerging bat virus spillover. These hypotheses include: pulsed viral excretion due to seasonal epidemics, local persistence due to waning immunity within bats, or episodic shedding from persistently infected bats. We discuss the evidence for each hypothesis and show that differentiation among these scenarios is essential for predicting and managing spillover.

Using serology to understand the dynamics of concurrent viral infections in pteropid bats

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Objectives: Fruit bats of the genus *Pteropus* are reservoirs for henipaviruses throughout their range. *Pteropus medius* is the natural reservoir for Nipah virus in India and Bangladesh, and mechanisms of spillover to humans primarily involves contamination of date palm sap with excreta. Serological dynamics have provided insight into patterns of Nipah virus infection in this host, but other viruses, including Nipah-like viruses have been identified through pathogen discovery techniques. Little is known about infection patterns of other viruses within this species, or their likelihood of infecting other animals or people. **Methods**: We screened sera from a single population of *P. medius* in Bangladesh collected quarterly over six years for IgG antibodies against henipaviruses (NiV, HeV, CEDV), filoviruses (EBOV, MARV), and Menangle virus, using assays containing virus-specific solubilized glycoproteins or F proteins in a Luminex platform. **Results and Conclusions:** Here we present preliminary observations of comparative temporal patterns for multiple viral agents that suggest co-circulation in this population. We also discuss challenges in interpretation of serology

when studying viral infections in wildlife, particularly when multiple antigenically related viruses may be present.

Estimating viral richness and viral sharing in bats: integrating previously-published and newly-acquired field data

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Objectives: A handful of studies published over the last 8 years have sought to identify the host, ecological, and evolutionary factors that best explain species-level differences in viral richness in bats. Similarly, a few studies have also aimed to answer the golden question: Do bats carry a significantly larger number of total viruses, or a larger number or proportion of zoonotic viruses than other mammals? Our objective is to address these critical questions using statistical models and large datasets collated from the literature and acquired from the field. **Methods:** We collated data from the past 75 years of published for over 2800 mammal-virus associations, representing 754 mammal species and 586 ICTV-named viral species. We fit a series of generalized additive models to these data to identify and examine the functional form of significant predictor variables for total and zoonotic viral richness. Using our best-fit models we also estimate expected viral richness for each host species under a scenario of 'maximum' research effort. We map these viruses in geographic space. We also use species accumulation curves to estimate viral richness from standardized, field-acquired data from the USAID PREDICT project (http://www.healthmap.org/predict/). Network models and statistics were used to compare patterns of viral sharing among bats between the literature and field-acquired datasets. **Results:** For the all mammal analyses: The best-fit model for total viral richness per wild mammal species explained 49.2% of the total deviance, and included a per-species measure of disease-related research effort, phylogenetically corrected body mass, geographic range, mammal sympatry, and taxonomy (order) After controlling for research effort, the proportion of zoonotic viruses per species is predicted by phylogenetic relatedness to humans, host taxonomy and human population within a species range—which may reflect human–wildlife contact. We demonstrate that bats harbor a significantly higher proportion of zoonotic viruses than all other mammalian orders. For the bat field-acquired data we show significant differences in viral richness estimates across bat genera and viral family, as well as differences in the rates of saturation. Clustering in bat host-virus networks follow some predictable patterns and identify additional bat species to target for viruses of interest. **Conclusions:** These host-specific analyses and estimates of viral richness, including the unobserved or 'missing' viruses, allow us to better identify and target which species and regions should be preferentially targeted to characterize the global bat virome.

Optimised sampling efforts and screening assays identify several MERS-related coronaviruses in South African bats

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Objectives: Bats are considered reservoir hosts for all mammalian alpha- and beta-coronaviruses (α-, β-CoV). Following the emergence of SARS in 2002/03 and the subsequent identification of *Rhinolophus sinicus* as the likely ancestral SARS-CoV source, a wide diversity of bat CoV has been described worldwide. We work in transdisciplinary collaborations with ecologists and zoologists to define CoV diversity and ecology in South African bats. In addition to general "opportunistic" surveillance, species-specific studies of *Neoromicia capensis* and *Rhinolophus spp* are conducted, including longitudinal studies of bat colonies to determine shedding patterns and diversity of viruses present. **Methods:** Since 2011, 24 different bat species have been sampled along rainfall and altitudinal gradients across different biomes; namely Fynbos, Forest, Nama Karoo, Grassland, and Savanna. Sample types include faecal pellets, saliva and urine swabs, and when voucher specimens are sacrificed for museum collections, also blood and organs. Sequences of the 816bp RGU fragment (Drexler et al., 2010) for species classification were used to construct ML trees in MEGA v7. **Results:** An improved screening method greatly increased the CoV detection rate. Of 686 samples tested, 92 from 9 bat species were screening-positive: 66 for α-CoV, 19 for β-CoV, and 7 for both. The majority of sequences identified are α-CoVs, with ~20% prevalence for *N. capensis*. Preliminary analyses of partial RdRp, nucleocapsid and spike gene fragments of novel β-CoV identified in Neoromicia and Pipistrellus bats are closely related to BtCoV PML-PHE1/RSA/2011 (NeoCoV), previously found by us in a *N. capensis* and belonging to the same viral species as the recently emerged MERS-CoV, responsible for the ongoing

outbreak in the Arabian Peninsula. **Conclusions:** Extensive, dedicated sampling efforts allowed detection of α- and β-CoV from a wide range of bat species across large parts and different biomes of South Africa. An improved screening PCR approach yielded significantly more positive samples. There is substantial CoV diversity in southern African bats, including, most importantly, additional MERS-CoV-related CoV, which will hopefully help to address the unresolved question of the origin of this zoonotic pathogen.

Coronavirus diversity in bats from urban, rural and forest areas of Atlantic and Amazon Forest biomes, Brazil.

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Objectives: Epidemiological and phylogenetic studies indicate that four out of six coronavirus capable of infecting humans are the result of spill over events of virus from bats to humans. Despite the great diversity of coronaviruses in bats, the large number of bat species in Brazil (15% of the world's bat diversity) and the presence regions classified as hotspot for zoonotic pathogen emergence only few studies have analyzed the circulation of coronaviruses in Brazilian's bats. This study aims to evaluate the diversity of CoV circulating in bats in Brazil, covering different species, habitats, and life history of the hosts. **Methods:** We analyzed 840 bats from 53 species and five bat families with a pancoronavirus detection assay. Intestine, lungs, serum and rectal/oral swabs were obtained from bats from forest, urban, and rural areas located in the Atlantic and Amazon Forest biomes. **Results:** Distinct coronavirus lineages were detected in in bats from all sites screened. The coronavirus RNA was detected in 27 individuals from eleven bat species including *Artibeus lituratus(4), Carollia perspicillata (5), Eumops glaucinus(1), Glossophaga soricina (3), Mimon crenulatum(1), Molossus rufus(2), Molossus molossus (1), Myotis nigricans(1), Myotis riparus (1), Phyllostomus discolor(1)* and *Sturnira lilium (7)*. The analysis of coronavirus phylogenetic relation from nucleotide sequences obtained showed the circulation of the 25 Alphacoronavirus genotypes (α-CoV) and two Betacoronavírus (β-CoV), distributed in thirteen lineages (eleven α-CoV and two β-CoV). Results indicate the presence of a great coronavirus diversity in bats from Brazil including potential new and already described lineages. We describe the detection of a bat coronavirus genetically related with Alphacoronavirus-1 species, which are a group of closely related viruses with an evolutionary history of recombination and cross-species transmission between domestic and livestock animals. We also report the circulation of Betacoronavirus lineage "C", related to emergent highly pathogenic coronavirus CoV-MERS, in South American bats commonly found in urban areas, representing the first detection of coronavirus Clade C in this subcontinent. **Conclusions:** Our report points to the great diversity of CoV genotypes in New World bats, more specifically in the Atlantic Forest Biome, providing a better understanding of CoV diversity, host range and biogeographic distribution.

Preliminary Evidence of a Novel Alphacoronavirus and Secondary Acquisition of Tymoviridae and Partitiviridae in Little Brown Bats (*Myotis lucifugus*) in Southcentral Alaska.

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Objective: We sought to analyze the virome of the most common bat species in Alaska, *Myotis lucifugus*, the little brown bat. Swabs, tissue, and fecal samples were collected from habitats in close proximity to barns, farm buildings, and human habitations in southcentral Alaska. **Methods**: Total RNA extracts were screened by RT-PCR and CoV ORF1a, and primary RNA samples were used in library preparation for short-read, paired-end next generation sequencing on an Illumina HiSeq platform. **Results**: Sanger sequencing of amplicons confirmed the presence of an alpha-coronavirus phylogenetically related to

persistent alphacoronaviruses detected in bats in Colorado and the Rocky Mountains. Aligning to a reference *M. lucifigus* virus from Colorado, bat alphacoronavirus CDPHE15/USA/2006, we assembled a full-length genome (28,515nt) identifying the novel alphacoronavirus/bat/Alaska/s7/2014. A high degree of thermodynamically stable stem-loop RNA structures are predicted by Mfold within 700nt of 5' and 3' termini of genome**.** While nucleotide conservation to the Colorado virus was 96%, notable amino acid differences were identified in coronavirus proteins. In two distinct bat samples, preliminary results indicate the likely presence of tymovirus (eg. Dulcama mottle virus) probably acquired through ingestion of insects feeding on infected plants. In addition, initial results indicate presence of alpha-partitivirus closely aligned to *Rosellina*-type associated with spruce/alder and other partitivirus-like sequences. Secondary acquisition of virus obtained by feeding or incidental infection by fungi (eg. gamma-partitivirus associated with *P. destructans*) has been previously described for bats collected from similar ecological settings (eg. Thapa et al. 2016). **Conclusions**: We continue to further refine these initial for better resolution of the virome of Alaska bats.

Are big brown bat cells different than human cells in their innate immune response to coronavirus and viral ligands?

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Objectives: Bats are hosts for viruses such as those that closely resemble coronaviruses (CoV) that cause severe acute respiratory syndrome (SARS), Middle East respiratory syndrome (MERS) and porcine epidemic diarrhoea (PED). Despite the serious nature of these diseases in other mammalian hosts, bats naturally infected with CoV or experimentally infected with MERS-CoV do not demonstrate clinical signs of disease. We challenged big brown bat (*Eptesicus fuscus*) cells and human cells with MERS-CoV or viral ligands to study the differences in their interferon and inflammatory responses. **Methods:** *E. fuscus* kidney cell line and bone marrow derived cells, human fibroblast and epithelial cells were challenged with either MERS-CoV or poly(I:C), a double stranded RNA surrogate. Transcripts for several innate immune response genes were quantified using qRT-PCR. Interaction between the bat TNF promoter and a potential repressor of the promoter, c-Rel, was detected by chromatin co-immunoprecipitation and bat c-Rel, TLR3, RIGI and MDA5 transcripts were knocked-down using specific siRNA. **Results:** Both human and bat cells, when stimulated with poly(I:C), contained higher levels of transcripts for interferon beta than unstimulated cells. In contrast, only human cells expressed robust amount of RNA for TNFα, a cell signaling protein involved in systemic inflammation. We further observed that poly(I:C) signaled primarily through TLR3 in big brown bat cells. We examined the bat TNFα promoter and found a potential repressor (c-Rel) binding motif. We demonstrated that c-Rel binds to the putative c-Rel motif in the promoter and knocking down c-Rel transcripts significantly increased basal levels of TNFα transcripts. Both human and bat cells support replication of MERS-CoV to comparable levels. **Conclusions:** We have identified a novel transcription repressor, c-Rel, that inhibits an increase in TNFα transcripts in bat cells after poly(I:C) stimulation. We have also showed for the first time that poly(I:C) signals through TLR3 in bat cells. We are currently studying the modulation of the innate immune response in bat cells by MERS-CoV and individual MERS-CoV and bat coronavirus proteins. Identifying adaptations in the bat innate immune response might allow us to extrapolate the knowledge in identifying potential drug targets in spill-over species, such as humans.

Reverse genetic analysis of bat influenza viruses: A journey full of surprises.

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Our understanding of conventional influenza A viruses was recently challenged by the identification of two novel genome sequences of influenza A-like viruses from bat specimens by next-generation sequencing. Serological surveys indicate that these viruses circulate in various bat species in Central and South America. However, no viable viruses could be isolated from bats, impeding further characterization of these viruses. Interestingly, analysis of the viral surface proteins revealed that the entry machinery of these viruses differ significantly from all known conventional influenza A viruses and may only support entry into bat cells. This talk will summarize recent progress obtained by reverse genetic analysis of bat influenza A-like viruses, including the observation that the host tropisms of these viruses might be larger than anticipated.

Towards understanding bat influenza A-like viruses

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Objectives: Bats harbor many viruses, which are periodically transmitted to humans resulting in outbreaks of disease (e.g., Ebola, SARS-CoV). Recently, bat influenza A-like virus HL17NL10 and HL18NL11 sequences were identified; however, no viruses were isolated from bats. This discovery aroused great interest in understanding the evolutionary history and pandemic potential of bat-influenza virus. **Methods**: Using synthetic genomics, we rescued a modified bat-influenza virus that had the HA and NA coding regions replaced with those of A/PR/8/1934 (H1N1). **Results**: This modified bat-influenza virus replicated efficiently in vitro and in mice, resulting in severe disease. The results indicate that internal genes of bat influenza A-like viruses are functional to support virial genome transcription and virus replication. Mini-genome replication studies and virus reassortment experiments demonstrated that bat influenza A-like virus has very limited genetic and protein compatibility with Type A or Type B influenza viruses, yet it readily reassorts with another divergent bat influenza A-like virus. **Conclusions**: In conclusion, our data indicate that the bat influenza A-like viruses recently identified are authentic viruses that pose little, if any, pandemic threat to humans; however, they provide new insights into the evolution and basic biology of influenza viruses.

Experimental Infection of Jamaican Fruit Bats (*Artibeus jamaicensis*) with a Rescued Bat HL18NL11 Influenza A-like Virus

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Objectives: Nucleotide sequences of two novel influenza A-like viruses, HL17NL10 and HL18NL11, were recently discovered in New World little yellow shouldered fruit bats (*Sturnira lilium*) and flat-faced fruit bats (*Artibeus planirostris*), respectively. Serological studies indicated high prevalence to these viruses among many species of Phyllostomidae leaf-nosed fruit bats of Central and South America, including Jamaican fruit bats (*Artibeus jamaicensis*). **Methods**: Infectious viruses have not been isolated from bats, therefore an infectious clone of HL18NL11 was generated by reverse genetics technologies that produced particles resembling influenza viruses from transfected cells by electron microscopy. Susceptibility of Jamaican fruit bats to rescued HL18NL11 bat influenza A-like virus was determined during a 28-day challenge experiment via intranasal inoculation. **Results**: The bats exhibited no overt clinical signs of disease nor fever. However, rectal swabs had up to 10^4 $TCID_{50}$ equivalents of HL18NL11 vRNA by real-time PCR in each bat on days 2, 4 and 7 post inoculation, but not day 15 or 28, and in the lungs of one of the bats on day 28 when they were euthanized. Serology showed moderate antibody titers to nucleoprotein by ELISA. Histopathology revealed mild pathology, particularly in the one bat with detectable vRNA in its lung. This bat's lungs showed multifocal mild-to-moderate histiocytic and lymphoplamacytic interstitial pneumonia. Pleocellular infiltrates were especially prominent around adventitia of pulmonary arterioles. Immunohistochemistry with mouse antibody to recombinant H18N11 nucleoprotein revealed virus antigen in the lungs of this bat. **Conclusions**: This is the first study to demonstrate susceptibility to bat influenza viruses and suggests that viral persistence up to 28 days may occur in some bats, supporting the hypothesis that Jamaican fruit bats may be a natural reservoir host of the HL18NL11 virus.

Seroprevalence of alphaviruses, flaviviruses and Rift Valley fever virus in Ugandan bats

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Objectives: Arboviruses including Rift Valley fever virus (RVFV), chikungunya virus (CHIKV) and Sindbis viruses have previously been isolated from naturally-infected East African bats, however the role of bats in arbovirus transmission cycles is poorly understood. The aim of this study was to investigate the exposure history of Ugandan bats to a panel of arboviruses. **Methods**: Insectivorous and fruit bats were captured from multiple locations throughout Uganda between 2009 – 2013. All bat captures were conducted under the approval of IACUC protocols 1731AMMULX (Maramagambo samples) and 010-015 (all other samples). Bats were captured using harp traps or mist nets, taking appropriate biosafety precautions. All serum samples were frozen at -80°C until they were tested for neutralizing antibodies against West Nile virus (WNV), yellow fever virus (YFV), Dengue 2 virus (DENV-2), Zika virus (ZIKAV), CHIKV, o'nyong-nyong virus (ONNV), Babanki virus (BABV), and RVFV by plaque reduction neutralization test (PRNT). **Results**: Sera from up to 626 bats were screened for neutralizing antibodies against each virus. Key findings include the presence of antibodies against ONNV in approximately 15% (44/303) of Egyptian rousette bats (*Rousettus aegyptiacus*) from Maramagambo forest in western Uganda, and antibodies against RVFV in Ethiopian epauletted fruit bats (*Epomophorus labiatus*) captured from Kawuku (5/52) and Egyptian rousette bats from Kasokero cave (3/54). **Conclusions**: Antibodies reactive to flaviviruses were widespread across bat taxa and sampling locations.The data presented demonstrate the widespread exposure of bats in Uganda to arboviruses, and highlight particular virus-bat associations that warrant further investigation.

Presence of zoonotic bat pathogens correlate with reproductive seasons in South African bat populations
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In 2003 we initiated passive surveillance on bats in South Africa with the initial objective to identify rabies–related lyssaviruses, but this has since expanded to include several other possible zoonotic viral and bacterial pathogens. The project has identified viruses in the following families; *Rhabdo, Paramyxo, Bunya, Filo*, *Adeno-, Herpes-, Picorna, Orthomyxo, Circo, Parvo, Papilloma* and *Coronaviridae* as well as the following bacterial pathogens; *Leptospira*, *Rickettsia and Bartonella.* **Objectives:** To determine longitudinal circulation of pathogens we initiated seasonal sampling from 2012 in two cave systems in South Africa. This sampling specifically focused on the reproductive seasons of *Rousettus aegyptiacus* and *Miniopterus natalensis*. **Methods:** Serum was analysed for rabies related lyssavirus, Lagos bat virus, antibodies using a virus neutralization assays. Tissue, urine saliva and fecal samples were tested for the presence of viral nucleic acids using RT-PCR/PCR specific for several viral families. Illumina MiSeq 16S rRNA gene sequencing on low-biomass individual bat samples was used to identify bacterial pathogens. **Results:** Longitudinal studies, specifically focused on measuring the presence of LBV antibodies in *Rousettus aegyptiacus*, indicated cyclic fluctuation of antibodies with a marked increase shortly after the parturition period, which identified this as a high risk period for spill-over. We showed that seasonal bat reproduction is a major driver shaping temporal variations in microbial community structure. A strong temporal shift in oral, fecal and urinary microbiota was also associated with bat reproduction, with significant associations between the microbiota and the sex, or reproductive status. **Conclusion**: This cumulative evidence can be used to indicate periods of increased viral and bacterial circulation, which can be used to make public and veterinary health decisions on spill-over risks.

Body mass index of the Egyptian fruit bat, *Rousettus aegyptiacus*: An indicator of infection status
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Body mass in conjunction with forearm length has long been used to determine body mass indices for bats. These indices have been further linked to diseases detected in bats, with a low body mass index being a potential indicator of infected bats. **Objectives**: We correlated body measurements to body mass, enabling us to determine

the best measurement that could be used to build body mass indices which can be correlated to disease status of *Rousettus aegyptiacus.* **Methods**: This study focuses on the Egyptian fruit bat (*Rousettus aegyptiacus*) in the Limpopo Province of South Africa. Data was gathered over a two year period, 2015 and 2016, and consisted of measurements of various body parts. **Results**: Wilcoxon Matched pair tests indicated a significant difference in body weight between the two sampling years (V = 34476, p = 0.002466). A strong correlation was found between body mass and forearm length when both years are considered (S = 17252000, p-value < 2.2e-16), as well as for the first (S = 3487900, p-value < 2.2e-16) and second year (S = 1250500, p-value < 2.2e-16) of the study with a strong correlation value; R > 0.78 in all cases. The correlation between mass and forearm length was significant for both males and females during both years (p-value < 2.2e-16), but the correlation value was always lower for females. Other body measurements correlated significantly with body mass, but only forearm length showed a strong correlation. **Discussion**: Forearm length is thus an indicator of body mass in Egyptian fruit bats, as has been found for insectivorous bats. As such, body mass in conjunction with forearm length could be used to build body mass indices, which could be used as a preliminary indicator of disease status for *Rousettus aegyptiacus.*

Environmental constraints drive the viral diversity of two sympatric Amazonian bat species
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Amazonia is a major biodiversity hotspot which encompasses a great diversity of bat species, as well as a wide variety of climates and vegetation formations. Landscape characteristics (*e.g*. climate, vegetation structure, anthropogenic disturbances) are relevant predictors of species richness and influence the host-pathogens relationships. However, the effects of contrasting environmental conditions on the viral diversity harbored by Amazonian bats have yet to be investigated. Through a metagenomic approach we characterized the viral diversity of two sympatric Amazonian bat species: the common vampire bat, *Desmodus rotundus* (*Phyllostomidae*) and the insectivorous bat, *Molossus molossus* (*Molossidae*). Then, through a statistical approach, we assessed the impact of the landscape characteristics by comparing the viral richness harbored by different populations of vampires and insectivorous bats inhabiting different environments (*e.g.*, forests, edge habitats, anthropized and urban areas). We identified 10,983 viral sequences related to 48 viral families known to infect a wide range of hosts (*i.e.*, bacteria, plants, insects and vertebrates). Most viruses detected reflect the dietary habits, especially within the insectivorous bat species which presented the highest diversity of plant and insect-related viral families. Diversity tests and phylogenetic relationships reconstructed for several mammal-related viral families (*e.g.*, *Bunyaviridae*, *Circoviridae*, *Foamyviridae*, *Herpesviridae*, *Papillomaviridae*) revealed a preferential transmission route within phyla of bats, as well as a potential association of viral diversity with the host's gut microbiota. Three structuring poles related to species traits and environments were identified, explaining the distribution of viral diversity and showed a strong correlation between the type of environment, host phylogeny, diet and viral diversity. The substantial viral richness detected in forest environments is likely due to a wider diversity of prey and favored by more frequent contacts between hosts and overlapping habitats. These findings provide significant insight into viral bat diversity in Amazonia and emphasize that environmental constraints and host features are the main drivers of viral diversity in bat species.

Seasonal and individual predictors of grey-headed flying fox (*Pteropus poliocephalus*) foraging movements in Adelaide, South Australia
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Objectives: The distribution of flying foxes in Australia is influenced by the unpredictable availability of their preferred diet, especially eucalypt blossoms. Recently, human activities, including destruction of native habitat and planting of non-native vegetation that provides predictable foraging, have altered the distribution and movements of flying foxes. The consequences of this change are important for both bat and human health, given that bats are reservoirs of Australian bat lyssavirus and Hendra virus, both of which cause fatal disease in humans. In 2010, grey-headed flying foxes (*Pteropus poliocephalus)* established a permanent roost in Adelaide, South Australia, several hundred kilometers outside their previous range. Despite incurring juvenile mortality due to extreme heat events, the population now numbers approximately 7000 and is expected to continue growing. **Methods:** As part of a larger study to characterize the health and behavior of the Adelaide flying fox population, we deployed lightweight GPS loggers on bats to track their foraging movements. Loggers recorded a bat's position every 30 seconds when flying and every 45 minutes when stationary, and also recorded acceleration,

speed, and altitude data. Forty foraging sites were ground-truthed to identify feeding resources. **Results:** Five flying foxes were tracked in winter 2016 and 9 in summer 2017, resulting in 112 nights of movement data. Bats exhibited individual variation in movement patterns, with some foraging repetitively, and others ranging more widely over the landscape. The nightly distance traveled depended on the interaction between sex and the ratio of weight to forearm length, but not on season. In the summer, bats foraged predominantly on urban resources, with figs and eucalypts being especially popular. **Conclusions:** This work provides insight into a recently-established, understudied bat population and is useful both to local Adelaide stakeholders as well as other urban citizens seeking to manage the bats that share their space. Foraging on urban resources, especially in residential yards, could increase the chances for disease transmission from flying foxes to humans and pets. Individual predictors of movement should be considered when building models of bat movement and disease risk.

Uganda Bat calls library-developing a tool to survey arthropod-borne viruses associated with Chiroptera
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Objectives: We continue to conduct studies of bats in different parts and habitats of Uganda with a number of particular goals: -

i. To continue to understand the occurrence and ecology of bats that may be reservoirs and/or vectors of viruses in Uganda (BM presentation),
ii. To develop a micro-chiroptera calls Library for the country
iii. Continue the development a fast approach that can be used to quickly survey and identify the bat fauna of different parts of Uganda.
iv. To investigate the roles of different species of bats in the ecology of viruses (RK presentation),

Methods: Through a DTRA supported project we particularly targeted to understand bat ecology and their potential roles in virus ecology. This was done through graduate training and research, training in field techniques of capture and processing of bats for detection of and characterization of viruses a pillar institutional players and a compilation of reference calls of micro-chiropteran bats for Uganda. Field biosurveillance training was held with participants from NADDEC, UVRI and Makerere University at Zika forest. A graduate student now preparing his dissertation, was recruited and completed an ecological study on bats in the Kaptum cave. Insect bats are captured using Mist nets, Herp traps and Hand net capture at roost sites. Bats are either free flown, ziplined or light tagged and hand released from which voucher calls are collected. Collected calls are processed using Kaleidoscope Pro version 31.7 for large files that need to be split for examination and processing in Sonobat4.0.6p. **Results**: Cumulatively, voucher calls for 50 species of micro chiropteran bats (over 50% of the Ugandan species) have been collected. Several of these are represented by multiple bats that way taking care of potential intra specific variations, potential ecological variations each of which could affect the call produced by the species. This presentation specifically shares our findings on call characteristics for a sample of the species and highlights the great overlap in signatures for species of Molosid bats, species of the Genus *Scotophilus*, while showing very nicely segregated call signals for Hipposiderid, Rhinolophid and a good number of verspertilionid bats. **Conclusions**: Our next steps are to attempt to collect voucher calls from species we haven't, collect additional calls from species already recorded but from few individuals, and to work with partners to develop a tool that could be used to rapidly identify calls collected from bat detection surveys from different parts of the country.

Dampening of STING-dependent IFN production: an implication of virus tolerance in bats?
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Objectives: Bats are known to harbour a number of zoonotic viruses, many of which are highly pathogenic in human but result in no clinical symptoms in bats. The mechanism of how bats coexist with viruses is still largely unknown. We previously reported the contraction of type I IFN locus and unusual constitutively expression of IFNA in bats. We hypothesis this may help bat to inhibit virus replication. However, as immune response can also do harm to the host, then how bats tolerate viruses and viral induced immune responses become a question. **Methods:** To address this question, we scanned a list of DNA and RNA sensors in bats. We then focus on STING, which played a key role in multiple DNA sensing pathways, for understanding how bats tolerate DNA viruses. We also tested the functionality of bat STING in a list bat immune or non-immune cells. **Results and Conclusions:** We found some of the viral DNA sensors are under faster evolution, implying a change of function. Further experimental data also confirmed the dampening of viral DNA sensing, more specifically STING- dependent IFN production pathway. We then identified a ubiquitous key point mutation in all bat species tested, which hugely

decreased the cGAS-STING sensing ability (80%) by gain-of-function studies. Lastly, we restored the functionality of STING and STING-dependent viral DNA sensing pathway by changing this site to human. We conclude that bat naturally own a dampened STING-dependent IFN production, probably to avoid over responses to virus. This observation provides a model of how bats tolerance thus long-term hosting these viruses.

Regulation of immune activation and dampened inflammation in Pteropid bats
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Objective: Natural reservoir hosts can maintain low-level infection of pathogens without succumbing to severe disease. Several bat species host viruses such as Ebola, SARS, Nipah, Hendra, and other pathogenic viruses and while these same infections cause mass-inflammation in humans and other animals they are mostly asymptomatic in the bat. As such, bats are a unique model for studying the host control of systemic inflammation. **Methods:** We utilised bat cell lines, primary cells and tissue with qPCR, Western Blot, FACS analysis, NGS transcriptomics and cellular proteomics to profile pathways and characterise signalling mechanisms. **Results:** Through studying immune activation to flaviviruses, influenza and reovirus, along with natural stimulants of innate immunity such as TLR and RLR ligands we are beginning to characterize key differences to their human counterparts for PRRs.. There appears to be differences also in the kinetics and activation signals required for Interferon activation also. In addition, our data, from investigation of primary bat immune cells and studying bat homologs, suggests that inflammasome activation pathways may be altered with dampened activation of downstream inflammation. **Conclusion:** Along with fundamental differences to cell biology, this may indicate an evolutionary adaptation that while supporting flight, may cause susceptibility to infection yet maintain a symbiotic state with several pathogens. Initial observations show several key mutations, altered kinetics and a decrease in sensitivity to induce signaling all appear to be involved. From this we can gain understanding into a mechanism for controlling excess inflammation in humans.

Delineating the phenotype and function of the B cell population in the fruit-eating bat, Pteropus Alecto.
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Objective: The unique ability of bats to act as reservoir for viruses that are highly pathogenic to humans suggests unique properties and functional characteristics of their immune system. However, the lack of bat specific reagents, in particular antibodies, has limited our knowledge of bat's immunity.
Methods: Here, using cross-reactive antibodies, we report the phenotypic and functional characterization of B cells based on anti-mouse I-Ab (MHC-II) and anti-bat IgG. **Results**: Using flow cytometry, we show their distribution amongst the major lymphoid organs and scanned electron micrographs of these sorted population reveal that they are morphologically similar to human and murine B cells. In addition, a large population of these cells test positive for CD19 mRNA, tested using SmartFlare RNA probes, and anti-human CD19 antibody. Uniquely, these cells are able to show an increase in calcium uptake upon cross-linking of their B cell receptor with the addition of secondary donkey anti-goat antibody, which is specific for the goat anti-bat IgG. We also demonstrate T cells and myeloid cells do not release calcium in the presence of IgG and secondary antibody. Furthermore, we also demonstrate that injecting LPS for 5 hrs show an increase in MHC-II$^+$IgG$^+$ B cell population in the spleen and blood. This demonstrates a T-independent B cell activation amongst the B cell population. In addition, this population of cells do not respond to Poly (I:C) stimulation. We also performed single cell RNA sequencing on sorted MHC-II$^+$IgG$^+$CD19$^+$ positive cells to identify various B cell subsets based on their gene signature. Initial analysis reveal that these cells show increased expression of CD19 and do not express CD3, CD8 and CD11b. **Conclusions**: Here, we demonstrate for the first time the phenotype and function of B cells in *Pteropus Alecto.* This provides us with a platform to isolate and further elucidate the role of these cells in infectious models.

Integrative measures for assessing "health" in free-ranging bats – zoonotic and conservation implications from a One Health perspective

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Objectives: Risks of zoonotic spillover are likely related to the overall health of the animal host. For bat hosts of viral zoonotic diseases, the relationship between health and spillover risk is complex, with poor health possibly favoring transmission by increasing viral load and shedding but also decreasing animal mobility and human-host contact. Unfortunately, determining the health status of free-ranging bats is fraught with difficulty. Challenges exist not only in deciding which diagnostic measures to use, but also in interpreting the results of these measures. Furthermore, without the ability to measure fitness in these long-lived mammals, our understanding of the consequences of "good" or "bad" health for a free-ranging bat is poor. Our objective is to provide a framework for defining bat health that will facilitate bat studies and will enhance our understanding of spillover risk, ecosystem health, and human health. **Methods:** We combined an extensive literature review of health metrics in free-range wildlife, including bats, with our own long-term field studies and experiences studying bat physiology and disease. **Results:** Literature review and our past work point to several findings: (1) a number of measures commonly used in other vertebrate taxa and in other mammals have not been fully deployed for bats – sometimes owing to methodological hurdles; (2) due to a lack of tools, and often small sample volumes, most bat studies have relied on too-few measures, such as BMI (which suffers from allometric problems and is often surprisingly uninformative), the ubiquitous neutrophil-to-lymphocyte (N/L) ratio, ectoparasite load, and highly variable immune metrics such as hemmaglutination assays; (3) newer molecular methods, such as transcriptomic approaches hold promise for improving our understanding of bat health, especially when integrated with other measures such as infection status. We will present preliminary data from our recent field studies of African fruit bats in which we have deployed 20+ field diagnostic measures in combination with infection status and a transcriptomic approach. **Conclusions:** We recommend the development of integrative health metric(s), which will allow for the determination of the most informative measures for future studies. We also implore researchers to document normative physiological measures for more species of bats, analyzed with regards to life history, ecology, and phylogeny.

Host-pathogen interactions during white-nose syndrome

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Objectives: We have employed a dual RNA-Seq approach to study gene expression of both host and pathogen during the fungal infection that causes white-nose syndrome (WNS) in bats. **Results**: We have found that when *Pseudogymnoascus destructans* is causing WNS, the most significant differentially expressed genes in the pathogen were involved in heat shock responses, cell wall remodeling, and micronutrient acquisition. These results demonstrate that this fungal pathogen responds to host-pathogen interactions by regulating gene expression in ways that may contribute to evasion of host responses. We have also found that host responses vary between susceptible and resistant species of bats in ways that may indicate that host responses contribute more to pathogenesis than to protection. This may be because, during hibernation, host immune responses are too costly and lead to premature depletion of energy reserves. We have also determined which host transcriptomic responses to fungal infection can occur during torpor and which require arousal to euthermy. We found relatively few host transcripts that showed significant changes in expression levels due to fungal infection in torpid bats compared to euthermic bats. **Conclusions**: These results support the view that torpor is a period of relative dormancy and suggest that periodic euthermic arousals exist to provide an opportunity for host responses to pathogens.

Resistance or Tolerance – How do European bats cope with *Pseudogymnoascus destructans*?
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Objectives: *Pseudogymnoascus destructans* (*Pd*), the causing agent of the White-nose disease, colonizes bats during hibernation. The cold-loving fungus affects the snout and all the hairless skin membranes of torpid bats where it causes lesions. The spreading epidemic in North America (so called White-nose syndrome) is characterized by mass mortalities and regional extinctions of certain bat populations. In Europe, *Pd* has been recorded since several decades as a widespread pathogen, yet it does not cause mass mortalities. Several studies confirm that *Pd* is native to Europe and appeared as a new pathogen in North America in 2006. If and how European bats adapted to the disease and why North American bats cannot cope with the fungus remains unclear. **Methods**: We analysed data from over 300 hibernacula across Europe to test for factors influencing mortality, including *Pd* infections on bats. **Results**: Our results show an overall low mortality rate of bats in Europe with no evidence of *Pd*-associated mortalities. Physiological data and blood samples from infected and non-infected European bats were analysed to investigate, if bats suffer from White-nose disease and how the immune systems reacts to fungal infections during hibernation. **Conclusions**: Our ecological, physiological and immunological results suggest resistance and tolerance of European bats towards *Pd*.

Modeling the impact of White-nose syndrome on two western bat species
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Objectives: The rapid westward spread of white nose-syndrome (WNS) through North America has become a critical conservation issue for endemic hibernating bat species with many Eastern populations experiencing steep declines over the last ~10 years. The continued spread of the psychrophilic fungus *Pseudogymnoascus destructans* into Western states over the last two years has the potential to impact many hibernating species. Disease outcome varies widely between species, with infection of some species (namely European and Asian species) being largely benign. The identification of species that may be threatened is paramount to development of effective conservation strategies. **Methods:** Using field obtained morphometric data in conjunction with experimentally obtained estimations of key metabolic parameters we applied a modified hibernation model that includes fungal growth dynamics for two currently unaffected North American bat species: *Myotis californicus* and *Myotis yumanensis*. **Results:** Infection of *P. destructans* would likely reduce the maximal time spent in hibernation for both Western *Myotis* species. Reductions of maximal time spent in torpor were predicted to be the most drastic in microclimates with relative humidity approaching saturation and temperatures between ~5 °C and 10 °C. Despite the increased rate of overwinter energy consumption, fat reserves were still predicted to be sufficient to overwinter throughout the majority of their distribution. **Conclusions:** *M. californicus* and *M. yumanensis* are predicted not to experience distribution wide population declines like those witnessed for *M. lucifugus* and *M. septentrionalis* in eastern North America. Continuing field studies will provide data on important model parameter estimations, more species, realized hibernacula microclimate selection, and providing data to empirically validate model predictions.

Variable behaviors influence species susceptibility to disease – surviving white-nose syndrome.
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White-nose syndrome (WNS) continues to spread through populations of hibernating bats in North America, causing unprecedented mortality in several species occurring in eastern parts of the continent. Despite this devastation, other bat species that come into contact with the causative fungus, *Pseudogymnoascus destructans*, somehow survive. We still do not understand factors influencing species and continental differences in bat

susceptibility to WNS, but variability of innate behaviors among taxa and regions may help explain disease survival. This talk focuses on evidence suggesting infected bats can exploit 'survival habitats' (e.g., hibernacula with palliative microclimates) and 'survival behaviors' (e.g., palliative ways of regulating body temperature during winter). Our search for survival habitats and behaviors in WNS bats illustrates the challenges of understanding how microorganisms influence their cryptic hosts, how unknown host behaviors can obscure understanding of disease, and how new bat research methods may help overcome some of these challenges.

Emerging Insights into the Geographic Distribution, Genetic Diversity and Evolutionary Origin of Bat-borne Hantaviruses

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Objective: The recent discovery of genetically distinct hantaviruses in multiple species of shrews and moles (order Eulipotyphla) prompted a further exploration of their geographic distribution, genetic diversity and evolutionary relationships by analyzing tissues and feces from bats (order Chiroptera). **Methods:** Total RNA, extracted from frozen, ethanol-fixed or RNAlater®-preserved archival tissues (lung, liver, kidney, intestine, intercostal muscle) and rectal swab/feces of 1,890 bats, representing 10 families (Emballonuridae, Molossidae, Mormoopidae, Nycteridae, Phyllostomidae, Vespertilionidae in the Yangochiroptera suborder, and Pteropodidae, Hipposideridae, Megadermatidae, Rhinopholidae in the Yinpterochiroptera suborder), collected in Asia (China, Korea, Malaysia, Mongolia, Myanmar, Philippines, Republic of Georgia, Vietnam), Africa (Côte d'Ivoire, Guinea, Liberia) and the Americas (Bolivia, Brazil, Guyana, USA) during 1981–2015, were analyzed for hantavirus RNA by nested RT-PCR. Phylogenetic analysis was performed using maximum likelihood and Bayesian methods. **Results**: Hantavirus RNAs were detected in 2 of 12 *Neoromicia nanus* from Côte d'Ivoire (Mouyassué virus, MOYV), 6 of 49 *Hipposideros pomona* and 1 of 5 *Hipposideros cineraceus* from Vietnam (Xuan Son virus, XSV), 1 of 12 *Aselliscus stoliczkanus* from Vietnam (Dakrong virus, DKGV), 2 of 13 *Taphozous melanopogon* from Myanmar (Laibin virus, LBV), and 1 of 15 *Rousettus amplexicaudatus* from the Philippines (Quezon virus, QZN). Multiple attempts to acquire whole genomes of the newfound hantaviruses were unsuccessful, except for DKGV and QZNV. Phylogenetic analyses indicated incongruent topologies for each genomic segment, presumably because of the limited sequences available for most of the hantaviruses harbored by bats, shrews and moles. However, in both the S- and L-segment trees, QZNV appeared to share a common ancestry with XSV and LBV. Based on the host cytochrome *b* sequences, the phylogenetic positions of bats in the Yinpterochiroptera and Yangochiroptera suborders were consistent with the phylogenetic relationships among the bat-borne hantaviruses. **Conclusions:** Other research teams have reported Magboi virus in *Nycteris hispida* from Sierra Leone, Makokou virus in *Hipposideros ruber* from Gabon, Huangpi virus in *Pipistrellus abramus* from China, Longquan virus in *Rhinolophus affinis, Rhinolophus monoceros* and *Rhinolophus sinica* from China, Laibin virus in *Taphozous melanopogon* from China, and Brno virus in *Nyctalus noctula* from the Czech Republic, bringing to 11 the number of bat-borne hantaviruses to date. As in shrews, moles and rodents, the same hantavirus species was occasionally found in more than one bat species, and the same bat host species occasionally harbored more than one hantavirus species, suggesting that the formerly held conventional view of one hantavirus species and one host species is no longer tenable. Moreover, the basal position of the chiropteran-borne hantaviruses in phylogenetic trees and the demonstration that bat species in both suborders harbor hantaviruses suggest that primordial hantaviruses may have emerged in an early common ancestor of bats or other members of the Laurasiatheria superorder, that includes shrews and moles.

Neotropical Bats that Co-habit with Humans Function as Dead-End Hosts for Dengue Virus

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Objective: Several studies have shown Dengue Virus (DENV) nucleic acids and/or antibodies present in Neotropical wildlife including bats, suggesting that some bat species may be susceptible to DENV infection. Here we aim to elucidate the role of house-roosting bats in the DENV transmission cycle. **Methods**: Bats were sampled in households located in high and low dengue incidence regions during rainy and dry seasons in Costa Rica. We captured 318 bats from 12 different species in 29 households. Necropsies were performed in 205 bats to analyze virus presence in heart, lung, spleen, liver, intestine, kidney, and brain tissue. **Results**: Histopathology studies from all organs showed no significant findings of disease or infection. Sera were analyzed by $PRNT_{90}$ for a seroprevalence of 21.2% (51/241), and by PCR for 8.8% (28/318) positive bats for DENV RNA. From these 28 bats, 11 intestine samples were analyzed by RT-PCR. Two intestines were DENV RNA positive for the same dengue serotype detected in blood. Viral isolation from all positive organs or blood was unsuccessful. Additionally, viral load analyses in positive blood samples by qRT-PCR showed virus concentrations under the minimal dose required for mosquito infection. Simultaneously, 651 mosquitoes were collected using EVS-CO_2 traps and analyzed for DENV and feeding preferences (bat cytochrome b). Only three mosquitoes were found DENV positive and none was positive for bat cytochrome b. Our results suggest an accidental presence of DENV in bats probably caused from oral ingestion of infected mosquitoes. Phylogenetic analyses suggest also a spillover event from humans to bats. **Conclusion**: Therefore, we conclude that bats in these urban environments do not sustain DENV amplification, they do not have a role as reservoirs, but function as epidemiological dead end hosts for this virus.

Novel Gammaherpesvirus in Bats: discerning the secrets of these oncogenic viruses

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Objectives: *Gammaherpesvirinae* is a subfamily of herpesviruses which often cause lymphoproliferative diseases and have been linked to two human lymphoid cancers – Burkitt's lymphoma and Kaposi's sarcoma. Anecdotal evidence suggests that bats have lower rates of cancer than other mammalian species. This phenomenon may be because bats have evolved efficient mechanisms for detecting and repairing damaged DNA as a by-product of flight. How such a mechanism affects the interaction of Gammaherpesviruses (which cause cancer) with their bat, hosts is largely unknown. **Methods and Results:** We have isolated a novel Gammaherpesvirus (*Eptesicus fuscus* herpesvirus – EfHV) from a North-American Big Brown bat (*Eptesicus fuscus*). We have used a big brown bat cell line to study the growth kinetics of the virus. We have also performed electron microscopy and PCR to confirm that the virus belongs to the herpesvirus family. To determine the sequence of the herpesvirus, we have performed next generation sequencing (NGS) using Illumina mi-seq. Using the sequence obtained, we have performed phylogenetic analysis from which we found that although the EfHV belongs to the sub-family of Gammaherpesvirus, it forms a distinct branch within the sub-family. In addition to that we have identified the different proteins present in the virion by performing mass spectroscopy and have found that the virion components are similar to other herpesviruses. We have also infected cells of different species with the EfHV to understand the spectrum of different species that this virus is capable of infecting and we have found that it is able to infect human, monkey, porcine and feline cell lines apart from the bat cell line. **Conclusions:** The phylogenetic analysis shows that EfHV is a distant relative of all other gammaherpesviruses known so far. It might have evolved together with the big brown bat. Further studies looking at the interaction of EfHV and big brown bat might help us understand more about the persistent infection in bats and their unique was of resisting cancer.
Funding Source: NSERC

Experimental Infection of Jamaican Fruit Bats (*Artibeus jamaicensis)* with Zika Virus

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Objectives: Zika virus (ZIKV) emerged in the New World with the 2014 outbreak in Brazil. It has spread to much of South America, Central America, Mexico and the Caribbean, with hundreds of thousands of cases. While disease presentation may be subclinical to mild and include symptoms of maculopapular rash, conjunctivitis, and arthralgia, infection of pregnant women can lead to fetal microcephaly. Additionally ZIKV infection can induce Guillain-Barre syndrome. In the 1950s and 1960s bat species were investigated as possible reservoirs for ZIKV. In total, five different species of bats were found to be susceptible to the virus. Bats seroconverted, had viremia,

and, in one experimental infection study bats developed fatal neurological disease. This warranted further investigation of ZIKV in bats to determine their use as an animal-model, and to better understand the potential role of bats in viral ecology. **Methods:** Nine Jamaican fruit bats (*Artibeus jamaicensis*) were subcutaneously inoculated with $7.5x10^5$ pfu of ZIKV strain PRVABC59 and monitored over the course of 28 days, during which there were no conspicuous signs of disease. Bats were euthanized at 2, 5, 10 and 28 days post-inoculation to assess the course of infection and antibody responses. **Results:** Bats seroconverted by day 28 by ELISA with ZIKV-infected, fixed Vero E6 cells. Low levels of viral RNA were detected in one brain and one urine sample. IHC detected ZIKV antigen in lung and testes of one bat, and brains and salivary gland of two others. Pathology was consistently observed in the lungs, heart, testes and brain. Pneumonia was observed in four bats, cardiomyocyte necrosis in three bats, degeneration and lymphocyte infiltration in the testes of two bats, and neuronal degeneration in the hypothalamus and cerebellum in three bats. **Conclusions:** These results provide evidence that Jamaican fruit bats are susceptible to ZIKV and may serve as an animal model to study neurological components and sexual transmission of the virus. Low viral load in urine and tissues suggests the role of bats in viral ecology may be minimal.

Long-term monitoring of *Bartonella* bacteria in a captive colony of fruit bats and experimental evidence of bat flies as vectors of bartonella

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Objectives: Few experimental studies have monitored long-term infection dynamics in bat populations. This is especially true for vector-borne bacteria, where there can be significant challenges in maintaining both host and vector populations in controlled settings. In order to understand the importance of vector populations in the long-term maintenance of infection prevalence and bacterial diversity, we advocate for the use of semi-natural, long-term experiments capable of detecting changes in infection dynamics linked to the force of infection by vectors. **Methods:** Using blood samples taken from a captive colony of ~100 fruit bats (*Eidolon helvum*) in Accra, Ghana from July 2009 - March 2012, we monitored the dynamics of *Bartonella* spp. infection in the bat population using molecular techniques. Over this period, the bat fly population (*Cyclopodia greefi*) infesting the captive bats declined, but was then supplemented with additional flies from wild *E. helvum* in January 2012. We hypothesized that prevalence and species diversity of *Bartonella* infections in the colony will vary with changes in the bat fly population. **Results:** *Bartonella* prevalence and diversity peaked in March 2010 with 77% of bats infected and 8 *Bartonella* spp. present, then began to decline until July 2011 with only 15% of bats infected and 4 *Bartonella* spp. present. After the reintroduction of flies in January 2012, prevalence increased to 43% in March 2012 with 6 species present. Bats that received flies were equally likely to become positive after January 2012 as bats that did not receive flies, which may be attributable to dispersal of flies among bats after reintroduction. Additionally, changes in relative *Bartonella* spp. abundances showed that the species lost over time were uncommon in bats, but some of these uncommon species became more abundant after the reintroduction of flies. **Conclusions:** This experiment indicates that *C. greefi* bat flies are likely vectors of bartonella in *E. helvum* and play an important role in the maintenance of bacterial diversity in bats. Ongoing occupancy modeling work will explore the influence of within-host processes (including bacterial interactions and host resistance to infection) and alternative transmission routes on the long-term infection dynamics in individual bats.

Posters

1. Predicting the epizootiology of temperate bat disease: Is it all about the bats?James N. Aegerter[1], Ashley C. Banyard[2], Anthony R. Fooks[2], Graham C. Smith[1]

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Predicting the dynamics of disease in wild bats, their epizootiology, and the risks these pose to people, the economy or other biodiversity is complicated. Bats may be the evolved hosts for disease, effective maintenance hosts, or accidental spill-over hosts (we cannot always distinguish which), whilst their unique life-style permits the exceptional natural movement of disease, as well as an exceptional potential to vector disease into homes, farms or other sensitive sites. These diseases may pose social or economic concerns (i.e. to public or livestock health), or produce conservation concerns. Further, diseases may well also be endemic, exotic or newly emerging, and importantly their dynamics today occur in the contexts of rapid land-use change and climate change. With decision-makers relying on the quality of epizootiological predictions, and substantial uncertainty about the pathogen, its pathology in wild bats, a changing environment, and the abstraction of these into mathematical form, it is surprising that little effort has been made to construct and validate mechanistically realistic models of bat populations to act as the solid foundation for higher-level disease modelling. Here we aim to produce a generic tool to provide some evidence based predictions of bat disease epizootiology, founded on a coherent representation of bat ecology and behaviour deployed through an IBM (Individual Bat Model). Importantly, this is founded on an independently validated understanding of their ecology and population dynamics, both of which need to emerge as model behaviour before disease is added. We recognise at least two divergent life-history strategies and lifestyles; ‘slow’ bats, typified by cave hibernators, include a seasonal hierarchical spatial and population structure; ‘fast’ bats show larger but less structured communities. Both accommodate the emerging understanding of bats as social animals as well as assuming that spatial heterogeneity drives some form of meta-population process. Early work has illustrated the surprising variation/instability in demographic structure driven by environmental variation close to range edges (many British bats are at their cold edge in the UK), as well as highlighting basic gaps in knowledge which are pivotal in robust predictions of disease dynamics (males in summer – Where? When? And how much?).

2. **Comparative loss of function screens highlight common cellular pathways required by mumps virus for replication in bats and humans**
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Objectives: Bats have been implicated as an important source of new and emerging paramyxoviruses. The identification of bat-borne paramyxoviruses closely related to mammalian paramyxoviruses suggests a possible risk of zoonotic transmission of these paramyxoviruses. Mumps virus (MuV) a contagious virus of the genus *Rubulavirus*, was thought to be an exclusive human pathogen with no animal reservoir. Recently, the complete genomic sequence of a mumps-like rubulavirus was obtained from an African bat. In order to ascertain if bat and human cells are capable of supporting the replication of MuV, and to identify cellular proteins involved in the viral life cycle, we performed comparative genome scale siRNA screens using a human and novel bat siRNA library. **Methods**: Comparative genome scale siRNA screens with MuV were performed. The human MuV siRNA screen (Qiagen) was previously performed in our lab using A549 cells, a human lung adenocarcinoma cell line. A custom bat siRNA library was designed to target 18,328 genes of the *Pteropus alecto* genome. The bat siRNA screen was performed in PaKi cells, a *Pteropus alecto* kidney cell line. **Results**: The coatomer complex I, a known dependency factor was identified as required for MuV replication in both human and bat cells. Eukaryotic initiation factor 3 (eIF3) is a multiprotein complex that functions during the initiation phase of eukaryotic translation was also identified as a host factor. Interestingly, ABCE1, identified as a pan-paramyxovirus host factor, was not required for MuV replication in bat cells. **Conclusions**: This study is the first to utilize a bat genome scale siRNA screen and provides a novel overview of cellular proteins and pathways that impact this important pathogen.

3. **Implementation of a RT-PCR Assay to Detect Henipaviruses in Trinidad Bats**
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Objectives: Since the emergence of Hendra in Australia, and Nipah in Malaysia and Bangladesh, evidence of henipaviruses in bats has been reported in Thailand, Cambodia, India, Papau New Guinea, China, and Madagascar. Cedar virus, a novel henipavirus, has been isolated from bats in Australia. There has been evidence of seropositivity among humans and *Eidolon helvum* (Straw-coloured fruit bat) bats in Cameroon, as well the publishing of the genome sequence of a henipa-like virus from a bat sample in Ghana. More recently, sequences related to henipaviruses were identified in New World bats, and Brazilian bats were found to have antibodies against henipa-like viruses, though no viral isolate has yet been obtained. This suggests that henipaviruses are likely to exist in other regions, including the Western hemisphere, presenting a need to investigate host populations. The goal of this study is to design a PCR assay to screen bat samples from Trinidad to detect novel henipa or henipa-like viruses.
Methods: Using published primer sets from Tong, et al, and van Boheemen, et al, PCR assays were developed to screen various tissue samples collected from bats in Trinidad. Both primer sets will be evaluated for their ability to detect henipaviruses using viral RNA standards for Hendra, Nipah Bangladesh, and Nipah Malaysia. The 132 samples are from 30 bats, including the species *Saccopteryx bilineata* (greater sac-winged bat), *Carollia perspicillata* (Seba's short-tailed bat), and *Artibeus planirostris* (Flat-faced fruit-eating bat) (sensu Larsen, 2007). Tissues harvested include brain, kidney, liver, spleen, lung, and fetal tissue.
Results: The PCR assay is able to detect viral RNA standards of Hendra, Nipah Bangladesh, and Nipah Malaysia. The assay will be further optimized to screen tissue samples. Samples that screen positive by this assay will be sequencinged.
Conclusions: To our knowledge, no henipaviruses have yet been detected or isolated from New world bats, though studies suggest their presence. Thus, screening for novel henipaviruses in Trinidad bats will help elucidate the full geographic range of these viruses, allowing a better understanding of risks of emergence and outbreaks in humans.

4. **Genomic characterization and pathogenic potential of a novel evolutionarily-divergent alphacoronavirus isolated from *M. lucifigus* bats in Alaska.**
Jonathan C. Rupp[1], Maegan Lange[1], Megan Howard[2], Anitha Sundarajan[3], Jonny Sena[3], Faye D. Schilkey[3], Molly Murphy[4], Douglas Causey[1], Eric Bortz[1].

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4- Dept. of Veterinary Medicine, University of Alaska Fairbanks

Objectives: Coronaviruses (CoV) are zoonotic pathogens with the potential to cross species barriers from bats into other mammals, including marine mammals, swine and humans. Novel bat-origin coronaviruses have been responsible respiratory disease in humans, notably betacoronaviruses (OC43, HKU-1, SARS and MERS) and alphacoronaviruses (229E and NL63). Thus, it is important to identify the reservoirs of CoV in bats and their potential for transmission, and pathogenicity, in other mammalian species. We sought to analyze the virome of the most common bat species in Alaska, *Myotis lucifugus,* the little brown bat.

Methods: Swabs, tissue, and fecal samples were collected from habitats in close proximity to barns, farm buildings, and human habitations in southcentral Alaska. Total RNA extracts were screened by RT-PCR with coronavirus primers matching CoV ORF1a, and amplicon sequencing. Complete genomes of novel viruses were sequenced by next-generation sequencing (NGS) RNA-seq.

Results: Sanger sequencing of amplicons confirmed the presence of an alphacoronavirus phylogentically related to persistent alphacoronaviruses detected in bats in Colorado and the Rocky Mountains. Primary RNA samples were used in library preparation for short-read, paired-end next generation sequencing on an Illumina HiSeq platform. Aligning to a reference *M. lucifigus* virus from Colorado, bat alphacoronavirus CDPHE15/USA/2006, we assembled a full-length genome (28,515nt) identifying the novel alphacoronavirus/bat/Alaska/s7/2014. A high

degree of thermodynamically stable stem-loop RNA structures are predicted by Mfold within 700nt of 5' and 3' termini of genome**.** While nucleotide conservation to the Colorado virus was 96%, notable amino acid differences were identified in coronavirus proteins. The major CoV surface spike (S) protein exhibited 26 amino acid changes, including 14 in the globular head containing the putative receptor-binding domain, suggesting divergence based on immune evasion or receptor-specificity. Another 6 amino acids were altered in the fusion hinge. Protease cleavage sites were not conserved. Nucleoprotein (N) and ORF3 also exhibited amino acid differences.

Conclusions: Understanding the evolution and pathogenicity of this novel evolutionarily-divergent alphacoronavirus provides insight into the role of bats in virus transmission, and ecological assessment of bat-borne virus reservoirs in North American ecosystems.

5. Preliminary Evidence of Secondary Acquisition of Tymoviridae and Partitiviridae in Little Brown Bats (*Myotis lucifugus*) in Southcentral Alaska.

Douglas Causey[1] , Jonathan C. Rupp[1], Maegan Lange[1], Megan Howard[2], Anitha Sundarajan[3], Jonny Sena[3], Faye D. Schilkey[3], Molly Murphy[4], Eric Bortz[1]

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We sought to analyze the virome of the most common bat species in Alaska, *Myotis lucifugus,* the little brown bat. Swabs, tissue, and fecal samples were collected from habitats in close proximity to barns, farm buildings, and human habitations in southcentral Alaska. Total RNA extracts were screened by RT-PCR and CoV ORF1a, and primary RNA samples were used in library preparation for short-read, paired-end next generation sequencing on an Illumina HiSeq platform. Sanger sequencing of amplicons confirmed the presence of an alphacoronavirus phylogenetically related to persistent alphacoronaviruses detected in bats in Colorado and the Rocky Mountains. In two distinct bat samples, preliminary results indicate the likely presence of tymovirus (eg. Dulcama mottle virus) probably acquired through ingestion of insects feeding on infected plants. In addition, initial results indicate presence of β-partitivirus closely aligned to *Rosellina*-type associated with spruce/alder and other partitivirus-like sequences. Secondary acquisition of virus obtained by feeding or incidental infection by fungi (eg. γ-partitivirus associated with *P. destructans*) has been previously described for bats collected from similar ecological settings (eg. Thapa *et al.* 2016). We continue to further refine these initial for better resolution of the virome of Alaska bats.

6. Molecular Screening of Zika and Dengue Viruses in Bats (*Artibeus jamaicensis, Glossophaga longirostris* and *Molossus molossus*) from Grenada, West Indies.

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Background: In recent years Zika virus (ZikV) has changed from an uncommon and poorly documented infection to a global public health concern. Dengue virus (DenV) has long-standing human health concerns worldwide, including Grenada, and has been detected in bats from other tropical countries. **Objective**: To determine if Grenada bats are infected with ZikV and DenV and thus possible reservoir hosts for these viruses. **Methods**: Forty-nine bats from 3 different genera and feeding behaviours (frugivorous, nectivorous and insectivorous) were trapped and humanly euthanized. ZikV RT-PCR was performed on serum, testes, spleen and brain samples, and a DenV RT-PCR multiplex was performed on serum. Amplicons of the expected sizes were sequenced for confirmation. **Results**: Physical exams prior to euthanasia and sample collection indicated all bats were clinically healthy. All 3 bat species collected tested positive for both viruses. Sera from 27 bats out of 41 tested were positive for ZikV (65.9%) and sera from 12 bats out of 19 tested were positive for DenV (63.2%). All DenV positive bats were infected with serotype 2, with one of these bats testing positive for both DenV serotype 2 and 4. Brains from 22 bats out of 48 tested were positive for ZikV (45.9%). Testes from 2 bats out of 12 tested were ZikV positive (16.7%) and a spleen from one bat out of 22 tested was ZikV positive (4.5%). **Conclusions**: The results demonstrate that frugivorous, nectivorous and insectivorous bats in Grenada are infected with both ZikV and DenV. Of interest is that despite many bats testing positive for ZikV in the brain, all bats appeared clinically healthy with no signs of neurologic dysfunction. Histopathology and immunohistochemistry are pending to

determine if infection is associated with lesions. Virus quantification is currently underway to determine if the level of viremia for either ZikV or DenV is high enough to consider the different bat species as potential reservoir hosts.

7. Serologic evaluation of Alphavirus and Flavivirus exposure in bats in Grenada

Diana Stone[1], Christine Cornish[1], Amy C. Lyons[2], Yan-Jang S. Huang[2], Dana L. Vanlandingham[2], Stephen Higgs[2], Bradley Blitvich[3], Abiodun A. Adesiyun[4], Sharlene Santana[5], Leith Leiser-Miller[5], Sonia Cheetham[1].

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Objective: Determine exposure to Alphaviruses and Flaviviruses in bats in Grenada. **Methods:** Fifty bats were trapped in August, 2015 in Grenada. Sera from all bats were tested for antibodies to flaviviruses: West Nile virus, Japanese Encephalitis virus, St. Louis Encephalitis virus, Bussuquara virus and dengue virus serotypes 1-4 (DENV-1,2,3,4) using the plaque reduction neutralization test (PRNT). Forty three of the 50 samples were tested for antibody to alphaviruses: Western Equine Encephalitis virus, Venezuelan Equine Encephalitis virus and Eastern Equine Encephalitis virus using epitope-blocking ELISA and 42 samples were tested for antibody to the alphavirus Chikungunya (CHIKV) using PRNT. **Results and Conclusions:** Two species of fruit bats were sampled, *Artibeus jamaicensis*, (48), and *A. lituratus*, (2). Fifteen of the 42 tested positive for neutralizing antibodies to CHIKV at $PRNT_{50}$ with titers 1:10 to 1:640. All 43 bats tested negative for epitope blocking antibody to the other alphaviruses except one positive for Venezuelan Equine Encephalitis virus. All 50 bats tested negative for neutralizing antibody to flaviviruses except one which had a Bussuquara virus $PRNT_{80}$ titer of 20. **Discussion:** Historically, DENV has been endemic in Grenada. CHIKV was introduced to the island in 2014. Bats for this study were trapped a year after the peak human CHIKV epidemic. Of interest is that in a separate study molecular detection confirmed the presence of both DENV and CHIKV RNA in bats serologically tested in this study. Of the 15 CHIKV seropositive bats, one was positive for CHIKV RNA. Of the 50 DENV seronegative bats, 6 showed detection of flavivirus RNA with a band compatible with DEN3. Thus, the negative DENV serology is unanticipated, but may reflect lack of neutralizing antibody responses developed for DENV. Future studies will characterize the humoral immune response to DENV in naturally exposed Grenada bats and determine whether non-neutralizing antibody responses are present. The type of immune response to DENV in bats may promote persistent infection and high-titer viremia and thus contribute to viral maintenance. Our results and those of the molecular study confirm that Grenada fruit bats are exposed to CHIKV and DENV, but their role in the epidemiology of these viruses is currently unknown.

8. **Isolation and molecular characterization of Bukakata orbivirus, a novel virus from a Ugandan bat, and associated pathology in experimentally infected Jamaican fruit bats (*Artibeus jamaicensis*)**

Fagre AC, Kityo R, Lee J, Mossel E, Crabtree, M, Nalikka B, Nakayiki T, Kerbis J, Gilbert, A, Bergren, N, Nyakarahuka L, Lutwama J, Stenglein M, Byas A, Malmlov A, Bergren N, Rice L, Miller B, Schountz T & Kading, RC.

Objectives: In 2013, a novel orbivirus (*Reoviridae: Orbivirus*) was isolated from an Egyptian fruit bat (*Rousettus aegyptiacus*) in Uganda. Preliminarily named "Bukatata orbivirus" after the region where the infected bat was captured, this virus is the fourth identified orbivirus of bats. The genomes of all four bat orbiviruses (Bukakata, Ife, Fomede, and Japanaut viruses) were sequenced to assess their phylogenetic placement within the genus *Orbivirus*, and develop hypotheses regarding virus-vector associations. **Methods:** Whole genomes of all four viruses were sequenced using an Illumina platform and assembled *de novo*. To begin studying the effect of infection with Bukakata orbivirus on a bat host, three male Jamaican fruit bats (*Artibeus jamaicensis*) were inoculated intraperitoneally with 5.3 $\log_{10}$ pfu Bukakata orbivirus and monitored daily for signs of clinical disease. **Results:** Phylogenetic analysis placed Fomede and Bukakata orbiviruses in the tick-borne clade, and Japanaut and Ife in the mosquito/*Culicoides* clade. On day 12, all three bats were diffusely hyperemic and tachypneic and, thus, were humanely euthanized. Histopathologic lesions of perivascular inflammation, hemorrhage and edema were present in varying degree of severity in the liver, lung and kidney of all three bats. Additional lesions included meningeal hemorrhage in two of the bats and evidence suggestive of early hepatic vasculitis in the other. Eosinophilic and suppurative gastroenteritis affected all bats with one containing intraluminal bacilli, suggesting secondary bacterial infection. **Conclusions:** Immunohistochemistry and qPCR will be performed to assess

relative abundance of virus in various organ systems to optimize future analyses. Future experimental infections will be performed to monitor temperature, physiological and immune parameters, virus shedding and viremia throughout the course of infection. These preliminary data are critical in the assessment of the potential role of bats as reservoirs for arboviruses.

9. **Using GIS to Guide Ebola Virus Disease Ecology Field Investigations**

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Objectives: In the health field GIS is being used to track epidemics in real time and to create predictive models of outbreak potential. We have investigated the feasibility of using a maximum entropy model (Maxent) to assist in determining the target species and optimum locations and times to direct field sampling efforts. **Methods:** We developed an ecological niche model of Ebola virus (EBOV) using the location of Ebola virus disease (EVD) outbreak index cases as presence points we developed an ecological niche model to predict geographic locations that had environmental conditions similar to those of known outbreaks. To determine which environmental parameters were important in constructing the model, a correlation matrix was constructed using ArcGIS and highly correlative parameters were eliminated and the model reconstructed. Additionally, home ranges of African mammals were overlaid on a map and compared to the model to determine which species inhabit the geographical regions predicted to be suitable for a spillover event. **Results:** The model was used to highlight environmental factors common to the location of the EVD index cases from 19 environmental parameters and altitude that were used to construct the model. A list of 66 mammals including 26 bat species with home ranges that overlap the modeled range of EBOV was produced. **Conclusions:** While there is no conclusive evidence that bats serve as the reservoir for Ebola virus (EBOV) i.e. there is no wild EBOV bat isolate, there is evidence that they may play a role in maintaining the virus in nature. Combining what is known about the natural histories of bat species and animal species known to be susceptible to EVD such as great apes, duikers and forest hogs coupled with environmental factors predicted to be important, we can further prediction when and where spillover events may occur and tailor our sampling efforts to target these conditions. Additionally, as there is a dearth of knowledge on the natural history of deep forest fruit bats we are planning to monitor the short term daily movements of *Hypsignathus monstrosus* with the aim of being able to predict where the movements of the bats and susceptible species may commonly intersect.

10. **Bat - infection interactions: Signals of evolution, ecology, immunity and deforestation**

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Objectives: Bats are ecologically diverse and these ecological differences may lead to differences in infection prevalence and identity. We sought to discover the evolutionary and ecological signatures of differences in bat behavior and environment on bat-infection patterns, as well as to understand how these patterns are impacted by human activity. Regions where a high diversity of hosts occur with prevalent deforestation, human habitation and livestock rearing are of great concern for potential spillover. Accordingly, we aimed to characterize infections of potential spillover importance in an altered landscape. **Methods**: Using a combination of genomics, targeted sequence capture and tests of positive selection, we screened 60 species of bats distributed globally for evidence of selection in response to viruses. Additionally, we screened the speciose and ecologically diverse bat fauna of an agricultural landscape in Costa Rica for eight viral groups (Herpesviridae, Astroviridae, Adenoviridae, Paramyxoviridae, Coronaviridae, *Lyssavirus*, Filoviridae, Influenza A), *Bartonella* bacteria and ectoparasites to detect pathogen sharing, immunological and behavioral patterns of infection and the impact of humans on these relationships. **Results**: Evolutionarily, viral sharing has been important for shaping bat immune evolution. However, ecologically most infections are host specific and regulated by host immunity with species that are more frequently exposed less likely to yield detectable pathogen nucleic acids. In deforested areas, these patterns shift in a sex-specific manner, disproportionately impacting females with potential for population stability. **Conclusions**: This study yields evolutionary insights into the unique relationship between bats and viruses, identifying the environmental factors that are driving adaptation. Additionally, it represents one of the broadest infection screening studies in the Neotropics, which has the highest density of bat diversity but is less frequently screened than the Old World. Our data suggest that there are few pathogens of spillover concern circulating in this landscape, but that humans may be having a detrimental impact on bat health.

Daytime behavior of *Pteropus vampyrus* and *Acerodon jubatus* in the natural habitats: a cue of viral transmission

11. Yupadee Hengjan[1], Didik Pramono[2], Hitoshi Takemae[1], Ryosuke Kobayashi[1], Karla Cristine Doysabas[1], Keisuke Iida[1], Takeshi Ando[5], Supratikno[2], Chaerul Basri[2], Yuli Sulistya Fitriana[4], Eko M.Z. Arifin[6], Yasushige Ohmori[1], Ken Maeda[3], Srihadi Agungpriyono[2] and Eiichi Hondo[1]

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Objectives: The large flying fox (*Pteropus vampyrus*) are well-recognized host of Nipah virus. Base on serologic studies, the golden-crowned flying fox (*Acerodon jubatus*) are infected with Ebola Reston virus. To estimate the risk of disease emergence, it is important to understand the behavior of flying foxes. This study aimed to clarify diurnal behavior of *P. vampyrus* in Leuweung Sancang conservation area, Indonesia (7º 43′ 45.12″ S, 107º 54′ 10.08″ E), and *A. jubatus* in the Subic Bay Freeport, the Philippines (14º 46′ 31.54″ N, 120º 19′ 14.90″ E). **Methods:** Quantitative behavioral data were collected using instantaneous scan sampling and all occurrence focal sampling methods. **Results:** Unexpectedly, many flying foxes were awake during daytime (*P. vampyrus*: 46.9 ± 10.6%, *A. jubatus*: 23.7 ± 3.1% of scanned bats), and showed various activities. The commonly observed behavior were wing flapping and self-grooming behaviors. Males engaged in sexual activity more than females (*P. vampyrus*: 6.5 ± 1.6 % in males and 0.2 ± 0.1 in females, *A. jubatus*: 1.6 ± 0.5 % in males, 0% in females), sometimes accompanying with aggression behaviors between males and females. There was no significant difference in negative social behaviors (fighting and wing spreading) between males and females of *P. vampyrus*, whereas, the difference was found in *A. jubatus* (2.6 ± 0.7 % in males, 0.1 ± 0.04 % in females). The positive social behaviors (maternal care, mutual grooming and playing) were rarely found in *P. vampyrus*, but never in *A. jubatus*. Physical communications, not only among flying foxes, but also direct and/or indirect contacts between *P. vampyrus* and non-human primate (*Trachypithecus auratus*) were observed (3.3 ± 0.5 times per day). Specifically, periodic disturbance by tourists and unidentified aerial predators like raptors was observed at the roosting site of *A. jubatus*. *A. jubatus* shared the same roosting site with *P. vampyrus*, this enables the contacts between the two species of flying foxes, an average 25.4 ± 6.3 times per day. **Conclusions:** These observations would provide a cue to know how viral transmissions among flying foxes, other wildlife and humans in South-East Asia.

12. The study of whole spike gene of bat coronavirus from Thailand using Next Generation Sequencing

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Objectives Bats have been recognized as the natural reservoirs of a vast variety of viruses, including as host to Coronaviruses – a viral family of public health importance. Bat coronaviruses have been intensively studied since the discovery of Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) and have expanded even more after the emergence of Middle East Respiratory Syndrome Coronavirus (MERS-CoV), both of which are purposed to have originated from bats. Since spike protein is correlated with host cell receptor binding and membrane fusion, a better understanding of sequence diversity for this gene will help determine the potential for host-switching and zoonotic potential of CoVs. The aim of our study was to characterize the spike gene of bat coronaviruses from Thailand. **Methods** we PCR amplify about 4 kb of whole spike gene from seven PCR positive coronavirus of *M. magneter* and *R. shameli* bats from northern part of Thailand and sequencing using Next Generation Sequencing (NGS). Phylogenetic tree of the full alignment of whole spike gene sequences was estimated by maximum likelihood method. **Results** The average of 1,306,845 sequences of spike gene per sample was obtained from NGS. Phylogenetic tree of all seven spike sequences are grouped into the same clade in the alpha Coronavirus (α CoV) and mostly related to the Bat Coronavirus-1A (BatCoV-1A). **Conclusions** Even though seven spike genes of coronaviruses in this study showed sequence different from emerging disease beta coronavirus group B and C (β CoV B and β CoV C); nevertheless, more positive bat coronaviruses should be investigated including whole genome sequencing of bat coronaviruses that may useful for more understanding host-viral evolution and potential for host switching or spillover.

13. **Assessment of the cross-species potential of two emerging coronaviruses, SARS-CoV and MERS-CoV, by Protein-Protein Molecular Docking analyses**
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Objectives: Coronaviruses are a virus family with broad host range, and have spilled over from their natural reservoirs into various mammalian species, including humans. For humans, four of them cause common cold and circulate exclusively in the human population. In addition, SARS-CoV and MERS-CoV, recently emerged in the human population and are associated with severe respiratory illness. Where do these zoonotic viruses come from, and how did they cross the species barrier? These questions are generally difficult to address. The critical residues at interaction interface of host receptors (DPP4 for MERS-CoV and ACE2 for SARS-CoV) are believed to impact the binding ability of the receptors with viruses' surface-located spike. The diversity of available protein sequences limits our understanding of the receptor-mediated pathogen-host interactions for bat coronaviruses. Computational molecular docking is a bioinformatics tool, which allows us to explore the potential receptor-spike interactions in silico. The aim of this study is to analyze the diversity of SARS-CoV and MERS-CoV receptors from different mammalian hosts, to predict the host range using modeling and molecular docking. **Methods:** Up to 109 DPP4 and 94 ACE2 sequences from mammalian hosts were downloaded from genbank or acquired by sequencing, covering 60 and 51 different families respectively. The putative crystal structures were homologically modeled, and protein-protein docking was performed using Autodock Vina on NIH HPC Biowulf cluster. **Results:** Both of DPP4 and ACE2 receptors sequences from the hosts have relative high diversity. The docking results point out wide but family specific of host range of MERS-CoV and SARS-CoV. Virtual mutagenesis studies explored the impact of each critical residue of DPP4 on binding interaction for *Homo sapiens*, *Mesocricetus auratus*, *Desmodus rotundus*, *Canis lupus familiaris* and *Felis catus*. **Conclusions:** Although currently in silico analysis of spike-receptor interactions utilizing molecular docking methods still are in its early stages of development, the generated results could be utilized to perform large screens of potential virus reservoir, and intermediate hosts associated with emerging coronaviruses, and could potentially be utilized to estimate the distribution of MERS-CoV and SARS-CoV in ecosystems.

14. **Hendra virus phylogeography in eastern Australia**
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Objectives: Hendra virus (HeV) is an emerging zoonotic paramyxovirus that causes sporadic fatal disease in horses and humans in mainland Australia. Australian flying foxes (*Pteropus* spp. fruit bats), the endemic host, are gregarious, semi-migratory species that occupy the tropical and subtropical forests of coastal Australia. Despite the vast range of flying foxes, current outbreaks of Hendra virus have been restricted to a narrow band in southeast Queensland and northern New South Wales. Transmission dynamics of HeV between flying foxes is poorly understood, which limits our ability to identify potential points for management and spillover prevention. We used a phylogeographic framework to explore the spatial structure of HeV over eastern Australia, and to investigate factors that contribute to maintenance and spread of HeV in flying foxes. **Methods:** A three-year surveillance field study was initiated to improve understanding of Hendra virus diversity and disease dynamics in wild flying foxes, generating partial sequences from 26 colonies across eastern Australia. We incorporated sequenced isolates from spillover events in horses, and applied discrete and continuous Bayesian phylogenetic approaches to explore patterns in the dynamics and spatial spread of Hendra virus. Analysis was performed on a 2015 bp intergenic region between the nucleoprotein and phosphoprotein genes. **Results**: Preliminary analysis indicates a broad spatial structure, with lineages clustering loosely in space and time. However, we also find that multiple variants co-circulate in one colony at any given time, and that identical variants may co-circulate in geographically disparate colonies. Our ongoing approach is to identify drivers in the spatial spread and diversity of Hendra virus by examining the role species composition, roost structure, and migratory behavior play in shaping the geneology of Hendra virus. **Conclusions**: These data suggest that host factors (e.g., species composition within roosts) and/or environmental factors may play a role in HeV circulation within and between bat colonies. This work represents a novel approach to understanding the transmission dynamics and evolution of Hendra virus, as well as the functional connectivity of flying fox populations in eastern Australia.

15. **Viral Zoonosis in Georgian Bats**

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Objectives: Bats are reservoir-hosts of viral agents (lyssaviruses, paramyxoviruses, coronaviruses, and filoviruses), which are transmittable to humans and other animals. There are few bat virus detection studies linked to the Caucasus region. In Georgia, bat *Lyssavirus* (Rabies virus) is listed as a priority pathogen, and West Caucasian Bat Virus (WCBV) is the most genetically different member of the *Lyssavirus* genus. The goal of our study was to find WCBV and the newly discovered bat Coronavirus (bat-CoV) in Georgian bats. **Methods:** Bats that were used for sampling were collected in 2012 from four different regions in Georgia. Bat brains (n=236) were sampled and tested for the presence of lyssavirus antigen by the direct fluorescent antibody (DFA) test. A total of 186 bats of 11 different species were sampled for CoV confirmation. RT-PCR amplification assay targeting the 180 bp fragment within the RNA-dependent RNA polymerase RdRp gene and sequencing of the amplified product was used to confirm the presence of coronaviruses in bat specimens. The PCR product was sequenced on an ABI 3130 Automatic Sequencer. **Results:** None of the bats had detectable antigen consistent with an active infection of related *Lyssavirus* or WCBV. We found an outstanding diversity of CoV strains in Georgia; 54 bats tested positive for CoV. Sequence analysis demonstrated 97- 99% identity to five different types of CoV available at NCBI database. Most CoV positive bats were collected from Imereti, which is located in western Georgia. Bats with a higher prevalence of CoV were *Myotis blhytii* and *Rhinolophus ferrumequinum.* **Conclusions:** Our study revealed that we need additional research for excluding the existence of WCBV in Georgian bats. Future work will include determining the prevalence of rabies virus in these bat samples. To do this, we will perform rabies virus neutralization “Rabies Vaccine Response End-Point Titer (RFFIT)” assays. This was the first study addressing the genetic diversity of bat-CoV in this region. Further analyses and interpretation of the phylogenetic results for CoV will be a benefit for surveillance, system control, and response measures of emerging pathogens in Georgia.

16. Forestalling Future Outbreaks: Enhancing Capacity for Surveillance of Viral Hemorrhagic Fever Viruses in Sierra Leone

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Objectives: The first outbreak of Ebola virus disease in Sierra Leone exposed the limited in-country capacity for effective disease surveillance. Heavy reliance was placed on international support for human, technical and material resources. While the source of the outbreak has not been confirmed, human interactions with wildlife and their habitats continue unabated, raising fears of future outbreaks of zoonotic diseases. Building national level capacity, especially in research universities, would enhance Sierra Leone’s capability to forestall future outbreaks involving viral pathogens of public health concern. **Methods:** Through a collaborative agreement with the Viral Special Pathogens Branch at the Centers for Disease Control & Prevention, staff and students at Njala University have received field and laboratory training in ecological surveillance and molecular diagnosis of hemorrhagic fever viruses in bat populations. **Results:** Training in safe capture techniques, collection of blood/serum samples, necropsy techniques and the safe processing and storage of tissues specimens have been achieved over a period of 18 months for 12 Njala University staff and students. Further, three additional staff and students have been trained in molecular diagnostics using robotic nucleic acid extraction and qRT-PCR methods. These trainings, coupled with the acquisition of laboratory and field equipment and renovations of laboratory space on the Njala University campus and its field research station, are resulting in the inclusion of ecological surveillance and molecular diagnostics of viral pathogens in wildlife populations in the curriculum of Njala University in Sierra Leone. **Conclusions:** Strengthening technical and human capacity for disease surveillance in bats through long-term partnerships with research institutions could lay the foundation for preventing future outbreaks of global concerns.

17. Ecological aspects of bats in a cave frequented by members of the local community in Kaptum Cave in eastern Uganda.

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Few studies have addressed the ecology of cave bats in Uganda. This study assessed the diversity, roosting and feeding ecology, of micro bats (order *chiroptera*) as well as influence and frequency of human disturbance, in Kaptum cave of Eastern Uganda. Field observations were conducted between July/Augst 2016 and October/ November 2016 to document aspects of roost utilisation by the bats, their feeding choices and human influences on the cave in which 6 species of microchiropteran bats roosted. We used Mist nets and a Harp trap to capture individuals for examination and identification of species present. Infrared Trail trap Cameras were used to monitor roosting habits and activity patterns of the bats in the cave. A portable whether station was used to record the microclimatic conditions in the different sections of the cave in which the bats roosted to evaluate if there was any influence on choice roost. Kaptum cave has 6 species of insectivorous bats which seemed to prefer different sections of the cave. From evidence of insect remains in the roost, the diet of the bats in Kaptum cave consisted of eight insect orders (*Lepidoptera, Coleoptera, Orthoptera, Dictyoptera, Heymenoptera, Isopteran, Hemiptera, and Odonata*) with the order *Lepidoptera* constituting the bulk of insects preyed upon. At the moment we cannot separate the diet of the different species, since most insect remains were recovered in a section the cave we refer to as the Nycteris corner, because it was most used by these bats, but other species of Rhinolophids and Hipposiderids also frequented this corner in any 24hr period. We believe that the continued human presence in the cave could have implications for roost stability, but also could predispose the humans to potentially harmful aerosols associated with bats and bat guano.

18. **Middle East respiratory syndrome coronavirus spike plasticity in the context of the common vampire bat (*Desmodus rotundus*) DPP4 receptor.**

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Objectives: In 2012, a novel coronavirus, Middle East respiratory syndrome coronavirus (MERS-CoV), was discovered in humans and dromedary camels, although genetic evidence supports a bat ancestor. This range of animal hosts lead us to hypothesize that MERS-CoV can readily adapt to new hosts. The receptor for MERS-CoV, dipeptidyl peptidase 4 (DPP4) has previously been shown to act as a species barrier. By passing the virus over time on cells stably expressing the common vampire bat (*Desmodus rotundus*) DPP4 receptor, which MERS-CoV binds inefficiently, we will determine how potential adaptation in the spike glycoprotein may influence species tropism. **Methods:** We have compared the growth kinetics of MERS-CoV over 72hrs between different bat DPP4 receptors transfected on baby hamster kidney (BHK) cells, which are naturally unsusceptible to MERS-CoV. We then generated BHK cell lines stably expressing the *D. rotundus* DPP4 receptor. By passing MERS-CoV on these cells over time, we hope to observe adaptations in the viral spike protein that allow more efficient viral growth kinetics. Viral genomes containing the relevant mutations can be created through a reverse genetics system and tested for binding affinity and growth potential. **Results:** We show here that MERS-CoV can use DPP4 from different animal hosts, including a variety of bat species. Notably, MERS-CoV can bind and replicate using the *D. rotundus* DPP4 but very inefficiently compared to human DPP4, leading to delayed growth. We observed that MERS-CoV growth on cells stably expressing D. rotundus DPP4 displays a similar inefficient growth pattern as seen previously using a transfection method. **Conclusions:** Our data demonstrates that MERS-CoV can use a diverse set of host species receptors. Although we have successfully generated BHK cells stably expressing *D. rotundus* DPP4, sequencing of the MERS-CoV spike over many passages is needed to identify relevant mutations. The ability of the MERS-CoV spike to adapt to diverse host species receptors may play a significant role in cross-species transmission.

19. **Viral community dynamics of Australian Flying foxes**

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Objectives: Bats are reservoirs for a disproportionate number of zoonotic viruses, with spillover to people and domestic animals resulting in significant public health implications globally. In Australia, bat viral research has largely focused on Hendra virus, yet a diverse viral community has been detected in Australian Pteropid fruit bats (flying-foxes)[1,2]. Additionally, while the four Australian flying fox are capable of being infected with Hendra virus, not all species appear to be equally competent hosts[3,4]. In this context, interactions among co-infecting viruses and the dynamical consequences of these interactions are under- studied. We aimed to gain further insight into bat viral transmission dynamics by exploring dynamics within a multi-host-multi-pathogen framework. **Methods:** To characterise existing knowledge of the bat viral-host community in Australian flying foxes, a systematic literature review of published studies was undertaken and then complimented with additional unpublished data. Using urine samples collected from three of the four Australian flying-fox species in a related field study[6], we utilised a novel high-throughput multiplex PCR[5] to simultaneously detect up to 11 known bat paramyxoviruses. Within a Bayesian framework, we then modelled the monthly presence of different virus species at the roost level in relation to environmental drivers and the co-occurrence of other virus species. **Results:** Results support synchronous shedding pulses of multiple viruses, with significant co-circulation associations between certain virus species. **Conclusions:** Natural host-virus systems comprise complex communities, and our study explores how moving beyond single-pathogen-single host studies of bat pathogen dynamics towards broader consideration of the biotic interactions within viral and reservoir communities could progress our understanding of transmission and spillover of bat pathogens.

20. **The glycoprotein of Nipah virus in Thai bats associated with Nipah virus in Bangladesh**

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Objectives Bats have been recognised as a natural reservoirs of a large number of viruses including Nipah virus (NiV) and are associated with human activities which plays important role in the transmission of pathogens from bats to human. Study the glycoprotein NiV protein which plays important role in virus entry into host cells is a crucial in order to know the virus transmission. **Methods** Bat urine were collected from Luang Phrommawat temple, Chonburi province and screened for NiV nucleocapsid by using hemi-nested RT-PCR. The NiV positive urine samples were amplified the whole glycoprotein gene (1.8 kb). The whole sequences of nucleotide and amino acid of NiV glycoprotein were compared with sequences from both Malaysian and Bangladeshi strains from bats and humans. The phylogenetic tree was constructed by comparing amino acid sequence between NiV from Thai bat and NiV Bangladeshi patient. **Results** NiV glycoprotein sequence from Thai bats were homologous with Bangladeshi strain compared to the Malaysian strain. Furthermore, it shared 99.2-100% and 99.2-99.5% identity with nucleotide sequence of NiV glycoprotein from Bangladeshi bats and Bangladeshi patients, respectively. Amino acid sequence of NiV glycoprotein from Thai bats shared 99.8-100% and 99.5-99.7% identity with Bangladeshi bats and Bangladeshi patients, respectively. While, nucleotide sequence of NiV glycoprotein in Thai bats shared only 93.0-93.3% and 93.2% identity with Malaysian bats and Malaysian patients, respectively. Like nucleotide sequence, the amino acid sequence of NiV Thai bats shared only 95.7-96.0% and 95.7% identity with Malaysian bats and Malaysian patients. Phylogenetic analysis of NiV glycoprotein amino acid revealed that the NiV glycoprotein in Thai bats belonged to Bangladeshi patients. **Conclusions** This is the first step to understand the mechanism of NiV entry to the host. The results may indicates that NiV Thai bat strain has the potential to cause infection in humans. NiV glycoprotein and host receptors should be further investigated in order to understand the viral entry mechanism, host range, including intra- and cross-species transmission. Understanding the transmission of NiV from bats to humans is crucial in order to predict and prevent NiV outbreaks.

21. **Genomic characterization and pathogenic potential of a novel evolutionarily-divergent alphacoronavirus isolated from *M. lucifigus* bats in Alaska.**

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Coronaviruses (CoV) are zoonotic pathogens with the potential to cross species barriers from bats into other mammals, including marine mammals, swine and humans. Novel bat-origin coronaviruses have been responsible respiratory disease in humans, notably betacoronaviruses (OC43, HKU-1, SARS and MERS) and alphacoronaviruses (229E and NL63). Thus, it is important to identify the reservoirs of CoV in bats and their potential for transmission, and pathogenicity, in other mammalian species. We sought to analyze the virome of the most common bat species in Alaska, *Myotis lucifugus,* the little brown bat. Swabs, tissue, and fecal samples were collected from habitats in close proximity to barns, farm buildings, and human habitations in southcentral Alaska. Total RNA extracts were screened by RT-PCR with coronavirus primers matching CoV ORF1a, and Sanger sequencing of amplicons confirmed the presence of an alphacoronavirus phylogentically related to persistent alphacoronaviruses detected in bats in Colorado and the Rocky Mountains. Primary RNA samples were used in library preparation for short-read, paired-end next generation sequencing on an Illumina HiSeq platform. Aligning to a reference *M. lucifigus* virus from Colorado, bat alphacoronavirus CDPHE15/USA/2006, we assembled a full-length genome (28,515nt) identifying the novel alphacoronavirus/bat/Alaska/s7/2014. A high degree of thermodynamically stable stem-loop RNA structures are predicted by Mfold within 700nt of 5' and 3' termini of genome**.** While nucleotide conservation to the Colorado virus was 96%, notable amino acid differences were identified in coronavirus proteins. The major CoV surface spike (S) protein exhibited 26 amino acid changes, including 14 in the globular head containing the putative receptor-binding domain, suggesting divergence based on immune evasion or receptor-specificity. Another 6 amino acids were altered in the fusion hinge. Protease cleavage sites were not conserved. Nucleoprotein (N) and ORF3 also exhibited amino acid differences. Understanding the evolution and pathogenicity of this novel alphacoronavirus provides insight into the role of bats in virus transmission, and ecological assessment of bat-borne virus reservoirs in North American ecosystems.

22. **Spatial pattern of genetic diversity and selection in the MHC class II DRB of three Neotropical bat species**

Salmier A., de Thoisy B., Crouau-Roy B., Lacoste V. and Lavergne A.

Host–pathogen interactions—greatly influenced by environmental characteristics—are a major determinant of the extensive polymorphism of the Major histocompatibility complex (MHC) genes that play an important role in both resistance and susceptibility to diseases. Amazonia encompasses the greatest bat richness, as well as great landscape diversity. However, there are few studies regarding adaptation to infectious diseases of bats and even less in contrasting environmental conditions. We analyzed the genetic variability and positive selection signatures of the expressed MHC class II *DRB* exon 2 in three sympatric Amazonian bat species, *Carollia perspicillata*, *Desmodus rotundus*, and *Molossus molossus* inhabiting different environments (*e.g.*, forests, edge habitats, and urban areas). The role of the environment on the allelic composition and distribution of the *DRB* gene, as well as the effects of pathogen-mediated selection, recombination, gene conversion, demographic history and population structure on the MHC diversity were investigated. Overall, we identified 23 *DRB* alleles in 19 *C. perspicillata*, 30 *DRB* alleles in 35 *D. rotundus* and 20 *DRB* alleles in 28 *M. molossus*. We found clear evidence of at least two functional *DRB* loci as well as a trans-species mode of evolution within the Phyllostomidae family. Bats inhabiting forest environments presented higher number of alleles, revealing a heterozygote advantage likely associated with higher diversity of microorganisms in forest environments due to greater host species richness and better transmission-promoting parameters compared to disturbed environments. The *DRB* polymorphism was high in all sampling sites and for all species but different signatures of positive selection were detected depending on the environment, suggesting a local adaptation characteristic driven by an area-limited pathogen-mediated selection. The patterns of *DRB* diversity were similar to those of neutral markers for *C. perspicillata* and *M. molossus* while these patterns were different for *D. rotundus* for which a geographical structure was highlighted. These results supported that demographic process acts as an additional force in shaping *DRB* diversity. However, in structured populations, environmental constraints associated with characteristic pathogen pressures are the main drivers of MHC diversity.

23. Establishing a field collection scheme to investigate the role of African fruit bats as the natural reservoir of ebolaviruses

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Objectives: Filoviruses are among the most well-known and well-studied zoonotic pathogens, yet we know little about filovirus populations in their natural reservoirs. Phylogeographic and population genetic studies of filoviruses isolated from their natural reservoirs would shed light on the population structure and evolutionary history of these important zoonotic pathogens. African fruit bats including *Hypsignathus monstrosus* and *Epomops franqueti*, are the candidate natural reservoirs for filoviruses in the *Ebolavirus* genus; however, there have been no successful attempts to sequence or isolate *Ebolavirus sp.* from PCR-positive bats due to low viral copy numbers in the bats and difficulty associated with sampling from wild bat populations. We sought to increase the likelihood of acquiring live virus and viral whole genome sequences through extensive sampling from wild bat species in the Odzala-Kokoua National Park, Republic of Congo, within the geographical area of previous Zaire ebolavirus outbreaks. **Methods:** Multiple capture-release studies were performed to sample fruit bats over a period of four years. Bats were captured by mist netting near an *H. monstrosus* lekking tree and sampled for whole blood in addition to collecting nasal, urogenital, and rectal swabs. **Results:** In total, samples were taken from 456 *H. monstrosus* bats and 43 *E. franqueti* bats across four years of sampling. An additional 57 samples were taken from other bat species. Preliminary serological work shows 4.9% seroprevalence against Zaire ebolavirus in a subset of the *H. monstrosus* bats. **Conclusions:** The field collection efforts have yielded a large number of bats sampled which show a history of Zaire ebolavirus exposure. Future work will focus on detecting active infection with ebolavirus and isolation of live ebolavirus for whole genome sequencing.

24. **Co-infection in Georgian Bats**

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Objectives: Bats have been recognized as natural reservoirs for a variety of zoonotic pathogens. The prevalence of different pathogens in bats could be associated with colony size and migration patterns. In this study, bats were collected from four different Georgian regions (Kakheti, Imereti-Tskhaltubo, Samegrelo, Kvemo Kartli) and were tested for different pathogens that are endemic to Georgia. **Methods**: In total, 218 bats (*Eptesicus serotinus*-20, *Miniopterus shrebersii*-27, *Myotis blythii*-67, *Myotis emarginatus*-38, *Pipistrellus pygmaeus*-12, *Rhinolopus Euriale*-26, and *Rhinolopus ferrumequinum*-22) were tested for four bacterial agents (*Bartonella, Brucella, Leptospira,* and *Yersinia*). Bat kidneys were dissected, and their DNA was tested for *Bartonella*, and *Leptospira*. Spleen DNA was tested for *Brucella* and *Yersinia*, and the intestine DNA was tested for *Yersinia*. Triplex Real-Time PCR (rtPCR) Assay was performed to detect *Brucella* (IS711), *Bartonella* (tmRNA), and *Yersinia* (pal). Singleplex rtPCR was used to identify *Leptospira* (LipL32). Targeting the 16S rRNA gene, conventional PCR was performed to detect multiple bacterial strains. Cultured *Bartonella* isolates of the *gltA* gene were sequenced. **Results:** A total of 113 (51%) were positive for at least one of the four pathogens. Co-infection was detected in different bat species from Tskhaltubo and Kakheti. One Tskhaltubo bat was positive for *Bartonella*, *Brucella*, and *Leptospira*. Two bats from Kakheti were co-infected with *Bartonella* and *Brucella*: (*Myotisblythii* (n=1), and *Miniopterusschreibersii* (n=1). Eighteen bats were co-infected with *Bartonella* and *Leptospira*: *Myotisblythii* (n=15), and *Miniopterusschreibersii* (n=3). Sequencing analysis confirmed a co-infection with two different *Bartonella* sequences from 16 different bats: *Myotisblythii blythii* (n=3), *Miniopterusschreibersii schreibersii* (n=7), *Myotisblythii emarginatus* (n=1), *Rhinolophus euryale* (n=2), and *Rhinolophus ferrumequinum* (n=3). All bats were negative for *Yersinia*. **Conclusions:** Our results indicate that bat colonies in Tskhaltubo have the highest prevalence of infection and co-infection; since these bats are in enclosed, small spaces such as caves, this may be a reason we see a mixture of pathogens and mutation. In the past couple of years', Georgian caves have become a popular tourist attraction; from a public health standpoint, it is important to know what types of pathogens exists in these local bats.

25. Caves of Myanmar: a high-risk human-wildlife interface for zoonotic disease
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The Southeast Asian country of Myanmar has been deemed a “hotspot,” both in terms of its biodiversity and disease emergence potential. Despite this recognition, there is a paucity of data and limited surveillance on emerging infectious diseases in Myanmar, due in part to almost five decades of political isolation. Recent changes in the government have expanded economic development, strengthening trade with neighboring countries and opening border access to tourists and investors, further contributing to potential underlying drivers of disease emergence. Of particular import and concern are zoonotic diseases arising from human-animal contact. The vast cave and karst system of Myanmar presents an understudied interface between humans and wildlife, such as bats, rodents, and non-human primates. Caves, particularly where intricate Buddhist shrines have been installed, are popular destinations for local, national, and international visitors despite high-contact potential with animals and their excrement. This poster underscores the growing risk of bat-borne pathogen exposure in relation to cave utilization in Myanmar, exemplified by the popular tourist destination town, Hpa-An.

26. **Prevalence Patterns of Coronaviruses in Lyle's flying fox (*Pteropus lylei*) in Thailand**
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Objectives Coronavirus (CoV) surveillance in Lyle’s flying fox (*Pteropus lylei*); a medium-sized flying fox which forms large colonies high up in trees in areas close to humans and other animals, was conducted to characterize strain of CoV and determine prevalence patterns in Chonburi province, Thailand. **Methods** *P. lylei* bats were captured monthly during January - December 2012 for detection of CoV at three closed areas in Chonburi province, two human dwellings which were 0.6 (S1) and 5.5 km (S2) away from the bat roost, and a bat roosting site (S3). Two nested RT-PCR of RNA-dependent RNA polymerase (RdRp) from rectal swabs were used for CoV detection. The strain of CoV was confirmed by sequencing and phylogenetic analysis. **Results** From 390 *P. lylei* bats, 239 were male and 151 were female, while 101 were juvenile (forearm length ≤136 mm) and 289 were adult. CoVs were detected in 68 bats, 17.4% using family-wide CoV PCR but not by group C betacoronavirus assay. The positive samples were found in eight months in the year that the study was conducted, the highest in June 2012. Ten mother–pup pairs were captured. Samples from 10 mothers were negative. Rectal swabs from 9 unweaned pups were available for CoV PCR assays and three of them were positive. PCR positive pup was identified with a PCR negative mother. Phylogenetic analysis of conserved RdRp gene revealed that the detected CoVs belonged to group D betacoronavirus (n=64) and alphacoronavirus (n=4). **Conclusions** Younger bats appeared to play a more significant epidemiological role in harbouring CoV. Young age but not sex or gravidity, correlated significantly with CoV detection. CoV was found in unweaned pups whose mothers tested negative for CoV. One possible conclusion is transient shedding from mother during peri-partum to the young, may maintain the virus transmission within the population. The immune status of young and adult bats against CoV, in terms of susceptibility to infection, needs to be studied to explore this. Further study into the association of CoVs with natural hosts is necessary to understand their prevalence and maintenance patterns, to evaluate its zoonotic potential.

27. Genetically Diverse Filoviruses in *Rousettus* and *Eonycteris* spp. Bats, China, 2009 and 2015
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Bats have been implicated as natural reservoirs for filoviruses based on serological or nucleotide evidence from 19 bat species in 8 countries across Asia, Africa, and Europe. Previously, we discovered filovirus antibodies in several bat species in China. Here we report genetically divergent novel filoviruses are circulating in the *Rousettus* and *Eonycteris* bats from China. The 310-bp L-gene sequences exhibited 65–99% nucleotide (nt) identity among themselves and 61–78% nt identity with known filoviruses. Phylogenetic analysis of these sequences suggests that at least 3 distinct groups of filovirus are circulating in these bats. Q-PCR results showed these filoviruses were mainly located in the lung, with genome copy number varying from 29 to 523,582/mg of tissue. Thus, these filoviruses may have the potential to be transmitted through the respiratory tract. Co-infection with four different filoviruses was found in a single bat. ELISA and Western Blot showed the antibodies reacting more strongly to EBOV NP than RESTV NP in some filovirus RNA negative bats. One of the viruses named BtFilo9447 were tried to amplify the whole genome. The GP gene of BtFilo9447 shared 34-39% similarity on aa level and 35-53% similarity on nt level with known filoviruses. Our results demonstrate that fruit bats may are important reservoirs of filoviruses. Considering their feeding habitats, fruit bats are often in close contact with domestic animals and human populations. It is therefore necessary to establish long-term and proactive surveillance of these viruses and related diseases.

28. **Development of a monoclonal antibody to Jamaican fruit bat CD3γ**
Miles Eckley, Ann Hawkinson, Tyler Sherman, Tony Schountz, Corey L Campbell

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Objective: T cells have critical immunomodulatory roles in the innate immune response to infection. The CD3 cell-surface protein complex is required for T cell activation, and thus treating bats with therapeutic Aj-anti-CD3 IgG antibodies may have immunosuppressive effects. Monoclonal antibodies are of particular interest for this application because of their ability to bind to the Fc receptor of phagocytic and cytotoxic cells and label a pathogen for destruction. Our goal is to investigate the biological mechanisms by which T cells may induce immunopathology in response to viral infection. **Methods**: BALB/c mice were immunized and boosted with a KLH-conjugated 30mer peptide from Jamaican fruit bat CD3γ. Hybridoma cells were produced from the fusion of splenocytes with Sp2/0-Ag14 myeloma cells. Hybridoma cells were selected and cloned on methylcellulose plates, transferred to 24 well plates and supernatants screened. Candidates were identified by ELISA to 30mer peptide conjugated to BSA first, followed by flow cytometry of bat splenocytes. Antibodies were purified from supernatants by affinity chromatography using a protein A/G agarose resin bed. Isotype determination was done by ELISA using HRP labeled mouse anti-IgM, IgG2a, IgG1 and biotin labeled rat anti- IGg2b, IgA and IgG3 primary antibodies. **Results**: Three hybridoma clones for Aj-anti-CD3 IgG were purified from the cell culture supernatants and stored for later use. Each of the three hybridoma clones are expected to have produced a different isotype based on flow cytometry data. **Conclusions**: In future work, we will use Aj-anti-CD3 antibody labelling of T cells in vivo to deplete T cells and determine whether immunopathology to Tacaribe virus, which normally causes fatal infection, will be ameliorated.

29. **Bats and Immunity: Anti-Viral IFNγ Responses Differ Among Hosts**
C. Cotter, T. Schountz, C.L. Campbell

Arthropod-borne and Infectious Diseases Laboratory, Colorado State University

Anti-viral responses in bats (order Chiroptera) is largely unknown to researchers. Although bats account for 20% of all mammal species, they are relatively understudied in the scientific community (Baker et al., 2013). Bats are reservoir hosts for zoonotic diseases such as severe acute respiratory syndrome (SARs), rabies virus, and Ebola virus (Mandl et al., 2015). Reservoir hosts, generally, do not show pathogenic signs or succumb to disease when infected with such viruses. Current efforts by Kuzmin et al to better understand anti-viral responses in Egyptian rousette bat (*Rousettus aegyptiacus*) and human cells include a comparative study of host innate immune response to infection with Ebola virus or Marburg virus. They focused on the interferon (IFN) response. Kuzmin et al. demonstrated that bat IFNγ (type II IFN response) decreased viral replication in cell culture, whereas the human IFNγ produced by the human cells did not. Additionally, IFNγ stimulated the type I IFN (IFNα/β) response Kuzmin et al., 2017). My research focuses on Jamaican fruit bat (*Artibeus jamaicensis*—Aj) IFNg and its role in an anti-viral response to New World mammarenavirus Tacaribe (TCRV). *A. jamaicensis*, when infected with

TCRV, suffer fatal infections (Cogswell-Hawkinson, 2012). Most arenaviruses, TCRV excluded, produce a nuclear protein (NP) that blocks the type I IFN response at interferon response factor-3 (IRF-3) (Martinez-Sobrido et al., 2007). Pathogenesis of TCRV is still unknown; however I hypothesize that it interferes with the IFN response pathway by a different mechanism. Therefore, introduction of therapeutic Aj IFNγ to TCRV infected A. jamaicensis should be able to stimulate an appropriate, anti-viral innate immune response to rescue them from death. My project focuses on cloning, expressing, and purifying Aj IFNγ in order to synthesize a recombinant antibody for Aj IFNγ.

30. **Virome analysis of neotropical bats on the Caribbean island of Trinidad**

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Objectives: Bats are recognized as reservoirs for a number of important zoonotic viruses. The Caribbean island of Trinidad is richly diverse in bat fauna with 68 species recognized. Viruses detected in Trinidad bats include Rabies virus, Tacaribe virus, Rio Bravo virus, Tamana bat virus and more recently a bat coronavirus. The objective of this study was to identify and characterize known and novel viruses in Trinidad bat species. **Methods:** During the period 2012- 2016, bats were sampled from 19 locations in Trinidad. The novel virome capture sequencing platform for vertebrate viruses (VirCapSeq-VERT) was employed to sequence faecal swab samples from 73 bats belonging to seven neotropical species (*Desmodus rotundus, Carollia perspicillita, Uroderma bilobatum, Molossus molossus, Molossus rufus, Pteronotus parnellii* and *Artibeus spp*). Sequence reads were processed using the bioinformatics pipeline at Center for Infection and Immunity to remove host background and assemble contigs that were then subjected to homology search using MegaBlast against the GenBank nucleotide database. Sequences that showed poor or no homology at the nucleotide level were searched against the GenBank viral protein database using BLASTx. The bat fecal samples were also screened by consensus PCR for 8 viral families (*Arenaviridae*, *Herpesviridae*, *Coronaviridae*, *Orthomyxoviridae*, *Alphaviridae*, *Flaviviridae*, *Rhabdoviridae*, *Picornaviridae*) using broadly reactive degenerate primers as outlined in the laboratory protocol for the PREDICT II surveillance project. All PCR products were confirmed by sequencing. **Results:** Consensus PCR detected sequences of Herpesviridae (bat herpesviruses) and Coronaviridae (bat coronaviruses). Preliminary analysis of VirCapSeq-VERT data provided evidence of both known and potentially novel viruses, the majority of which belonged to the families *Anelloviridae*, *Herpesviridae*, *Coronaviridae*, *Orthomyxoviridae*, *Parvoviridae*, *Rhabdoviridae* and *Retroviridae*. The *Anelloviridae* and *Herpesviridae* were detected primarily in fruit bats. The *Orthomyxoviridae* family included Influenza A viruses and were identified in *Desmodus* and *Molossus* species. *Parvoviridae* were overwhelmingly from *Desmodus* and *Artibeus* bats from one trapping site within the same year. *Rhaboviridae* viruses were detected in Desmodus bats sampled from various locations throughout the sampling period. The Retroviridae were primarily previously described bat endogenous retroviruses. **Conclusions:** Our results indicate the presence of a wide range of both known and novel viruses in faeces from Trinidad bats. The limited identification of viruses by consensus PCR as compared to the deep sequencing technique implies that viral detection is more efficient by targeted deep sequencing. Further analysis including targeted PCR and sequencing to assemble full genomes is required to further characterise the viruses detected. Analysis of other tissues will be required to distinguish between bat viral infections and viruses associated with animal prey.

31. **Delineating the phenotype and function of major lymphocyte populations in the fruit-eating bat, Pteropus Alecto.**

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Objective: The unique ability of bats to act as reservoir for viruses that are highly pathogenic to humans suggests unique properties and functional characteristics of their immune system. However, the lack of bat specific reagents, in particular antibodies, has limited our knowledge of bat's immunity. **Methods and Results**: Here, using cross-reactive antibodies, we report the phenotypic and functional characterization of CD3+ T cell subsets, CD19+ B and NK1.1+ NK cells in the fruit-eating bat Pteropus alecto. Our findings indicate the predominance of CD8+ T cells in the spleen from wild-caught bats that may reflect either the presence of viruses in this organ or predominance of these cells at steady state. In addition, bone marrow of the bat contains over 30% T lymphocytes. This is significantly greater when compared to the T cell percentages in human and mouse bone marrow which ranges between 4% and 8%. Uniquely, a significant proportion of CD3+ T cells in bat spleen constitutively express IL-17A, IL-22 and TGF- at the mRNA level. Hence, the spleen may contain a substantial population of naïve T cells that are programmed to readily differentiate into TH17 cells or Tregs. Furthermore, mitogenic stimulation induced proliferation of bat immune cells and production of cytolytic molecules granzyme and perforin, and cytokines IL-2, IL-10, TNF and IFN. Additionally, we also demonstrate B cell function via calcium flux assay. **Conclusions**: This work paves the way towards a better understanding of bat's immunity that may offer new perspectives of therapeutic interventions for humans.

32. **Seasonal serological signals in viral infections for Madagascar fruit bats**

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Objectives: Considerable evidence supports a seasonal driver of bat-borne zoonoses, with most spillover events aligned with the synchronous reproductive season of the bat host in question. Previous modeling work proposes three possible mechanisms which could underpin such seasonality: classic Susceptible-Infectious-Recovered (SIR) dynamics with a seasonal influx of naïve juveniles, Susceptible-Infected-Recovered-Susceptible (SIRS) dynamics with periodic, waning immunity, and Susceptible-Infectious-Latent-Infectious (SILI) dynamics, by which hosts maintain virus persistently but shed seasonally. We fit variations on these contrasting dynamic models to age-seroprevalence data for henipavirus infections in Madagascar fruit bats in order to test these hypotheses. **Methods:** We live-captured, serum-sampled, and extracted lower premolar teeth (under anesthesia) from 340 Madagascan fruit bats (Eidolon dupreanum) over an eighteen-month seasonal trajectory. Serum samples were subjected to Luminex assay for henipavirus antibodies, and teeth underwent histological processing to quantify bat age, resulting in the construction of age-serprevalence curves for heniapivrus exposure in E. dupreanum. We fit variations on SI, SIR, SIS, and SIRS compartmental models to these data and used generalized additive models (GAMs) to investigate seasonal variation in antibody titers for both sexes, including several individuals recaptured across our time series. **Results:** Seroprevalence to henipavirus increased with age across the early years of life in our dataset, then declined to zero in later life. Field data were best fit by either frequency-dependent transmission models incorporating infection-induced mortality or by density-dependent transmission models, allowing for rapid waning of immunity. GAM analysis of seasonal trends showed significant seasonality in an animal's serostatus, corresponding to the nutritional calendar for male bats and the reproductive calendar for female bats. Recaptured individuals demonstrated considerable dynamism in antibody titers, changing serostatus in both directions across our time series. **Conclusions:** Our analyses suggest that henipavirus infections in E. dupreanum fruit bats are governed by highly dynamic transmission mechanisms, involving rapidly waning immunity and seasonal peaks and troughs in infection status. We reject a classic SIR model in favor of a more flexible SIRS or SILI model underpinning viral transmission among bat hosts in our system. More fine-scale field data will be needed to further parse remaining hypotheses.

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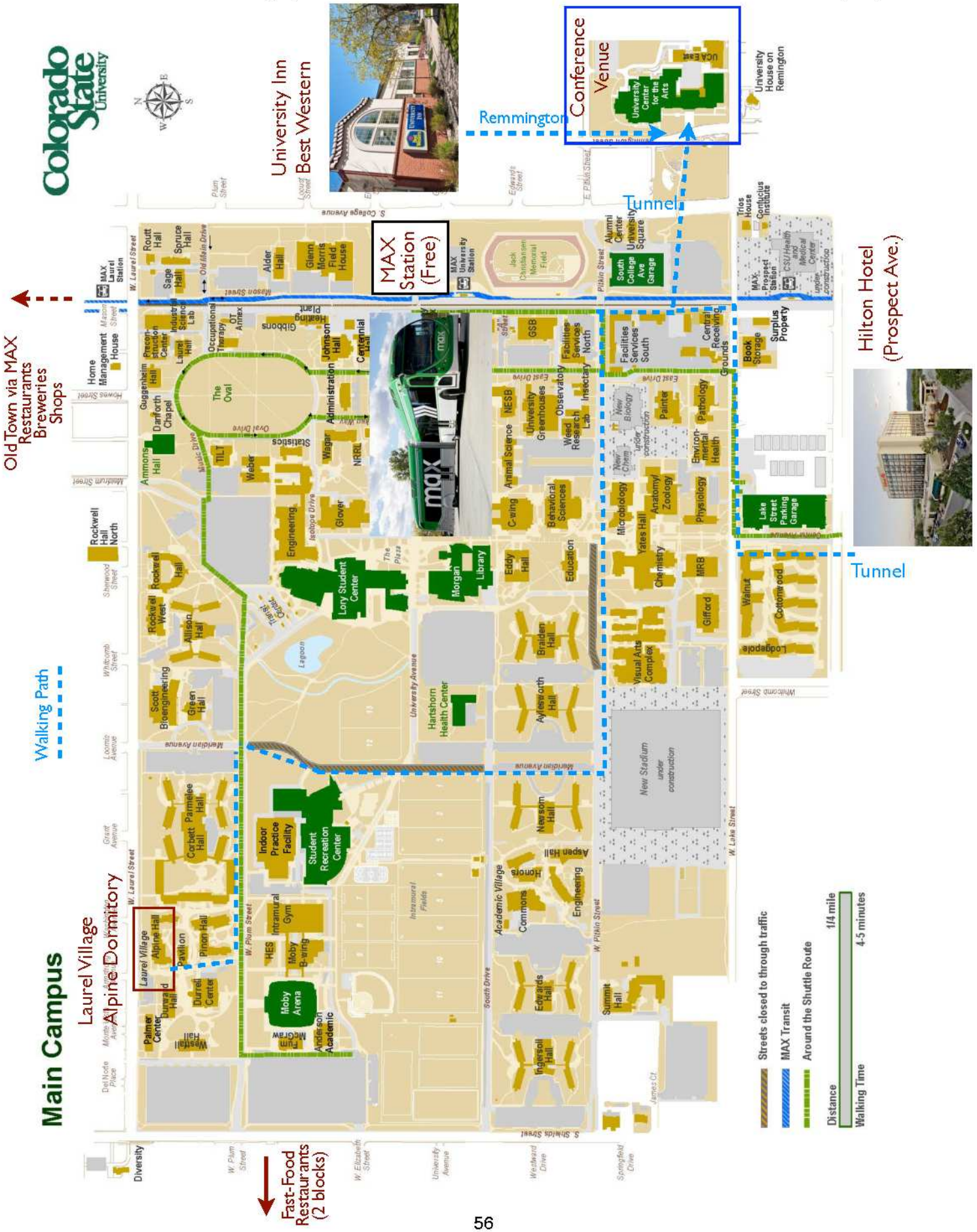
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From: Megan Hudson <
Sent: Wednesday, May 08, 2019 2:34 PM EDT
To: tgoldstein ; jkmazet Brian H Bird >; cryanp ; @ecohealthalliance.org ; Kading,Rebekah < >; tigga.kingston < ; eric.laing.ctr < >; ian.mendenhall ecohealthalliance.org < >; ecohealthalliance.org < jit8 gavin.smith ; mkariuki.njenga >; gustavo.f.palacios.ctr >; cxx1

CC: Stokes, Martha M CIV (USA) >; Marles, Jarrad M CIV DTRA J3-7 (USA) >; Tuttle, R Emerson CIV DTRA COOP THRT REDUCT (USA) Aleman, Nicki D CTR DTRA COOP THRT REDUCT (USA) >; Gano Cohen, Kelsey A CTR DTRA COOP THRT REDUCT (US) ; Lopez, Angelica Patricia (Angie) CTR DTRA COOP THRT REDUCT (USA) >; Katie Leahy ; Jessica Marks
Subject: Bat One Health Research Network Meeting - July 26 - 28, 2019
Attachment(s): "18th IBRC Phuket 2019[1][2][1].pdf","JKO-ATLV1-SERE-ISOPREP Instructions Feb 2019.docx"

Dear Bat One Health Research Network Participant,

On behalf the Defense Threat Reduction Agency, Biological Threat Reduction Program (DTRA BTRP) supporting global threat reduction networks for bat borne pathogens, we would like to extend a save the date for you to attend our Bat One Health Research Network (BOHRN) Steering Committee meeting in Phuket, Thailand. The meeting will be held 26 – 28 July 2019.

The BOHRN meeting coincides with the International Bat Research Conference (IBRC) 28 – 1 August 2019 in Phuket. If you are able to attend, we would also like to extend an invitation to attend IBRC.

We hope to achieve the following objectives during the Steering Committee Meeting:

1. Facilitate a multi-disciplinary forum for discussion on research methods and practices
2. Characterize global research interests and priorities, and align them with network research focus areas to develop shared resources on the BOHRN website
3. Discuss upcoming opportunities to support regional African bat networks and plan for a future effort in Africa

Should you accept this invitation, *Please follow the travel instructions below my signature block. Letters of Invitation will follow shortly.*

We hope you can join us!
Kind Regards,
Megan

Megan Hudson | ***Project Lead***
Global Systems Engineering, LLC
A Certified HUBZone Company
www.globalsyseng.com

Travel instructions:

Please respond with intent to join to megan.hudson and nicki.d.aleman.ctr *NLT 13 May.*

Please follow up with Nicki Aleman as soon as possible, if you intend to travel; you will likely need to provide Nicki with your passport information, to and from destinations, and travel dates. Logistics support coordinators will work with you to secure all your reservations. Please note that they try to work with your preferences, but must remain within the boundaries of the Department of Defense regulations for travel. *Please be advised, if your trainings are not completed by the assigned date (31 May), funding for travel and conference registration will not be provided.*

18th IBRC Phuket, Thailand - 28 July-1 August, 2019
(International Bat Research Conference)

Following the very successful IBRC conference in Durban, South Africa in 2016, we are pleased to announce that the 18th International Bat Research Conference will be held between 28 July and 1 August 2019 at the Slate Resort, Phuket, Thailand.

The meeting is hosted by Princess Maha Chakri Sirindhorn Natural History Museum, Prince of Songkla University, Thailand, supported by the Harrison Institute, UK.

Over 4 days, the meeting will feature a diverse range of presentations, symposia and workshops on numerous bat research and conservation topics. With an expected audience numbering some 400+ individuals, it is heartening to see that registrations and expressions of interest already include a broad cohort of students, young researchers, and leading authorities from Asia, the Americas, Africa, Australasia, and Europe. The conference is also providing a base on which a number of other bat-related networks are seeking to piggy-back in order to maximise their potential audience. Meanwhile, plenary speakers - all experts in their field - have been invited to address a series of highly topical issues such as bats and emerging disease, bat conservation in multi-occupation landscapes, and sequencing the bat genome. The conference is proving equally attractive to sponsors with a broad range of exhibitors.

As organisers, it is our hope that this meeting will bring together new, innovative ideas about the future of bat research and particularly the future of bat conservation. For this reason, the logo of the 18th IBRC symbolises that the future for bats is in our hands and it is for us to promote their conservation through strategic initiatives, education, and outreach.

We, however, still seeking partnership to support organising the meeting. The particularly crucial support that we really need at the moment is the travel grant for 'student and young/early career scientists'. We believe that support, in any kind, from your organisation will greatly increase the number of attendance and enhance the scientific atmosphere of the meeting.

We look forward to partner up and meeting with you.

Dr Pipat Soisook (pipat66@gmail.com)
Chairman of the Scientific Committee of the 18th IBRC
https://www.ibrc2019.com/

13 February 2019

JKO/ATLV1/SERE/ISOPREP Instructions for Civilian Personnel without an Official Government Email address or a Common Access Card who are Supporting BTRP.
Use your Work Email for Corresponding. Training not required by Foreign Nationals.

This process is for NEW ACCOUNTS ONLY. If you have logged into JKO before, use forgot user name /password if/as needed to recover your Username or Password. Contact JKOHelpDesk@jten.mil or 757-203-5654 for access issues.

To establish a JKO account, click on the following link. http://jko.jten.mil/index.html on the page that opens up, **click on enter JKO**. Read the Security Banner then **click OK**. On the page you are viewing now, under I DO NOT have a CaC, **click on Non-Government Personnel/Sponsored Account Registration**.
On the next page, fill out the requested information. **Enter the email for the Country Manager** you are supporting at BTRP. When you click submit, a notice will be sent to the country manager who will submit your account request.
If needed, John.T.Patterson2.civ@mail.mil can be used as the sponsor. It usually takes 24hrs to establish an account.

To complete:
1. JKO Course # JS-US007: Level I Antiterrorism Awareness Training: Valid for 12 Months.
Once logged into JKO, select the Catalog Tab at top of page and enter "antiterrorism" in title/keyword box, and click search. JS-US007 Level I Antiterrorism Awareness Training – (2hrs) should be listed. Click enroll to access course.

2. JKO Course J3TA-US1329, SERE 100.2 Level A SERE Education and Training in Support of the Code of Conduct (FOUO): Valid for 36 Months or AS REQUIRED BY THE FOREIGN CLEARANCE GUIDE. FREQUENCY SUBJECT TO CHANGE.
Once logged into JKO, select the Catalog Tab at top of page and enter "SERE" in title/keyword box, and click search. SERE 100.2 Level A SERE Education and Training in Support of the Code of Conduct (FOUO) - (4 hrs) should be listed.
Click enroll to access course.

ONCE ANTITERRORISM AND SERE TRAINING ARE COMPLETED, PLEASE SEND A COPY OF THE CERTIFICATES

DO NOT send form by email or regular mail. Once blocks 50-54 are completed the form is classified CONFIDENTIAL. Send using shipping instructions on page 2

3. DD Form 1833 Isolated Personnel Report (ISOPREP): Valid 12 Months or AS REQUIRED BY THE FOREIGN CLEARANCE GUIDE. FREQUENCY SUBJECT TO CHANGE.

If you have a DOD CAC, click on link below and follow instructions to complete your **initial ISOPREP**. You must be on a .mil or .gov domain computer system.
https://prmsglobal.prms.af.mil/prmsconv/Profile/Survey/start.aspx

If you need to update or want to verify your ISOPREP, contact one of the individuals listed below.

If you are in the local area, you may contact John.T.Patterson2.civ@mail.mil / 571-616-5938 to arrange completion of your ISOPREP at the BTRP office. If you receive an out of office response, you may contact theodore.w.carlson.civ@mail.mil / 571-616-6382 for assistance.

PLEASE FOLLOW THE INSTRUCTIONS for the Form.
If you do not have a DOD CAC, and are not in the local area, fill out DD Form 1833. This can be found by searching online. Instructions are included in form. Finger prints are not required. **Your SSN, DOB, Blood type, A Primary Next of Kin, and Your Company and Point Contact are needed. Section 9 blocks 50-54**

should be typed on separate piece of paper and included with the form. Make sure to follow the instructions for the 4 Statements and the Authentication Number. Need to be able to generate 4 questions from each statement. Do not use same # twice, no consecutive #'s, no zeroes. Submit two photos, a front view and right side profile view, from the shoulders up. Photos may be sent with the form or the preferred method is to email the **photos only** to John.T.Patterson2.civ@mail.mil

Mailing Instructions

Seal package with type of tape to retain postal stamp impressions. Prepare, package, and securely seal classified material in ways to MAXIMIZE evidence of tampering and MINIMIZE undetected deliberate compromise, or risk of accidental exposure. To minimize the risk of exposure of classified information, package documents so that classified material is not in direct contact with the inner envelope or container (e.g., fold so classified material faces together).
Double wrap classified information in two opaque, sealed envelopes, wrappings, or containers, durable enough to properly protect the material from accidental exposure and facilitate detection of tampering.
Do not place classification marking or any other unusual marks on the outer package that might invite special attention to the fact that the contents are classified

After completing form, fold so classified information faces together. Place folded form, disk or photos if you did not email them inside fully addressed and marked package as instructed and shown below.

Form

CONFIDENTIAL

DD FORM 1833

Inner Package

Full Name CONFIDENTIAL
Full Address (Mark Front and Back)

ATTN: CT-BT/John Patterson
and BTRP Country Managers
name
Defense Threat Reduction Agency
6200 Mead Road
Fort Belvoir, VA 22060-5624

CONFIDENTIAL
(Mark Front and Back)

Outer Package

Office Name Only
Office Address

See proper address below

Inner Package:

Mark inner package as shown above. Be sure to replace the BTRP Country Managers' name shown with the actual name you are supporting.

- Complete recipients and sender address
- Mark top/bottom and front/ back with CONFIDENTIAL markings.
- Seal package as stated at top of this page.

Place this package inside of another package (outer package).

Outer Package:

Mark outer package as shown above.

- Use only office name and office address. Do not use individual names.
- Do not use markings of any kind indicating classification or that the package contains classified material.
- Seal package as stated at top of this page.
- Send package via USPS, FEDEX, UPS, DHL, etc. Make sure you have a tracking # for Package.
- After sending package notify John.T.Patterson2.civ@mail.mil, and applicable BTRP Country Manager so we are aware to be watching for package.

Use correct address below depending on shipper. Make sure you have a tracking number for your package.

For Registered / Express mail via the US Postal Service	**For Express mail via Federal Express, DHL, UPS**
DEFENSE THREAT REDUCTION AGENCY 8725 JOHN J KINGMAN RD STOP 6201 FORT BELVOIR VA 22060-6201	DEFENSE THREAT REDUCTION AGENCY 6200 MEADE ROAD FORT BELVOIR VA 22060-5264

From: Megan Hudson
Sent: Wednesday, February 20, 2019 12:00 PM EST
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>; pilotdovih >; abubasha
; meryem.lemrani >; wava_38
; c demetria >; paalviola
ecohealthalliance.org >; ecohealthalliance.org
>; Kading,Rebekah ; sara.b
; sarabumrungsri ; julianas
wiantoro ; benjamin lee
; lisamariep pipat66
; vudinhthong ; iroro.tanshi
; benneth.obitte jjlutwama03
>; jit8 ; astghik.ghazaryan
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l.urushadze >; Katie Leahy >; Megan Hudson
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farlowscience ; payscue
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shahanajshanc ; ecohealthalliance.org ;
eric.laing. stsang@ ; bhbird
; ahandel ; tgoldstein >
CC: Stokes, Martha M CIV (USA) l>; Becker, Stephen M CTR DTRA J3-7 (US)
>; Katie Leahy >
Subject: Bat One Health Research Network
Attachment(s): "BOHRNVienna_FinalReport[1].pdf"

Dear all,

On behalf of Dr. Marty Stokes, please find the final report for the BOHRN Workshop in Vienna.

As discussed in Vienna, there are several action items for the BOHRN network. In order to move forward on several of these items, we ask that you take a few moments to answer the following questionnaire. This survey will help us to identify BOHRN's efforts and progress towards its overarching goals and evaluate the networks threat reduction efforts. Please follow the link and complete the survey no later than 28 February: https://www.surveymonkey.com/r/6FQPQR3

Additionally, please use the following Drop Box link for access to the BOHRN Workshop participant list with pictures and the quad charts submitted by all participants. You may also access the video of the BOHRN Workshop here.

We had hoped to make a more formal announcement regarding solicitation for BOHRN special projects around this time; however, BTRP is internally still reviewing necessary criteria for award and will not be ready to make a more formal announcement until the April / May timeframe. The announcement will be released via the www.bohrn.net website.

Please let us know if you have any questions or concerns.

Kind Regards,

Megan

Megan Hudson
Project Lead | Global Systems Engineering
6303 Little River Turnpike #208
Alexandria, VA 22312

http://globalsyseng.com

BOHRN

The Bat / One Health Research Network

The 1st Annual Bat / One Health Research Network Workshop

8-9 November 2018 • Vienna, Austria

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Workshop Overview

Executive Summary

The Bat/One Health Research Network (BOHRN) convened its 1st Annual Research Workshop in Vienna, Austria, 7-8 November 2018, in advance of the International Meeting on Emerging Diseases and Surveillance (IMED). This two-day workshop was organized and hosted by the Defense Threat Reduction Agency, Cooperative Threat Reduction Directorate, Biological Threat Reduction Program (BTRP) in its capacity as a sponsor of life-sciences research-based Threat Reduction Networks (TRNs). This event provided an opportunity to advance BOHRN's core agenda of enabling interdisciplinary collaboration at the interface of biological threat reduction, research, and conservation.

The BOHRN initiative was organized at a side-meeting of the 2nd International Symposium on Infectious Diseases of Bats in Fort Collins, CO on 29 June 2017. During this meeting participants established a Steering Committee and began preliminary actions to build a multi-disciplined, self-sustainable network to better characterize global threats of bat-borne pathogens and formalize community standards and conservation- conscientious practices for One Health disease research. During a series of follow-on meetings, members of the BOHRN Steering Committee identified objectives and developed a research strategy to prioritize and target common needs. The BOHRN 1st Annual Research Workshop in Vienna provided an opportunity to validate its research strategy with a wider audience.

The workshop began with a series of introductory presentations from Dr. Martha Stokes, DTRA BTRP, who provided background on her organization and the BOHRN effort. There were also a series of presentations from other subject matter experts who provided short lectures on areas were identified as knowledge gaps by members of the Steering Committee at previous BOHRN meetings (note: the full agenda may be found here). Next, workshop attendees participated in two breakout sessions. The first session focused on the research focus areas within the four (4) BOHRN Working Groups and aimed to solicit feed-back in real time on the short and long-term objectives within each network working group.

The second breakout session was initiated by an interactive exercise, facilitated by Dr. Tigga Kingston (Texas Tech University) and Dr. Jon Epstein (EcoHealth Alliance), mapping the intersectional of ecological and epidemiological research questions. Participants were then divided into regional groups with diverse and varying levels of expertise to sketch out hypothesis-driven research projects that mapped to BOHRN working group focus areas. Members of the BOHRN Steering Committee and other experts were on-hand to provide mentorship and guidance. At the end of the workshop, each project was presented orally by a member of the project team in a mock peer review session for feed-back and discussion.

The output and recommendations gathered from the small-group sessions will inform BOHRN next steps, which Dr. Stokes described at the conclusion of the workshop as a series of special grant awards for project proposals under BOHRN. She described the process as 'still under construction' but affirmed her leadership's commitment to maintain the network's initial momentum. While the exact mechanism and criteria for award are still being discussed, all interested parties may anticipate a call for proposals via the BOHRN website at some point in the spring of 2019.

There are a number of factors that make bats unique disease reservoirs, including their social behavior, distinct physiology and metabolism, ability to travel long distance, nocturnal activity, species diversity, and long life-span. BTRP anticipates that by taking a lead in funding bat-associated pathogen research, their organization can play a significant role in better characterizing the role of bats in global zoonotic disease ecology, coupled with assessing the impact of human-mediated interactions and environmental changes, to better understand threat reduction value of surveillance and intervention efforts.

Previous BOHRN Events

BOHRN Kick-off Meeting

- Concurrent with 2nd International Symposium on EID
- Sponsored by BTRP
- Took place in Fort Collins, CO – 29 June 2017
- **Outcomes:** (1) established a steering committee; (2) drafted terms of reference; (3) identified research areas of interest

BOHRN Steering Committee Strategy Mapping Meeting – 1

- Concurrent with Prince Mahidol Award Ceremony
- Sponsored by BTRP
- Took place in Bangkok, Thailand – 30 January 2018
- **Outcomes:** (1) prioritized research focus areas; (2) developed targeted action plans; (3) drafted associated workplans and timelines

BOHRN Steering Committee Strategy Mapping Meeting – 2

- Concurrent with International One Health Congress
- Sponsored by BTRP
- Took place in Saskatoon, Canada – 20-21 June 2018
- **Outcomes:** (1) completed workplans and timelines for research focus areas; (2) established BOHRN branding and website; (3) drafted communication and outreach strategy

BOHRN Biological Threat Characterization Discussion

- Concurrent with Western Asia Bat Network (WABNet) Kickoff Meeting
- Sponsored by BTRP, organized by EcoHealth Alliance
- Took place in Tbilisi, Georgia – 20 September 2018
- **Outcomes:** (1) identified and characterized regionally-focused gaps and needs (2) activated communication and outreach strategy;

Workshop Outcomes

Presentation Summaries

The following subject matter experts were invited to present on areas that were identified as knowledge gaps in BOHRN. Event participants received a pdf copy of each presenter's slides.

Dr. Jon Epstein

Dr. Jon Epstein, EcoHealth Alliance, presented on *Understanding the Ecology of Emerging Zoonoses*. His presentation focused on the three stages of disease emergence to help understand the complexities of spillover. Starting with the first stage, wildlife and domestic animal interactions, Dr. Epstein explained the movement of microbes into domestic animals. Human's increasing interactions with domestic animals leads to the second stage where the microbe has spilled over into the human population causing widespread outbreaks. The third and final stage of disease emergence is the outbreak reaching pandemic levels. Dr. Epstein proceeded to present two cases Nipah Virus spillover from Pteropid Bats and Nipah Virus spillover from date palm sap harvesting. Both cases were used to support evidence that the driver of spillover is human activity. However, as Dr. Epstein explained, this does not account for why human infections occur a small areas of these bat's known habitats. Therefore, it is important to understand why spillover is only occurring in these small areas, whether it is a rare event or there is a need for more broad spread surveillance.

Dr. Jonathan Towner

Dr. Jonathan Towner, from the Center for Disease Control and Prevention, presented on *Filovirus Maintenance in Nature: Potential Lessons Learned from Studying Marburg Virus*. Dr. Towner's presentation focused on the persistence of Marburg Virus (MARV) in nature supported by the recent study findings that Egyptian Rousette bats are identified as a natural reservoir for MARV. The study looked at bats during birthing and breeding seasons in the Python Cave of Uganda and focused on the impact seasonal pluses have on human spillover. From this study, Dr. Towner presented on the need for messaging to miners and the community to emphasize the importance of bats to the ecosystem and the effects of culling the bats in Python Cave. In addition, the presentation focused on discussing virus transmission from bat to bat, long-term immunity in bats, and the potential to recreate the study with Ebola Virus.

Dr. Brian Bird

Dr. Brian Bird, from the University of California-Davis, presented on *Synergies Between the Bench and the Field for Virus Discovery and Capacity Building*. Dr. Bird's focused on the work of the USAID PREDICT program and the Ebola Host Project. Dr. Bird began his presentation by explaining the challenges of targeted, risk-based surveillance the PREDICT program focuses on. He led into a discussion on virus discovery and detection from identifying viruses by consensus polymerase chain reaction (PCR) supplemented by high-throughput screening (HTS) to performing experiments to understand and rank the potential risk of the virus. Dr. Bird then explained the process PREDICT uses to strengthening laboratory efforts and used the Ebola Host Project in Sierra Leone as an example of

these efforts. The Ebola Host project has led to the training of numerous local scientists and the development of community outreach materials. Dr. Bird's presentation summarized the efforts in Sierra Leone to focus on Filoviruses which has led to identifying new Ebola viruses in insect eating bats before known human or animal sickness.

Dr. Susan Tsang

Dr. Susan Tsang presented on *Flying Foxes as Bushmeat in Sulawesi Indonesia, Building Community Outreach Initiatives Based on Novel Understanding of Who, Where, and Why*. Dr. Tsang began by identifying the common challenges in institutional capacity, identification of stakeholders, interagency coordination, and funding. Her presentation then focused on the flying foxes as bushmeat and the cultural understanding of the drivers for how and why bats are hunted. Dr. Tsang used the outreach initiatives in Sulawesi, Indonesia to emphasize that outreach must include regional level coordination to allow for national level communication at both the front and tail end of any project. In addition, outreach should be designed for the community and the importance of assessing effective ways to disseminate information. Dr. Tsang explained potential resolutions to the common challenges could include providing training on outreach, incorporating voices from all levels of policy, and demonstrating the value to other sectors for interdisciplinary funding.

Breakout Session 1 Overview

In advance of the first breakout session, Dr. Jon Epstein (EcoHealth Alliance) and Dr. Tigga Kingston (Texas Tech University) provided an update from the Steering Committee, summarizing a year's worth of Steering Committee Strategy Sessions. They presented two - three slides per Working Group, summarizing the group's mission, focus areas, objectives, measurements of success, challenges, and timelines. The new participants, who had not been part of previous BOHRN strategy sessions, were able to discuss the slides as a large group, before breaking out into smaller groups to provide constructive feedback and guidance based on their knowledge and experiences. Breakout session discussions led to the development of cross-cutting recommendations on capacity for in region repositories and curation of voucher material and the implementation of a data-sharing culture. The outcome of these suggested recommendations will ultimately build an additional working group.

Steering Committee Presentations

BOHRN planners collated and drafted the following material from the BOHRN strategy sessions, to provide a visual tool to solicit feedback from a group of new stakeholders. This information was presented in slide-form as an introduction to the large-group discussions and break-out group sessions.

Working Group 1: researching host-pathogen biology and interactions

MISSION: EXPLAIN THE DETERMINANTS OF PATHOGEN TOLERANCE, TRANSMISSION, AND SPILLOVER FROM BATS AT INDIVIDUAL AND POPULATION LEVELS

Established Working Group 1 Research Focus Areas

Bat physiology and immunology	Distributions of pathogen amongst species	Bat pathogen community biology	Modeling approaches for host dynamics and epidemiology

Objective		Outcomes
Complete a systematic review of knowledge gaps on model systems	→	Publish a systematic review of modeling systems and knowledge gaps that were defined
Identify modeling systems that are representatives of all geographic and phylogenetic areas	→	Modeling systems are defined, characterized, and validated
Evaluate the transmission risks and spillover pathogens to another animal host	→	Intrinsic and extrinsic risk factors are identified for major diseases and geographic areas

Overall Challenges: (1) Objectives require multidisciplinary team: (2) consortia would be needed for modeling systems review and validation

Established Working Group 1 Research Projects and Activities Priority Timeline

Short-term project / activity pipeline *6 -12 months*	Long-term project / activity pipeline *12 months +*
Map funding landscape ⇒ Identify funders ⇒ Host a funders meeting	Conduct long-term lab and field studies ⇒ Develop cell lines and bat animal models ⇒ IgM immunoassay ⇒ Develop methods for determining the age of bats ⇒ Determine the timing of viral shedding and the effects of environmental stresses ⇒ Determine co-infection in bat species ⇒ Determine temperate versus tropical variables associated with infection (hibernation periods / viral replication) ⇒ Understand climate change with respect to physiology ⇒ Develop heat stable preservatives ⇒ Develop smaller telemetry and physiology sensors

Working Group 2: researching pathogen surveillance, diagnostic capacity and epidemiology

MISSION: FORM REGIONAL NETWORKS TO ESTABLISH A COMMON METHODOLOGY FOR SURVEILLANCE OF HUMAN AND ANIMAL HEALTH; BETTER UNDERSTAND SPILLOVER RISKS AND EPIDEMIOLOGY OF BAT PATHOGENS

Established Working Group 2 Research Focus Areas

Molecular epidemiology	Geographic and phylogenetic distribution of pathogens	Detection, diagnosis, and reporting of bat-borne pathogens	Established guidance and protocols for sampling

Objective		Outcomes
Conduct a gap analysis of existing diagnostic tools	→	Publish review of epidemiology of known bat-borne pathogens
Conduct outreach to various groups of researchers and build awareness amongst public and science community	→	Established and linked regional networks of practice and expertise
Establish a common methodology for surveillance	→	A better understanding of the risks associated with spillover and established standards for surveillance and reporting

Overall Challenges: (1) The logistics and bureaucracy of creating a multidisciplinary team of international experts; (2) funding to support and sustain efforts to standardize surveillance

Established Working Group 2 Research Projects and Activities Priority Timeline

Short-term project / activity pipeline *6 -12 months*	Long-term project / activity pipeline *12 months +*
Conduct a gap analysis of diagnostic tools ⇒ Identify list of labs and contacts ⇒ Create a list for priority interventions / assistance ⇒ Analyze return data; publish resource lists	Conduct surveillance platform assessment ⇒ Conduct a literature review of previous surveillance platform assessments ⇒ Identify most beneficial platform for animal and human health data information sharing ⇒ Identify most logical platform for low resource settings ⇒ Identify the best field-forward platforms

Working Group 3: researching ecology (bat, domesticated animals and wildlife interface)

MISSION: DEFINE HOW AND TO WHAT EXTENT THE ECOLOGICAL CONTEXT OF BATS, AND THE HUMAN INFLUENCE ON THAT CONTEXT, INFLUENCE PATHOGEN DYNAMICS AND SPILLOVER THREATS

Established Working Group 3 Research Focus Areas

Bat behavior, distribution and movement	Effect of anthropogenic disturbance and modification on pathogen dynamics	Domesticated animals and wildlife behavior, distribution, and movement impact on interaction with bats

Objective		Outcomes
Engage the ecological community to define system uniqueness and interdependencies	→	Pathogen research community acknowledges and integrates ecological systems and interdependencies
Advocate for ecological design and analysis frameworks to pathogen research	→	BOHRN research projects are designed using a framework for well-balanced outcomes
Build capacity for disease researchers to gather ecological data to provide context for their studies	→	More funded studies return ecological data
Define emerging ecological principles that could inform spillover threats	→	Emerging ecological principles become widely accepted governing principles for practice
Establish key messages and conduct efforts to promote a culture of conservation amongst One Health researchers, practitioners, and stakeholders	→	BOHRN establishes itself as a consistent and unbiased perspective from the community and its statements are widely accepted and distributed

Overall Challenges: (1) Science communities have polarized and insular view of bats and diseases; (2) lack of collaboration and communication efforts

Established Working Group 3 Research Projects and Activities Priority Timeline

Short-term project / activity pipeline *6 -12 months*	Long-term project / activity pipeline *12 months +*
Conduct conservation / One Health literature review ⇒ Establish parameters ⇒ Conduct literature review ⇒ Quantify interdisciplinary relationships w/ assessment of numbers of publications ⇒ Publish results Establish ecology tool / training aid kits ⇒ Identify and source materials	N/A ⇒ N/A

- ⇒ Collect and build case-control studies for training
- ⇒ Develop training plans
- ⇒ Distribute through BOHRN

Working Group 4: researching human-bat interactions

MISSION: FULLY DEVELOP, UNDERSTAND, AND COMMUNICATE THE BAT AND HUMAN INTERFACE TO KEY STAKEHOLDERS AND COMMUNITIES

Established Working Group 4 Research Focus Areas

Hunting and commodity chain	Human behavioral risk characterization	Interactions in human dwellings	Ecotourism

Objective		Outcomes
Develop and test policy interventions for specific human-bat interfaces	→	Policy interventions for human-bat interfaces are developed and put into place
Communicate key findings to stakeholders	→	Effectively communicate and publish findings of studies
Develop global risk maps to assess existing data and validate risk maps	→	Publish global risk maps highlighting geographic areas of risk
Identify high-risk groups and develop education platforms to measure knowledge, attitude and practices	→	Getting community buy-in and understanding of concepts

Overall Challenges: (1) Truthful responses in behavior research on bat-human interactions; (2) accuracy of risk map and models; (3) cultural barriers and beliefs

Established Working Group 4 Research Projects and Activities Priority Timeline

Short-term project / activity pipeline *6 -12 months*	Long-term project / activity pipeline *12 months +*
⇒ Develop global risk maps ⇒ Survey high-risk groups for their KAP	Conduct research studies / support for ecology ⇒ Develop and validate education platforms ⇒ Research to measure changes in KAP ⇒ Validate ground-truth risk maps

⇒ Adapt education platforms / materials

Recommendations

BOHRN organizers invited many researchers from diverse backgrounds at varying levels of professional experience to the Vienna workshop. This approach facilitated lively discussions and prompted the Steering Committee to consider new objectives, priorities, and perspectives within their previously established Working Group bounds. The following recommendations were captured by note-takers, observers, and other members of the Steering Committee, and will be marked for further discussion and adjudication during BOHRN's next Steering Committee meeting which will be held at International Bat Research Conference (IBRC) in Phuket, Thailand 2019.

Working Group 1: researching host-pathogen biology and interactions

Breakout Session Recommendations: members of the breakout group accepted the overall mission and objectives that Working Group 1 had established and proposed adding two additional research focus areas: (1) the role of bat taxonomy in host-pathogen coevolution and (2) host specificity in bat-borne pathogens. Members of the breakout group also proposed the following additions to the priority timeline:

- ⇒ Establish species identification consensus tools and techniques – such as the role of bar coding and other methods
- ⇒ Host or link to public-facing databases (e.g., Vertnet, National Science Foundation digitized database)
- ⇒ Identify regional resource repositories for voucher materials
- ⇒ Establish sustainable freezer network
- ⇒ Develop funding models for in-country collection curation capacity building / field sample collection transfer (business plans, logistics, maintenance, training)
- ⇒ Establish a database of reagents
- ⇒ Establish a list of international regulatory experts for transport of select agent materials (e.g., Bombali ebolavirus discovery and the issues they had with reporting and transfer)

Working Group 2: researching pathogen surveillance, diagnostic capacity and epidemiology

Breakout Session Recommendations: members of this breakout group generally accepted the mission and objectives that Working Group 2 had established. They proposed amending the research focus area for "Molecular Epidemiology" to include "Molecular and Serological Epidemiology". They also proposed the following additions to the priority timeline:

- ⇒ Establish a set of common research questions and topics related to biosurveillance data-type (syndromic, diagnostic, environmental) associated with bat-borne pathogen threats
- ⇒ Establish a catalog of surveillance models
- ⇒ Develop a sera and antibody collection with a standardized pool of collection
- ⇒ Conduct studies that integrate bat ecology and pathogen research (One Health research team that collects virology and ecological data at the same time)

- ⇒ Establish a list of minimum biosecurity / biosafety protocols for research (lab / field) and recommended sample sets / study
- ⇒ Establish a list of laboratories with bat sample repositories (by region and country
- ⇒ Establish a registry of "Bat Experts" by region and country
- ⇒ Identify diagnostic capabilities (person / institution)
- ⇒ Develop a hypothesis map
- ⇒ Outline funding mechanisms for other BOHRN stakeholders

The breakout group also recommended that any efforts to seek "standardization" (surveillance platforms) should use the phrase "common framework" as methods and implementation will vary in different countries and regions.

Working Group 3: researching ecology (bat, domesticated animals and wildlife interface)

Breakout Sessions Recommendations: during the breakout session, members of this group did not have any substantial modifications to the Working Group's mission, focus areas, or objectives. They did provide several ideas long-term timeline priorities, which included:

- ⇒ Conduct ecological and taxonomic studies that support disease research (and threat reduction), this will create a demand for ecologists to collect samples and will ultimately capacity for ecology through training and networking
- ⇒ Identify ecological and taxonomic gaps at local levels

Since much of Working Group 3's approach was built around the development of training modules, the group discussed training and the importance of tailoring existing projects / programs. They talked about sustainability in bat research programs and mechanisms for incentivization, offering ideas such as scholarships at the end of a short research project or using a training workshop as a research candidate selection opportunity.

Working Group 4: researching human-bat interactions

Breakout Sessions Recommendations: members of this breakout group did not have any major changes to the Working Group's mission, focus areas, or objectives. They did, however, want to emphasize the importance determining *where* human behavioral risks are the highest and *what* drives specific human bat interactions and the need to map these interactions accordingly. With regard to the timeline priorities, they made the following recommendations:

- ⇒ Characterize the risk map with priorities
  - DTRA (BTRP) priority pathogens, USG priority pathogen threats, WHO regional threats
  - Chart recent pandemics with drivers (e.g., bush meat markets overlaid with outbreaks)
- ⇒ For database define the approach to obtain data; Bat Conservation International (example), Bat-Plant.com for ecology interactions

Breakout Session 2 Overview

The first breakout session provided a foundation for the second breakout session during which participants formed into regional teams to craft research projects within the bounds of the BOHRN Working Group research focus areas. BTRP intends to fund several high priority threat reduction projects in FY19-FY20 and developed this exercise to test the viability of the network's strategy thus far. The

projects that were developed will not be summarized in this report, as they may be part of future project proposal; however, the images below show the work, collaboration, and collegial spirit of this session.

Participant Feedback

After the BOHRN Workshop participants were sent an anonymous feedback survey via SurveyMonkey. The participants were asked the following six questions:

1. What did you like about this Workshop?
2. Do you think the objectives for the BOHRN Workshop were achieved? Please explain your answer.
3. What do you wish we did differently?
4. What does success of this network look like to you, for your field of study?
5. What do you think was the most important aspect of this Workshop?
6. Any other comments or suggestions?

Overall, the participants responded positively to the efforts accomplished at the first annual BOHRN Workshop. An appreciation for the multidisciplinary networking opportunities, the potential opportunities the network presents, and the alignment of breakout group work with the Workshop presentations was convey by all participants. One participant's comment reflects this in saying "the multidisciplinary networking opportunities for engaging the ecological context of emerging infectious disease and breakout sessions were a nice complement to the big group discussions." Participant feedback indicated that the BOHRN Workshop objectives were achieved but there was a need for further information on next steps and more opportunity for discussion after the final small group session. Suggestions for change were to extend the workshop for two whole days and provide more focus on funding the discussed research.

BOHRN Path Forward

As a result of this workshop, BTRP intends to release an announcement for research project funding in the early part of 2019. The official announcement will be released on the BOHRN website (www.BOHRN.net) and emailed to anyone who has participated in a BOHRN activity.

At the conclusion of the workshop, Dr. Martha Stokes presented draft criteria for project award consideration, which included:

- Performed in BTRP engagement countries
- Demonstrated commitment to capacity building in BTRP mission areas (biosafety and biosecurity, and biosurveillance)
- Demonstrated commitment to open science
    - Transparent sharing of knowledge and information
    - Should include a data curation plan and broad statement on information access
    - Sample sharing not require, but strongly encouraged and preferred
- Demonstrated commitment to One Health
    - Inter-disciplinary research teams
    - Local engagement plans or educational outreach

- Include early to mid-career project investigators
- Address cross-cutting themes of BOHRN
    - Projects should be tied to no less than two working groups
    - Projects should be tied to no less than one focus area within each working group
- Include mentorship from member of steering committee or a Steering Committee/Executive Committee-approved designee (correlates to respective working group(s))

These factors are still under consideration and BTRP may change any or all. The only information regarding "Criteria for Eligibility" for a BOHRN grant/project award will be released on BOHRN.net. The timeline for award will also be released on BOHRN.net.

Annex 1: Agenda

Day 1

Time	Session	Objectives
0700 – 0800	**Closed-door Steering Committee Meeting**	
0730 – 0810	**Photo Registration (for non-steering committee members)**	
0810 – 0845	**Welcome and Introductions** Marty Stokes *Biological Threat Reduction Program (BTRP)*	Welcome all participants, provide four slides about BTRP and TRNs All participants go around the room and introduce name and organization
0845 – 0900	**BOHRN Overview** Marty Stokes *Biological Threat Reduction Program (BTRP)*	Provide an overview about BOHRN, its mission and objectives; make sure to discuss (1) the funding opportunity; (2) the principles of capacity building / mentorship
0900 – 0910	**BOHRN Workshop Agenda, Objectives, and Housekeeping** Katie Leahy *Global Systems Engineering*	Provide overview of meeting objectives, scheme of maneuver, and other housekeeping items
Session 1: BOHRN Focus Group Progress and Work		
0910 – 0930	**Understanding the Ecology of Viruses** Jon Epstein *EcoHealth Alliance*	Discuss the challenges and understanding of the ecology of viruses such as Nipah and Ebola
0930 – 0950	**Host/Pathogen Interaction** Jon Towner *CDC- Division of High-Consequence Pathogens and Pathology*	Present on work focusing on viruses in the national reservoir hosts and determine the mechanisms by which the viruses are maintained in nature
0950 – 1010	**Laboratory Response** Brian Bird *UC Davis, School of Veterinary Medicine*	Synergies between the Bench and the Field: Rift Valley Fever and Ebola
1010 – 1030	**Building Policy and Community Outreach Initiatives Based on a Novel Understanding of Who, What, and Why** Susan Tsang *American Museum of Natural History and National Museum of the Philippines*	Discuss efforts to bridge policy gaps between local, national, regional, and international efforts
1030 – 1110	**Focus Area Research Mentor Progress Reports**	A representative or mentor from each group will present their Focus Area

		objectives, its long / short-term goals schedule, and progress Group 1: 10 min Group 2: 10 min Group 3: 10 min Group 4: 10 min
1110 – 1215	**Breakout Groups**	Participants will be broken into the focus area groups; their placement will be pre-arranged by decision of the steering committee and they will have a sticker on the back of their name card; they will be asked to listen in on the focus area group discussion, see if they could contribute to the group's direction
1215 – 1320	**Working Lunch**	
1320 – 1400	**Breakout Group Open Discussion**	Each group will present any changes to their schedules or objectives Group 1: 10 min Group 2: 10 min Group 3: 10 min Group 4: 10 min
Session 2: BOHRN Project Development Work		
1400 – 1430	**Doing Business with BTRP: Pathways to Contracts, Objectives for BOHRN and Beyond** Dr. Martha Stokes *BTRP*	20 Minute presentation of slides that Lance gave in Georgia, plus 1-2 developed with Scott V., plus 10 minutes for questions from the audience; this presentation will queue funding project development for focus area-specific RFPs
1430 – 1600	**Interactive Illustration Hypothesis Mapping Exercise**	Dr. Kingston and Dr. Epstein will facilitate an interactive hypothesis mapping session for the group
1600 – 1715	**Breakout Groups**	Breakout into blended project development groups. These groups will be based on seating arrangement (e.g., tables 1 and 2 will work together) to ensure that we have multi-disciplinary efforts.
1715 – 1730	**Close-out Day 1 and Review Day 2**	
1830 – 2000	**Dinner / Social Event** **Quad Chart / Poster Presentations**	

Day 2

Time	Session	Objectives
0900 – 1130	**Small Group Project Development Work**	Groups will come back to the main room to continue work in the smaller group project development
1000 – 1030	**Working Tea Break**	
1130 – 1300	**Working Lunch Break / Small Group Brief-outs**	
1300 – 1315	**Close-out / Group Discussion**	
TBD	**Steering Committee Meeting**	

Annex 2: Participant list

Name	Country	Organization
Abel Wade	Cameroon	National Veterinary Laboratory, Cameroon
Wanda Markotter	South Africa	University of Pretoria, Dept of Microbiology and Plant Pathology
Benneth Obitte	Nigeria	Texas Tech University
Iroro Tanshi	Nigeria	Texas Tech University
Joram Buza	Tanzania	Nelson Mandela African Institute of Science and Technology
Robert Kityo	Uganda	Makerere University, Kampala
Julian Lutwama	Uganda	Uganda Virus Research Institute
Astghik Ghazaryn	Armenia	Yerevan State University
Ioseb Natradze	Georgia	Ilia State University
Keti Sidamonideze	Georgia	National Center for Disease Control and Public Health -Georgia
Lela Urushadze	Georgia	National Center for Disease Control and Public Health - Georgia
Nesreen Alhmoud	Jordan	Royal Scientific Society
Meryem Lemrani	Jordan	Pasteur Institute in Morocco
Ehab Abu-Basha	Jordan	Jordan University of Science and Technology
Shusmita Dutta	Bangladesh	University of North Bengal
Ariful Islam	Bangladesh	EcoHealth Alliance
Shahanaj Shano	Bangladesh	Jahangirnagar Univeristy
Pilot Dovih	India	National Centre for Biological Sciences
Juliana Senawi	Malaysia	University of Kebangsaan Malaysia
Philip Alviola	Philippines	University of the Philippines-Los Banos
Catalino Demetria	Philippines	Research Institute for Tropical Medicine
Benjamin Lee	Singapore	Duke-NUS, Singapore
Sara Bumrungsri	Thailand	Prince of Songkla University
Pipat Soisook	Thailand	Princess Maha Chakri Sirindhorn Natural History Museum
Supaporn Wacharapluesadee	Thailand	WHO CC for Research and Training in Viral Zoonoses, King Chulalongkorn Memorial Hospital, Thailand
Vu Dinh Thong	Vietnam	Institute of Ecology and Biological Resources
Patrick Ayscue	United States	Metabiota
Brian Bird	United States	University of California- Davis
Bradford Brooks	United States	Metabiota
Jon Epstein	United States	EcoHealth Alliance
Jason Farlow	United States	Metabiotia
Tracey Goldstein	United States	University of California- Davis
Andreas Handel	United States	University of Georgia

Rebekah Kading	United States	Colorado State University
Tigga Kingston	United States	Texas Tech University
Eric Laing	United States	Uniformed Services Health Service University
Kendra Phelps	United States	EcoHealth Alliance
Mariano Sanchez-Lockhart	United States	United States Army Medical Research Institute for Infectious Diseases - Genomic Center
Jonathan Towner	United States	Center for Disease Control and Prevention, Viral Special Pathogens Branch
Susan Tsang	United States	Royal Scientific Society
Marty Stokes	United States	DTRA Biological Threat Reduction Program
Steve Becker	United States	DTRA A&AS
Katie Leahy	United States	Global Systems Engineering
Chris Russell	United States	Global Systems Engineering
Jason Hudson	United States	Global Systems Engineering
Megan Hudson	United States	Global Systems Engineering

From: Megan Hudson
Sent: Tuesday, March 27, 2018 2:52 PM EDT
To: Kading,Rebekah >; ecohealthalliance.org ; dreeder@ >; ecohealthalliance.org ; vkapur
CC: Katie Leahy >; Gano Cohen, Kelsey A CTR DTRA J3-7 (US) >; Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) >; Stokes, Martha M CIV (US) Becker, Stephen M CTR DTRA J3-7 (US) < >; Aleman, Nicki D CTR DTRA PARTNERSHIP AND INSP (US) >
Subject: BOHRN and OHC Invitation
Attachment(s): "BOHRNFactSheet.pdf","JKO SERE ATFP ISOPREP Instructions NOV 2016[1].doc"

All,

You are receiving this email, as part of a formal invitation to attend our BOHRN Steering Committee meeting and the 5th International One Health Congress (OHC) in Saskatoon, Canada. We understand you are very busy people, so please feel free to attend all or portions of the Conference. The OHC 2018 Provisional Conference Schedule can be found here. As previously emailed, CBEP will be doing one conference registration for all those who can attend some or all of the conference. The conference dates for both events will span 20-25 June 18.

Our meeting will take place 20-21 June (location TBD, though likely at the Hilton Garden Inn). Attached is the updated fact sheet, the agenda will follow shortly.

On behalf of Dr. Marty Stoke and Dr. Mary Lancaster, CBEP will be funding your travel and registration to the BOHRN and OHC. Specific instructions may be found below my signature block. Please let us know what portions of the week you will be able to attend. We will need to know what days of the conferences you will be able to attend for hotel room blocks and registration.

We very much hope you will be able to attend our meeting and some or all of the conference thereafter. Please let me know your plans and begin communication with Nicki at your earliest convenience. If you are only planning to stay for part of the OHC, please indicate the dates you will be attending when coordinating your travel.

V/r,

Megan Hudson

Megan Hudson
Task Lead | Global Systems Engineering
6303 Little River Turnpike #208
Alexandria, VA 22312

http://globalsyseng.com

Travel instructions:
Please contact Nicki Aleman NLT **9 April 2018** if you intend to travel; you will likely need to provide her with your passport information, to and from destinations, and travel dates. CBEP's logistics support coordinators will work with you to secure plane reservations. Please note that they try to work with your preferences, but must remain within the boundaries of the Department of Defense regulations for travel. *If your trainings are not completed by the assigned date, funding for travel and conference registration will not be provided.*

B O H R N

The Bat / One Health Research Network

Overview

There is a long tradition of international cooperation in scientific research. Scientific networks can be instrumental to bridge cultural boundaries and build trust, addressing the global threat of emerging infectious diseases. Current trends in scientific research funding, specifically competition for ever-decreasing research budgets, necessitate international collaborations focused around specific and prioritized research questions.

Scientists posit that the Ebola outbreak of 2014 began with a Guinean toddler playing in a bat roost amongst fruit bats that had migrated 2,500 miles from Central Africa. Understanding bat migration patterns, the effect of humans on those patterns, and the challenges of conducting disease surveillance in free-range bat populations, will enable relevant policy makers to better identify, plan, and prepare for the next pandemic. Additionally, research coordinated networks have the ability to significantly impact threat reduction by identifying and prioritizing coordinated approaches to close these and other pressing knowledge gaps.

The Defense Threat Reduction Agency (DTRA) Cooperative Biological Engagement Program (CBEP) is sponsoring a multi-regional disease surveillance research coordinated network to mitigate the threat of bat-associated pathogens of security concern. This network will identify and connect interdisciplinary expertise, convening an agile group to adapt to a wide spectrum of arising challenges and threats. The Bat / One Health Research Network (BOHRN) will enable shared learning and research opportunities, establish new research projects, and facilitate joint applications for funding; thus increasing the opportunity for peer review, especially if a cross-regional and multi-disciplinary team of authors is involved

The BOHRN kick-off meeting coincided with the 2nd International Symposium on Infectious Diseases of Bats in Fort Collins, CO on 29 June 2017. During this meeting, the group began preliminary actions to build a self-sustainable disease surveillance network and identified initial network objectives needed to develop a comprehensive research strategy to address bat-associated disease threats and mitigation solutions.

Network Objectives

- Facilitate interdisciplinary collaboration to identify research goals and needs for bat-borne disease research and broader threat reduction
- Create a common action plan that yields collaborative and sustainable projects which: (1) better inform policy makers; (2) better inform scientific community regarding funding targets and gaps in areas of research and development; (3) better define threat to global health security from bat-associated pathogens; and (4) improve national, regional, and global capacity to detect and respond to pathogens of security concern
- Enable better communication, coordination, and outreach at the research and conservation interface

Approach and Impact

BOHRN has four thematic focus areas, which were characterized and developed into research Working Groups at the kick-off meeting. These Working Groups (described below) will operationalize the network objectives by serving as subdivisions to the overall network to foster multi-national and multidisciplinary participation and mentorship. Each member of the BOHRN will identify with at least one Working Group based on field of research/practice. Working Group members will identify and prioritize research gaps and needs, and research project ideas will be solicited from BOHRN membership to address the identified gaps and needs.

Working Group 1: Host / pathogen biology interactions; specifically: (1) Bat physiology and immunology; (2) Bat pathogen community biology (e.g., co-infections and co-morbidities); and (3) Distribution of pathogens among species

Working Group 2: Pathogen surveillance, diagnostic capacity, and epidemiology; specifically: (1) Molecular epidemiology; (2) Distribution of pathogens geographically and phylogenetically; and (3) Detection, diagnosis, and reporting of bat-associated pathogens

Working Group 3: Ecology (bat, domesticated animal, and wildlife interface); specifically: (1) Bat behavior; (2) Domesticated animal and wildlife behavior, distribution, and movement impact; and (3) The effect of anthropogenic disturbance and modification on pathogen dynamics and spillover risks

Working Group 4: Human-bat interactions; specifically: (1) Hunting and commodity chain (e.g., bushmeat, guano, and pet trade); (2) Ecotourism; and (3) Interactions in human dwellings

Why Bats?

Bats act as natural reservoirs for over 60 pathogens, including some of the world's most deadly viruses, such as Nipah, Hendra, Marburg, and SARS viruses. Understanding the role of bats as a reservoir and the risk of pathogen transmission from bats to humans and other animals could be a key to discovering novel pathogens, mitigating the impact of emerging and re-emerging pathogens, and preventing future pandemics.

There are a number of factors which make bats unique disease reservoirs, including their social behavior, distinct physiology and metabolism, ability to travel long distances, nocturnal activity, species diversity, and long life span (10-20 years). These specific bat characteristics, coupled with the impact of human-mediated interactions and environmental changes, create research challenges to understanding the role of bats in global zoonotic disease ecology. BOHRN w ill create opportunities for policy makers, scientists, conservationists, funders, and students to identify community challenges, develop priority research lists and implement associated action plans that target needs and gaps. The opportunities created will work at all levels to build awareness of bat-associated disease burden and transmission risks and improve the prevention, detection, diagnosis, and reporting of pathogens of security concern.

U.S. DoD and Health Security

BOHRN outcomes will also support the Global Health Security Agenda (GHSA) Zoonotic Disease Action Package, which has a five-year target for countries to adopt measured behaviors, policies, and/or practices that minimize the spillover of zoonotic diseases from lower animals into human populations.

Although not directly involved in implementation, DTRA CBEP supports the GHSA goals and milestones, and synchronizes with GHSA country projects through the DoD GHSA Coordination Cell. DTRA CBEP is the DoD' premier biological nonproliferation division protecting the United States and its allies from especially dangerous pathogens by collaborating with partner countries and the international community to minimize the threat of deliberate, accidental, and natural infectious disease outbreaks through enhanced biosafety, security, and surveillance measures. DTRA CBEP investments build capacity to detect, diagnose, and report disease events and help reduce the magnitude and response costs of biological incidents.

Additionally, DTRA CBEP promotes scientific and technical collaborations among partner nations and the international community in the disciplines of biological safety, security, and surveillance to build constructive and sustainable international partnerships that address threats posed to health security. These science diplomacy-based activities engage scientists in peaceful application of biotechnology; building partner country disease surveillance capabilities; promoting adherence to international codes of conduct, security, and safety; and enhancing transparency and confidence building.

Although DTRA CBEP is committed to supporting BOHRN, there is no guarantee or obligation for DTRA CBEP to fund projects resulting from the network or its members.

Points of Contact

Dr. Mary Lancaster, DTRA CBEP

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Dr. Marty Stokes, DTRA CBEP

Pacific Region Science Lead
martha.m.stokes.civ@mail.mil

BPERN Access Network

https://wss.apan.org/s/DTRA/CTR/BPERN/default.aspx

Fact Sheet References

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16 Nov 2016

JKO – SERE 100 – ATFP – ISOPREP Completion Instructions

- These instructions are for Civilians and Contractors without a Common Access Card (CAC).
- When emailing, use your Work Email address. - Training is not required by Foreign Nationals.

1. JKO Course # JS-US007: Level I Antiterrorism Awareness Training: Valid for 12 Months.
Training can be accessed via link below. You do not need a JKO account to access training.
Click link below. When site opens up, click OK to close DOD Security Banner after reading.
Click on Non-CAC users under JS-007 Level I Antiterrorism Awareness Training, and follow instructions.
https://jkodirect.jten.mil/Atlas2/faces/page/login/Login.seam

2. JKO Course J3TA-US1329, SERE 100.2 Level A SERE Education and Training in Support of the Code of Conduct (FOUO): Valid for 36 Months or AS REQUIRED BY THE FOREIGN CLEARANCE GUIDE. FREQUENCY SUBJECT TO CHANGE.
To complete SERE training follow these instructions. Click on the following link. http://jko.jten.mil/index.html on the page that opens up, click on enter JKO. Read the Security Banner then click OK to close. On the page you are viewing now, under **I DO NOT have a CaC, select Non-Government Personnel/Sponsored Account Registration.**
On the next page, fill out the requested information. In the Reason for Account, after you enter reason, add the CBEP Country Manager and Country you are supporting. Not providing this information will cause delays. Then click submit. My email is John.T.Patterson2.civ@mail.mil.
When you click submit it will send a notice to me. I will verify reason with Country manager and submit request. The JKO office will contact you with your logon information. Once you have obtained your log on information, return to https://jkodirect.jten.mil/Atlas2/faces/page/login/Login.seam to log into JKO. Once logged in, select the Catalog Tab at top of page and enter "SERE" in title/keyword box, and click search. SERE 100.2 Level A SERE Education and Training in Support of the Code of Conduct (FOUO) - (4 hrs) should be listed. Click enroll to access course.
If you get an out of office notice from me, you will have to resubmit your request using the CBEP Country Manager's email address that you are supporting, they can sponsor you. You may want to check before submitting request.

Contact JKO at JKOHelpDesk@jten.mil or 757-203-5654 for access issues.

DO NOT send form by email or regular mail. Once blocks 50-54 are completed the form is classified CONFIDENTIAL. And must be sent using shipping instructions on page 2

3. DD Form 1833 Isolated Personnel Report (ISOPREP): Valid 12 Months or AS REQUIRED BY THE FOREIGN CLEARANCE GUIDE. FREQUENCY SUBJECT TO CHANGE.

If you have a DOD CAC, click on link below and follow instructions to complete your **initial ISOPREP**. You must be on a .mil or .gov domain computer system.
https://prmsglobal.prms.af.mil/prmsconv/Profile/Survey/start.aspx

If you need to update or want to verify your ISOPREP, contact one of individuals listed below.

If you are in the local area, you may contact John.T.Patterson2.civ@mail.mil / 703-767-5938 to arrange completion of your ISOPREP at the CTR office. If you receive an out of office response, you may contact theodore.w.carlson.civ@mail.mil / 703-767-6382 for assistance. Use these same contacts for updates.

If you do not have a DOD CAC, and are not in the local area, fill out DD Form 1833. This can be found by searching online. Instructions are included in form. Finger prints are not required. Section 9 blocks 50-54 should be typed on separate piece of paper and included with the form. Once completed, form is classified as Confidential and must be sent following instructions on page 2. Your SSN is needed. You Blood type is needed. Your DOB is needed. Make sure to follow the instructions for the 4 Statements and the Authentication Number.

Submit two photos, a front view and right side profile view, from the shoulders up. Photos may be sent with the form or the preferred method is to email the photos only to John.T.Patterson2.civ@mail.mil

DO NOT send form by email or regular mail. Once blocks 50-54 are completed the form is classified CONFIDENTIAL. Send using instructions below

Mailing Instructions

Seal package with type of tape to retain postal stamp impressions. Prepare, package, and securely seal classified material in ways to MAXIMIZE evidence of tampering and MINIMIZE undetected deliberate compromise, or risk of accidental exposure. To minimize the risk of exposure of classified information, package documents so that classified material is not in direct contact with the inner envelope or container (e.g., fold so classified material faces together).
Double wrap classified information in two opaque, sealed envelopes, wrappings, or containers, durable enough to properly protect the material from accidental exposure and facilitate detection of tampering.
Do not place classification marking or any other unusual marks on the outer package that might invite special attention to the fact that the contents are classified

After completing form, fold so classified information faces together. Place folded form, disk or photos if you did not email them inside fully addressed and marked package as instructed and shown below.

Form	Inner Package	Outer Package
CONF IDEN TIAL	Full Name CONFIDENTIAL Full Address (Mark Front and Back) ATTN: J3CTB/John Patterson and CTR	Office Name Only Office Address See proper address

Inner Package:

Mark inner package as shown above. Be sure to replace the CTR CBEP Country Managers' name shown with the actual name you are supporting.

- Complete recipients and sender address
- Mark top/bottom and front/ back with CONFIDENTIAL markings.
- Seal package as stated at top of this page.

Place this package inside of another package (outer package).

Outer Package:

Mark outer package as shown above.

- Use only office name and office address. Do not use individual names.
- Do not use markings of any kind indicating classification or that the package contains classified material.
- Seal package as stated at top of this page.
- Send package via USPS, FEDEX, UPS, DHL, etc. Make sure you have a tracking # for Package.
- After sending package notify John.T.Patterson2.civ@mail.mil, and applicable CTR CBEP Country Manager so we are aware to be watching for package.

Use correct address below depending on shipper. Make sure you have a tracking number for your package.

For Registered / Express mail via the US Postal Service	**For Express mail via Federal Express, DHL, UPS**
DEFENSE THREAT REDUCTION AGENCY 8725 JOHN J KINGMAN RD STOP 6201	DEFENSE THREAT REDUCTION AGENCY 6200 MEADE ROAD

FORT BELVOIR VA 22060-6201	FORT BELVOIR VA 22060-526

From: Megan Hudson >
Sent: Tuesday, July 03, 2018 10:43 AM EDT
To: nisreen.hmoud < >; c_demetria < ;
Kading,Rebekah >; tamar_kutateladze ;
ksidamonidze >; l.urushadze ;
spwa ; epstein ;
ian.mendenhall
CC: Stokes, Martha M CIV (US) ; Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) ; Katie Leahy
Subject: BOHRN Meeting Survey

All,

We hope you enjoyed the BOHRN meeting and IOHC. As a follow up to the meeting we have a short survey for you to complete. Your feedback is imperative for moving forward and coordinating the next steps for the TRN. Therefore, if you could please complete the survey NLT Monday, 9 July.

Thank you again for your hard work and participation.

Survey link: https://www.surveymonkey.com/r/BPQWX55

v/r,

Megan

Megan Hudson
Task Lead | Global Systems Engineering
6303 Little River Turnpike #208
Alexandria, VA 22312

http://globalsyseng.com

From: Megan Hudson >
Sent: Thursday, September 06, 2018 10:54 AM EDT
To: cryanp epstein < ; Kading,Rebekah ; vkapur < >; tigga.kingston ; olival ; dreeder ; raina.plowright ; ian.mendenhall@ < ; c demetria < >
CC: Stokes, Martha M CIV (US) ; Katie Leahy >; Aleman, Nicki D CTR DTRA PARTNERSHIP AND INSP (US) ; Becker, Stephen M CTR DTRA J3-7 (US) >
Subject: BOHRN November IMED Meeting Invitation
Attachment(s): "JKO SERE ATFP ISOPREP Instructions NOV 2016.doc","ITO_Information.docx","IMED_BOHRN Concept Note.docx","WG_ProgressChart.docx"

All,

On behalf of Dr. Marty Stokes you are receiving this email, as part of a save the date to attend our BOHRN Steering Committee meeting and International Meeting on Emerging Diseases and Surveillance (IMED) 8 – 12 November 2018 in Vienna, Austria.

Our meeting will take place on 8 – 9 November (hotel/meeting location TBD). The BOHRN steering committee meeting will aim to meet the objectives the group identified in Saskatoon. The following objectives were suggested based on your survey responses:

1. Prioritizes funding needs based on working groups' characterization of gaps and needs, to help organize and develop funding initiatives; and
2. Analyze progress of action plans and their yields establishing collaborate and sustainable projects

To facilitate these objectives, we will be asking each working group to present their progress. The progress updates for each working group are imperative to the outcomes for this meeting.

As discussed during the June BOHRN meeting, an objective of this meeting is to develop our outreach and populate working groups. Please send any nominations of subject matter experts or other participants who would be beneficial to this discussion **no later than 10 September 2018**.

IMED will take place 9 – 12 November at the Hilton Vienna. The 2018 IMED will focus on innovation and changes in political and societal responses to outbreaks. The theme of IMED aligns with our overall BOHRN objectives and we encourage all BOHRN members to stay and participant in the conference. **Therefore, we need you to confirm your attendance to BOHRN and IMED NLT 14 September.**

v/r,

Megan

Megan Hudson
Task Lead | Global Systems Engineering
6303 Little River Turnpike #208
Alexandria, VA 22312

http://globalsyseng.com

Travel instructions:
Please contact Nicki Aleman **NLT 14 September 2018** if you intend to travel; you will likely need to provide her with your passport information, to and from destinations, and travel dates. CBEP's logistics support coordinators will work with you to secure plane reservations. Please note that they try to work with your preferences, but must remain within the boundaries of the Department of Defense regulations for travel.

BOHRN Background

In 2013, CBEP began leveraging, enhancing, and convening TRNs to accelerate its programmatic targets and end states. CBEP employs this approach as a way to connect its active funded research projects with other projects to improve global health security, building consistency in data sets, and facilitate more confident decision-making by policy makers. Relationship-based networks around the globe, made up of interdisciplinary researchers, allow for novel and transformative scientific solutions for the world's high-impact infectious disease threats.

BOHRN connects multidisciplinary and One Health expertise to address research-based capability gaps and threats posed by bat-associated pathogens of security concern. The group maintains the standards of all research networks that are supported by CBEP, in which members convene as a body of experts and researchers to: (1) share information, data, samples, and protocols; (2) coordinate research activities; (3) build training events and awareness-building workshops at all levels of decision-making authority; (4) develop community standards and best research practices; (5) create mentorship-based opportunities for students, trainees, and early-career researchers to convene, present, and share ideas; (6) establish a community of international research leaders and champions; and (7) reduce outbreak and disease transmission risks.

Why Bats?

Scientists hypothesize that some of the world's most deadly emerging zoonotic diseases are found in bats, including Nipah, Hendra, and Marburg viruses. However, because bats contribute significantly to the health and diversity of many environments around the world, a conservation-minded approach to their study is necessary. There are a number of factors which could make bats unique disease reservoirs, including their social behavior, distinct physiology and metabolism, ability to travel long distances, nocturnal activity, species diversity, and long life span (10-20 years, compared with a rat's average life of two years).[1] These special bat characteristics, coupled with the impact of human-mediated interactions and environmental changes, create research challenges to understanding the bat's role in the global zoonotic disease ecology, which is further complicated by being difficult animals to study within a typical laboratory setting.

BOHRN is a global network of conservationists, disease ecologists, and clinical virologists who have organized to better understand how bat-borne disease threats filter through ecological systems. BOHRN creates opportunities for policy makers, researchers, conservationists, funders, and students to identify community challenges, develop priority research lists and associated action plans that target needs and gaps, and work at all levels to build awareness of bat-associated disease burden and transmission risks to improve the prevention, detection, diagnosis, and reporting of pathogens of security concern.[2] This group, under sponsorship from CBEP, has established objectives to collaborate on multi-disciplinary research and establish standards for lab and field research practices.

BOHRN Mission and Vision

BOHRN convenes multi-disciplinary and One Health-focused scientists, policy makers, research scientists, and medical/veterinary practitioners with interests in bat-related research involving pathogens of security concern. The network builds on community standards and best practices for research. BOHRN identifies and shares information on research funding opportunities offered by multiple institutions. Most importantly, this network fosters international relationships among collaborators, agencies, and organizations, which can produce long-term, sustainable partnerships that withstand changes in government and organization budgets, priorities, postures, and policies.

All members play a role in operationalizing the objectives of BOHRN, strengthening linkages and reducing overlap in global research on high-priority pathogens of bats (especially zoonosis) to maximize

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[1] Hayman, David T.S., "As the bat flies," *Science* 02 Dec 2016: Vol. 354, Issue 6316, pp. 1099-1100 http://science.sciencemag.org/content/354/6316/1099

[2] Schountz, Tony, "Immunology of Bats and Their Viruses; Challenges and Opportunities," *Viruses,* 2014 Dec; 6(12): 4880-4901. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4276934/

the efficient use of expertise and resources and accelerate the coordinated development of better disease surveillance and control methods.

BOHRN Objectives

This network will identify and connect interdisciplinary expertise, convening an agile group to adapt to a wide spectrum of emerging challenges and threats. By accomplishing the below objectives BOHRN will enable shared learning and research opportunities, establish new research projects, and facilitate joint applications for funding; thus, increasing the opportunity for peer review, especially if a cross-regional and multi-disciplinary team of authors is involved.

- Facilitate interdisciplinary relationships and collaboration to identify research goals and needs for bat-associated disease research and threat reduction; and
- Unify CBEP regions to create a common action plan that yields collaborative and sustainable projects that achieve the following end states:
    - Better informed policy-makers;
    - Better informed scientific community regarding funding targets and gaps in areas of research and development;
    - Better defined threat to global health security from bat-associated pathogens; and
    - Improved national, regional, and global capacity to detect and respond to pathogens of security concern; and
- Enable better communication, coordination, and outreach at the research and conservation interface.

BOHRN – International Meeting on Emerging Diseases and Surveillance

During the BOHRN meeting, the steering committee voted on options for the next full BOHRN meeting. Several conferences in October – December 2018 were suggested. The group decided that the objectives for the International Meeting on Emerging Diseases and Surveillance (IMED) best met the overall goals of BOHRN. IMED is organized by the International Society for Infectious Diseases and will take place in Vienna, Austria from 9 – 12 November 2018. The conference draft agenda reviews the following objectives: methods and models of disease surveillance, detection and prediction, lessons from epidemic emerging zoonoses, animal health threats biosecurity, agents of bioterrorism and biological warfare infections, and migration of human and animal vector borne diseases. The meeting aims to unite human, veterinary, and environmental specialists on approaches to pathogens in a broad ecological context. These goals align directly to the BOHRN objectives and provide opportunities for the steering committee to socialize the network while gaining tools and information from the interdisciplinary collaboration to aid in accomplishing the working group actions

The BORHN steering committee agreed upon a two-day meeting on 8-9 November to coincide with IMED. The following objectives are suggested:

1. Prioritizes funding needs based on working groups' characterization of gaps and needs, to help organize and develop funding initiatives; and
2. Analyze progress of action plans and their yields establishing collaborate and sustainable projects

The following items are topics for discussion during this meeting:

- Draft initial Request for Approvals
- Develop initiatives for a funding discussion
- Review and begin developing abstracts for working group actions
- Discuss literature review scoping
- Plan and draft agenda for Uganda Training Event
- Read out from Georgia Biological Threat Characterization Discussion (BTCD)
- Identify and catalog existing tool kits for website database
- Develop an approach to outreach and populating working groups
- Report out of working group progress
- Strategy session for future International bat meeting and conferences

Proposed Agenda

Day 1 – 8 November 2018 (Thursday)

- 1000 – 1045 Welcoming Remarks
- 1045 – 1100 House Keeping and Admin
- 1100 – 1130 Updates on BOHRN BTCD
- 1130 – 1145 Working Break
- 1145 – 1300 Updates on Breakout Group Progress
- 1300 – 1400 Lunch
- 1400 – 1600 Breakout Sessions
- 1500 – 1530 Working Break
- 1600 – 1630 Brief-out of Breakout Sessions
- 1630 – 1645 Close-out Discussion

Day 2 – 9 November 2018 (Friday)

- 0900 – 1000 Review of Day 1
- 1000 – 1030 Large Group Discussion – BOHRN Funding
- 1030 – 1045 Working Break
- 1045 – 1145 Breakout Session
- 1145 – 1215 Lunch
- 1215 – 1345 Uganda Training Event
- 1345 – 1415 Large Group Discussion – Future Training Events
- 1415 – 1430 Working Break
- 1430 – 1500 Build Next Meeting Agenda
- 1500 – 1600 Next Steps

Breakout Group Timeline

During the June 2018 One Health Congress and BOHRN meeting in Saskatoon, Canada, meeting attendees “broke out” into four working groups. They were instructed to continue work on the objectives and goals set at previous meetings, creating workplans short and long-term intentions. Due to scheduling issues, all of the working groups were not fully represented, so other members were asked to fill-in for different groups. The following write-up describes the outcomes from the breakout group session. Progress updates from each group will be presented during the November IMED Meeting.

Group 1: Host-Pathogen Biology and Interactions

Group 1: Host-Pathogen Biology and Interactions **Focus Area 1:** Bat physiology and immunology **Focus Area 2:** Bat pathogen community biology (e.g., coinfections and comorbidities) **Focus Area 3:** Distribution of pathogens amongst species **Focus Area 4:** Develop modeling approaches for host dynamics and epidemiology	
MISSION STATEMENT: Explain the determinants of tolerance, transmission, and spillover of pathogens by bats at individual and population levels.	
Objective 1	Complete a systematic review of the knowledge gaps on modeling systems
Objective 2	Identify model systems that are representative of all geographic and phylogenic areas
Objective 3	Evaluate the transmission risk and spillover of pathogens to other animal hosts
Projects or Activities	**Timeline / Responsible Authority / Needs (e.g., funding or other support**
Develop cell lines and bat animal models	Long-term lab study
IgM immunoassay	Long-term lab study
Develop methods for determining the age of bats	Long-term lab/field study
Determine the timing of viral shedding and the effects of environmental stresses	Long-term lab/field study
Determine co-infection in bat species	Long-term lab/field study
Determine temperate versus tropical variables associated with infection (hibernation periods / viral replication)	Long-term lab/field study; study species that live in both temperate and tropical locations; study climate change
Understand climate change in respect to physiology	Long-term lab/field study; study species that live in both temperate and tropical locations; study climate change
Map funding landscape / reach out to program officers from agencies	Short-term project (within 6-months) to map funders Long-term project (within 1-year) to host a funders meeting

	Need to identify funders with different interests in the same biological/ecological system to provide long-term funding
Develop heat stable preservatives	Long-term lab/field study
Develop smaller telemetry and physiology sensors	Long-term lab/field study

Group Notes

Group 1 discussed ways the need to mine existing studies for data, which could extend the longevity of data collection and the breadth of data sets. They additionally requested a funders' meeting to identify other program officers and tech companies that would be interested in BOHRN research projects. The group suggested providing opportunities for training, which could include EDGE at Los Alamos National Laboratory for bioinformatics and next generation sequencing. The group discussed the need to identify funders with different interest in the same biological/ecological system that can provide more longer-term funding and to also engage with biologists from regions that have expertise on bat ecology and history.

Group Research Mentors

Dr. Mary Lancaster, DTRA CBEP

Dr. Jon Epstein (EcoHealth Alliance) *– note: ordinarily works Group 2*

Dr. Lela Urushadze (NCDC, Georgia) *– note: ordinarily works Group 4*

Dr. Joram Buza (Nelson Mandela-African Institute of S&T, Tanzania) *– note: invited, could not attend*

Dr. Vivek Kapur (Penn State University) *– note: invited, could not attend*

Dr. DeeAnn Reeder (Bucknell University) *– note: invited, could not attend*

Dr. Gavin Smith (Duke NUS Medical School, Singapore) *– note: invited, could not attend*

Group 2: Pathogen Surveillance, Diagnostic Capactiy, and Epidemiology

Group 2: Pathogen Surveillance, Diagnostic Capacity, and Epidemiology **Focus Area 1:** Molecular epidemiology **Focus Area 2:** Distribution of pathogens geographically and phylogenetically **Focus Area 3:** Detection, diagnosis, and reporting of bat-associated pathogens **Focus Area 4:** Establish commonly used guidance on sampling	
MISSION STATEMENT: Form regional networks to establish a common methodology for surveillance and sustain the surveillance for both human and animal health. In addition to understanding spillover risk and epidemiology of bats	
Objective 1	Fully establish a baseline of animal health and public health laboratories for equipment, staff, and diagnostic tools
Objective 2	Build awareness amongst the research, public health, and other science communities
Objective 3	Establish a common methodology for surveillance
Projects or Activities	**Timeline / Responsible Authority / Needs (e.g., funding or other support)**
Develop assessment tool and conduct capability assessments in laboratories to establish baseline requirements for conducting NGS and other diagnostic protocols for detecting novel and routine diseases from bats	Timeline: Immediate: identify laboratories to assess (likely National Reference Labs, Ministries or Departments of Public (human) and Animal Health) 1-9 Months: create, distribute, and receive feedback questionnaires from labs 9-12 Months: conduct lab visits (as necessary) to identify inconsistencies and fill in knowledge gaps 12-18 Months: assess data, send feedback to labs, and publish report on findings Needs: Technical support and funding
Conduct outreach through meetings with multisectoral stakeholders and social media	Timeline: Immediate: identify opportunities for side meetings at larger animal and public health events with topics related to diagnostic surveillance; identify POCs to serve on One Health committees 6 Months: present research findings and publications; form country-specific One Health committees to sustain awareness and serve as organizers for regional meetings (e.g., 2-3 Animal and Public Health researchers / university) 12 Months: form outreach teams that can network through social media, perform website updates, and survey additional information from other networks and associations Needs:

	Identify potential funders for logistics and planning support; need technical support for social media, web design, and communications
Establish a common methodology for diagnostic surveillance	Timeline: Long-term, after completion of needs assessment tool and implementation 2+ years to implement Needs: Funding for equipment and technical training; resources to develop EQA

Group Notes

Group 2 worked to emphasize the need for commonality (technique, tools, communication, and lexicon) and communication. They worked to offer a plan that identifies baseline tools for lab-based disease surveillance and sets up a system of multi-sectoral outreach and communication.

Group Research Mentors

Dr. Catalino Demetria (Research Institute for Tropical Medicine, Philippines)

Dr. Tamar Kutateladze (NCDC, Georgia)

Dr. Jon Epstein (EcoHealth Alliance) *– note: worked in Group 1*

Dr. Abel Wade (National Veterinary Laboratory, Cameroon) *– note: invited, could not attend*

Dr. Keti Sidamonidze (NCDC, Georgia) *– note: worked in Group 3*

Group 3: Ecology Setting (Bat, Domesticated Animals, and Wildlife Interface)

Group 3: Ecology Setting (Bat, Domesticated Animals, and Wildlife Interface) **Focus Area 1:** Bat behavior, distribution, and movement **Focus Area 2:** Domesticated animals and wildlife behavior, distribution, and movement and impact on interaction with bats **Focus Area 3:** Effect of anthropogenic disturbance and modification on pathogen dynamics and spillover risk	
MISSION STATEMENT: Define how and to what extent the ecological context of bats, and human influence on that context influence pathogen dynamics and spillover threats.	
Objective 1	Improve coordination at the One Health / conservation interface
Objective 2	Define ecological principles that could inform spillover threats
Objective 3	Conduct conservation-minded messaging and outreach
Projects or Activities	**Timeline / Responsible Authority /** **Needs (e.g., funding or other support)**
Quantify interdisciplinary relationship through assessment of publications that feature animal and/or public health, zoonotic disease focus and awareness	Timeline: 6-months post-identification of search parameters Needs: Require BOHRN help in defining search parameters (set as agenda item for next meeting) Research and lit review assistance
Define lit review search parameters for study	Timeline: 6-months Needs: Identify target journals for publication; research guidelines for conducting and publishing a lit review
Publish position paper advocating for improved relationships amongst conservation and One Health communities and suggesting collaborative research projects as a way to bridge differences	Timeline: 1-year (NLT summer 2019) Needs: Research assistance
Develop a repository of tool kits, safety and research guidelines for protecting human and bat health; publish available materials on the BOHRN website	Timeline: 6-months to collect information into training guides for use at field workshops

	Needs: Research assistance; meeting support
Conduct tactical field training activities and a “train the trainer” model	Timeline: 6-months (next BOHRN meeting) establish goals and objectives 9-months establish first training event (Uganda) Needs: Planning / funding / logistics support Funding support for implementation
Build case-control studies for training purposes in messaging	Timeline: 6-months for use during training events Needs: BOHRN group support for case-control study ideas
Participate in One Health / conservation conference panels	Timeline: International Bat Research Conference (IBRC) June 2019 Needs: Participation from BOHRN

Group Notes

Group 3 focused on engaging the ecological community and analyzing frameworks for pathogen research through assessing One Health interactions and developing workplans to include conferences for outreach. Their workplan offers the ability to establish key messages throughout the ecological community.

Group Research Mentors

Dr. Rebekah Kading (Colorado State University)

Dr. Keti Sidamonidze (NCDC, Georgia) *– note: ordinarily works in Group 2*

Dr. Paul Cryan (USGS Fort Collins Science Center) *– note: invited, could not attend*

Dr. Tigga Kingston (Texas Tech University) *– note: invited, could not attend*

Dr. Robert Kityo (Makerere University, Uganda) *– note: invited, could not attend*

Group 4: Human-Bat Interactions

Group 4: Human-Bat Interactions	
Focus Area 1: Human behavioral risk characterization **Focus Area 2:** Hunting and commodity chain (e.g. bushmeat, guano, and pet trade) **Focus Area 3:** Ecotourism **Focus Area 4:** Interactions in human dwellings	
MISSION STATEMENT: Characterize relationships and interactions between bats and humans and communicate findings to key stakeholders and communities.	
Objective 1	Identify and characterize high-risk interfaces
Objective 2	Develop risk maps to assess existing data and validate risks
Objective 3	Communicate findings to key stakeholders
Objective 4	Develop and test policy interventions for specific human bat interfaces
Projects or Activities	**Timeline / Responsible Authority / Needs (e.g., funding or other support)**
Convene a series of funders' meetings	Timeline: 12 months Needs: Assessment of available funders and timeline of BOHRN projects needing funding Funding platform on BOHRN website
Conduct survey that identifies risk groups and interfaces	Timeline: 12 months Needs: Literature assessment of current risk groups and interfaces
Develop risk map	Timeline: 12 – 36 months Needs: Literature review Research assistance
Conduct literature / research review	Timeline: 6 months Needs: Research assistance
Create a database of expertise, active research projects and activities	Timeline: 36 months Needs: Funding for database creation Development of platform on BOHRN website
Perform a seasonality study	Timeline: 36 months Needs: Research assistance Funding

Group Notes
Group 4 focused on a series of projects that would help assess the risk groups and characterize the interactions between bats and humans. Long-term the group's focus is to develop a way to effectively communicate these findings to stakeholders and the community

Group Research Mentors
Dr. Ian Mendenhall (Duke-NUS)
Dr. Supaporn Wacharapluesadee (WHO CC, King Chulalongkorn Medical Hospital, Thailand)
Dr. Nesreen Alhmoud (Royal Scientific Society, Jordan) *– note: worked in Group 3*
Dr. Lela Urushadze (NCDC, Georgia) *– note: worked in Group 1*
Dr. Kevin Olival (EcoHealth Alliance) *– note: invited, could not attend*

STEERING COMMITTEE MEMBERS		
Mendenhall	Ian	Duke-NUS, Singapore
Epstein	Jonathan	EcoHealth Alliance, U.S.
Kading	Rebekah	Colorado State University, U.S.
Urushadze	Lela	R. Lugar Center for Public Health Research, National Center for Disease Control and Public Health (NCDC), Georgia
Kutateladze	Tamar	R. Lugar Center for Public Health Research, National Center for Disease Control and Public Health (NCDC), Georgia
Sidamonidze	Keti	R. Lugar Center for Public Health Research, National Center for Disease Control and Public Health (NCDC), Georgia
Wacharapluesadee	Supaporn	WHO CC for Research and Training in Viral Zoonoses, King Chulalongkorn Medical Hospital, Thailand
Demetria	Catalino	Research Institute for Tropical Medicine (RITM), Philippines
Alhmoud	Nesreen	Royal Scientific Society, Jordan
Buza	Joram	Nelson Mandela African Institute of Science and Technology, Tanzania
Kapur	Vivek	Penn State University, U.S.
Wade	Abel	National Veterinary Laboratory of Cameroon (LANAVET)
Kingston	Tigga	Texas Tech University
Cryan	Paul	USGS Fort Collins Science Center, U.S.
Reeder	DeeAnn	Bucknell University, U.S.
Smith	Gavin	Duke-NUS, Singapore
Kityo	Robert	Makerere University, Uganda
Plowright	Raina	Montana State University, U.S.

From: Kingston, Tigga
Sent: Thursday, September 17, 2020 9:50 AM EDT
To: nisreen.hmoud < ; joram.buza ;
cryanp ; c_demetria >; epstein
ecohealthalliance.org>; Kading,Rebekah >; vkapur
; Kingston, Tigga ; kityrob >;
tamar kutateladze >; ian.mendenhall
>; ecohealthalliance.org >; dreeder
; ksidamonidze < ; gavin.smith
>; l.urushadze >; spwa
>; abelwade >; katie.leahy
>; martha.m.stokes. <
CC: martha.m.stokes.civ ; Kading,Rebekah < >;
Guzal Masharipova
Subject: BOHRN STEERING COMMITTEE - membership, photos and profiles

Hi everyone
I hope this finds everyone well and safe!

You should have recently received an email from Rebekah inviting everyone that has participated in BOHRN activities to join the member directory. I see that most of you have already done so – thanks! This is a friendly reminder with the info again on how to do this at the bottom of the email.

Other questions for the Steering Committee

a. Confirm that you are OK with your photo on the Steering Committee page https://www.bohrn.net/member
b. Update your SC profile – if you click on your photo or name you come to your page. (here is mine, which I need to update. https://www.bohrn.net/tigga-kingston). If you would like to update it, please send through as a word file to Guzal Masharipova (copied here). Guzal is our wizard behind the website and has worked some miracles to get the membership directory plugged in and is now updating other elements of the website.

Thank you so much! I think Marty will update the SC more broadly with what is going on with BOHRN in the near future – there were budget cuts early in the year, changes in leadership at DTRA BTRP, but it looks like the dust is settling and now is a good time for BOHRN to be active and secure a prominent place in the revamped program/portfolio.

Lastly, BOHRN is a member of the Global Union of Bat Diversity Networks (GBatNet) that brings together 14 networks to secure sustainable bat populations https://gbatnet.blogspot.com/p/about.html. GBatNet recently received support from the US's National Science Foundation for five years which will provide great opportunities for BOHRN to interact with the rest of the global bat research community. You can read the public abstract here https://www.nsf.gov/awardsearch/showAward?AWD_ID=2020595&HistoricalAwards=false

If you have any questions, please do get in touch.

Best
Tigga

Tigga Kingston, PhD
she/her/hers
Professor
Department of Biological Sciences
Texas Tech University
Lubbock, TX 79409-3131
USA

http://kingstonlab.org
http://www.seabcru.org

Here is a reminder on the how to join the membership directory

1. Go to https://www.bohrn.net
2. Click on "Join"
3. Create an account, fill out your profile
4. Check the boxes to affirm that you agree with having your information visible to others within the member page, and with the BOHRN mission statement (above)
5. Click "Continue" to be brought to the Members page.
6. Your profile will automatically be entered into the directory, butthis may take a few hours to sync and be visible on the website.
7. From the Members page you should be able to view other member profiles as well as search the directory.

Please feel free to spread the word, and encourage trainees/students/post-doctoral researchers on your teams to join!!

From: Jon Epstein ecohealthalliance.org>
Sent: Monday, July 22, 2019 7:01 PM EDT
To: Wade Abel < >; Nisreen Alhmoud < >; joram buza
Paul Cryan >; Catalino Demetria ; Kading,Rebekah
; Kingston, Tigga <t >; Robert Kityo < Ian
MENDENHALL PhD >; Kevin Olival, PhD Plowright,
Raina >; Tamar Kutateladze ; DeeAnn Reeder
Keti Sidamonidze < ; Gavin Smith ;
Lela Urushadaze ; Supaporn Wacharapluesadee <
CC: Katie Leahy >; Stokes, Martha M. < >; Megan Hudson
>
Subject: BOHRN steering committee - preparation for data discussion

Dear BOHRN Steering Committee Members,
As part of our upcoming meeting, Marty and Katie would like us to discuss data curation and data standardization for BOHRN projects. The plan is to begin the discussion during the SC meeting, and then have a broader discussion, on day three, with the full group. On Sunday, Noam Ross from EHA will present some specific ideas around data standardization to kick start the discussion, focusing on how we might approach developing a common database or data collection standard that can be used across BOHRN projects to facilitate broader analyses. Noam works with Kevin on the PREDICT Modeling & Analytics team and has substantial experience with data management and curation.

We'll also discuss whether and how we might want to make existing datasets available to the BOHRN network, to create opportunities for scientists to leverage them to develop new projects or perform new analyses. For this part, Marty has requested that we come prepared with a list or description of datasets, (e.g. those already published) that we have in hand that could be made available to the BOHRN network.

If you have any questions, don't hesitate to reach out to Katie Leahy Marty, or me. I look forward to seeing you all in Phuket soon.

Safe travels.

Cheers,
Jon

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street, Ste. 1701

New York, NY 10001

web: ecohealthalliance.org

From: Megan Hudson >
Sent: Monday, November 19, 2018 4:33 PM EST
To:

Kading,Rebekah

Subject: BOHRN Workshop Feedback

Dear all,

We hope you enjoyed the BOHRN workshop and found it as productive as we did. As a follow up to the workshop we have a short survey for you to complete. Your feedback is imperative for moving forward and coordinating the next steps for the BOHRN. Therefore, we would appreciate it if you could please complete the survey NLT Monday 26 November.

Thank you again for your hard work and participation this past week.

Survey link: https://www.surveymonkey.com/r/9CZ5MKH

Kind Regards,

Megan

Megan Hudson
Task Lead | Global Systems Engineering
6303 Little River Turnpike #208
Alexandria, VA 22312

http://globalsyseng.com

From: Katie Leahy >
Sent: Sunday, January 28, 2018 10:28 PM EST
To: lance.r.brooks6.civ ; Newman, Carl I CIV DTRA J3-7 (US) <carl.i.newman.civ >; Lancaster, Mary J CIV (US) >; christopher.r.lewis ; Kading,Rebekah ; DeeAnn Reeder Cryan, Paul ; Vivek Kapur >; Gavin James Smith ; Tigga Kingston ; abelwade Ian Mendenhall tamar kutateladze Keti Sidamonidze ; Lela Urushadze < ; joram.buza c demetria >; Kevin Olival < Jon Epstein >
CC: Stokes, Martha M CIV (US) >; Simmi Ghai ; S Wacharapluesadee >
Subject: BPERNet: Transportation Times and Other Useful Information (30 and 31 January 2017)

Hello, everyone! Welcome to Bangkok. On behalf of the Executive Committee (Dr. Martha Stokes and Dr. Mary Lancaster), we are so pleased that you are able to join us this week for our BPERNet planning meeting and other PMAC activities.

Please use this email as your resource for information regarding transportation, logistics, and other coordinating information for 30 January – 31 January.

30 January – BPERNet Meeting at Chulalongkorn Hospital

1. **The bus will depart from the Renaissance Hotel promptly at 0800** ; please be in the lobby for head count at 0745
2. We will provide coffee and light refreshment during the meeting; you will take lunch at one of the many canteen options at the hotel; please bring about 200 - 300 thai baht (~10 USD) for lunch

31 January – PMAC / BPERNet Field Trip

1. **The bus will depart from the Renaissance Hotel promptly at 0630** ; please be in the lobby for head count at 0615; please make sure that you are on time, as we are caravanning with a delegation from the Centara Hotel and will receive a police escort to move us quickly through traffic
2. We will provide a box breakfast for the bus ride
3. Please make sure that you dress appropriately for this field trip; we strongly suggest covered shoes and loose, comfortable clothing; in addition to this mode of dress we also suggest that you bring accompaniments for spending a day outdoors amongst bat roosts; such as:
    a. Hat
    b. Sunscreen
    c. Sunglasses
    d. Bug spray
    e. Water bottle

We will provide information regarding the Ambassador's reception at the close of tomorrow's meeting.

Again, we are so excited to have you all here. Please do not hesitate to reach out to me or Megan Hudson (copied) if you have any questions.

V/r,

Katie Leahy

Katie Leahy
Program Manager | Global Systems Engineering
6303 Little River Turnpike, Suite 208
Alexandria, VA 22305

http://globalsyseng.com

From: Megan Hudson
Sent: Monday, February 05, 2018 10:32 AM EST
To: BounheuangK < >; cryanp < >; Kading,Rebekah < >; vkapur >; ecohealthalliance.org ; ecohealthalliance.org < ; ian.mendenhall@ ; l.urushadze gavin.smith nus.edu.sg < abelwade ; c demetria >; spwa ; kityrob >; tamar_kutateladze >; nisreen.hmoud ; joram.buza >; Tigga Kingston >; DeeAnn Reeder >; Keti Sidamonidze >; jason >
CC: martha.m.stokes >; mary.j.lancaster >; Katie Leahy
Subject: BPERNet Follow Up

All,

We hope you enjoyed the last week and found the BPERNet meeting and field trip as productive as we did. As a follow up to the meeting we have a short survey for you to complete. Your feedback is imperative for moving forward and coordinating the next steps for the RCN. Therefore, if you could please complete the survey NLT Friday, 9 Feb.

Thank you again for your hard work and participation this past week.

Survey link: https://www.surveymonkey.com/r/GTJSTJV

v/r,

Megan

Megan Hudson
Project Manager | Global Systems Engineering
6303 Little River Turnpike #208
Alexandria, VA 22312

http://globalsyseng.com

From: Megan Hudson >
Sent: Tuesday, March 13, 2018 8:56 AM EDT
To: Tamar Kutateladze Kading,Rebekah < >; DeeAnn Reeder ; Cryan, Paul >; Vivek Kapur Gavin James Smith abelwade >; Ian Mendenhall Keti Sidamonidze >; Lela Urushadze >; c_demetria >; Jon Epstein ecohealthalliance.org>; cryan.paul >; Kingston, Tigga ; S Wacharapluesadee >; Kevin Olival ecohealthalliance.org>
CC: Stokes, Martha M CIV (US) >; Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) >; Katie Leahy
Subject: BPERNet Name Change

All,

Thank you for you participation in our survey to consider renaming the BPERNet. From your responses and submitted words to consider, we have decided to move forward with Bat One Health Research Network, BOHRN.

In the next few weeks more information will be rolled out to include the start of an information sharing website. We are still actively planning for a meeting as part of the One Health Congress in June and will follow up with information.

v/r,

Megan

Megan Hudson
Task Lead | Global Systems Engineering
6303 Little River Turnpike #208
Alexandria, VA 22312

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From: Katie Leahy
Sent: Wednesday, February 14, 2018 9:45 AM EST
To: Tamar Kutateladze ; Kading,Rebekah < >; DeeAnn Reeder ; Cryan, Paul < ; Vivek Kapur >; Gavin James Smith ; abelwade < >; Ian Mendenhall < >; Keti Sidamonidze >; Lela Urushadze c_demetria >; Jon Epstein ecohealthalliance.org>; cryan.paul ; Kingston, Tigga ; S Wacharapluesadee ; Kevin Olival ecohealthalliance.org>
CC: Stokes, Martha M CIV (US) Lancaster, Mary J CIV (US) >; Megan Hudson
Subject: BPERNet Read-out
Attachment(s): "Bangkok BPERNet ExecSum_v3.docx"

All,

Please find the draft report from our meeting last week. This report includes an executive summary, action items, participant list, working group outcomes, lessons learned from your feedback, and the original slides from the end-of-day brief-out.

We ask that you provide constructive comments (e.g., content changes) no later than 20 February 2018. It is our intent to adjudicate and incorporate any comments with Mary and Marty and then publish a final report on 22 February 2018.

Also, thank you, to everyone who provided feedback via the survey monkey poll. We will be incorporating all of your comments into our meetings going forward.

V/r,

Katie Leahy

Katie Leahy
Program Manager | Global Systems Engineering
6303 Little River Turnpike, Suite 208
Alexandria, VA 22305

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TABLE OF CONTENTS

MEETING OVERVIEW

EXECUTIVE SUMMARY

The Bat-associated Pathogen and Ecology Network (BPERNet) Executive and Steering Committees met as a side meeting to the Prince Mahidol Award Conference (PMAC) on 30 January 2018 at the Chulalongkorn Hospital and University in Bangkok, Thailand. This meeting served as a follow-up to its kick-off meeting in Fort Collins, CO in June 2017, where the group chartered research objectives and terms of agreement. Members of the Executive Committee (EC) and the Steering Committee (SC) chairmen developed an agenda to meet the following objectives: (1) define working group focus areas, resource needs, and outreach plans; (2) build strategy maps to identify, prioritize, and address BPERNet research gaps and needs; and (3) discuss short and long-term processes to collect and collate applications to the network. A complete agenda from the meeting in addition to a list of its participants may be found in **Annex A** and **Annex B**, respectively.

The meeting kicked off with welcome remarks from Professor Sutep Gonlachanvit; followed by a review of the interim progress in developing the group Terms of Reference. The Executive Committee leads, Dr. Martha Stokes (CBEP SEA Science Lead) and Dr. Mary Lancaster (CBEP Africa Science Lead) facilitated a review of the network objectives, outlined progress since its last meeting, and set the guidelines for the meeting. Participants then broke out into their research focus areas to begin developing their strategic maps that outlined what the working group should achieve, how success will be measured, risks and needs, and a list of investments, activities and projects to accelerate short and long-term objectives.

Ultimately, meeting organizers and facilitators agreed that the meeting achieved its objectives. Working within their focus group areas, and then interactively using the World Café Method, they were able to develop ambitious multi-year strategies and characterize associated challenges and risks to achieving their goals. The group agreed on the importance of its momentum to develop supportive structures for communication and outreach both internally and externally to firmly establish itself as a unique global network of multi-disciplined researchers who aim to answer complex questions at the nexus of One Health.

The meeting's success is evident in the responses from the SC. The SC was given an opportunity to provide feedback via an anonymous survey shortly after the conclusion of meeting. Unanimously the group agreed that the meeting was productive and outlined a path forward for BPERNet. All members noted that their contributions were beneficial and there is consensus about taking steps to moving forward with research and publications. The survey was sent to all participants via email and a summary of the responses can be found below.

BACKGROUND

In 2014, the Defense Threat Reduction Agency (DTRA) Cooperative Biological Engagement Program (CBEP) began leveraging, enhancing, and convening research networks to accelerate its programmatic and research driven targets and end states. CBEP uses this approach as a way to connect its active funded research projects with other projects to help influence effective change for global health security; translating data into policy. Further, by using relationship-based research networks around the globe, made up of interdisciplinary relationships, it will allow for novel and transformative scientific solutions for the world's largest infectious disease threats.

The Bat-associated Pathogen and Research Network (BPERN) is a CBEP research network that connects multidisciplinary and One Health expertise to address challenges and threats posed by bat-associated pathogens of security concern. The BPERN maintains the standards of all research networks that are supported by CBEP, in which members convene as a body of experts and researchers to: (1) share information, data, samples, and protocols; (2) coordinate research activities; (3) build training events and awareness-building workshops at all levels of decision-making authority; (4) develop community standards and best research practices; (5) create mentorship-based opportunities for students, trainees, and early-career researchers to convene, present, and share ideas; (6) establish a community of international research leaders and champions; and (7) reduce outbreak / transmission risk.

Some of the world's most deadly emerging zoonotic diseases are found in bats, including Nipah, Hendra, and Marburg viruses. There are a number of factors which make bats unique disease reservoirs, including their social behavior, distinct physiology and metabolism, ability to travel long distances, nocturnal activity, species diversity, and long life span (10-20 years, compared with a rat's average life of two years).[1] These special bat characteristics, coupled with the impact of human mediated interactions and environmental changes, create research challenges to understanding the bat's role in the global zoonotic disease ecology, which is further complicated by being difficult animals to control within a typical laboratory setting. The BPERN creates opportunities for policy makers, researchers, conservationists, funders, and students to identify community challenges, develop priority research lists and associated action plans that target needs and gaps, and work at all levels to build awareness of bat-associated disease burden and transmission risks to improve the prevention, detection, diagnosis, and reporting of pathogens of security concern.[2]

MISSION AND VISION

The BPERNet brings together a multidisciplinary and One Health-focused group of scientists, policy makers, research scientists, and medical/veterinary practitioners with interests in bat-related research involving pathogens of security concern. The network builds on community standards and best practices for research. The BPERNet identifies and shares information on research funding opportunities offered by multiple institutions. Most importantly, this network fosters international relationships among collaborators, agencies, and organizations, which can produce long-term, sustainable partnerships that withstand changes in government and organization budgets, priorities, postures, and policies.

All members play a role in operationalizing the objectives of the BPERNet, strengthening linkages and reducing overlap in global research on high-priority pathogens of bats (especially zoonosis) to maximize the efficient use of expertise and resources and accelerate the coordinated development of better disease surveillance and control methods.

---

[1] Hayman, David T.S., "As the bat flies," *Science* 02 Dec 2016: Vol. 354, Issue 6316, pp. 1099-1100 http://science.sciencemag.org/content/354/6316/1099

[2] Schountz, Tony, "Immunology of Bats and Their Viruses; Challenges and Opportunities," *Viruses,* 2014 Dec; 6(12): 4880-4901. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4276934/

NETWORK OBJECTIVES

This network will identify and connect interdisciplinary expertise, convening an agile group to adapt to a wide spectrum of arising challenges and threats. By accomplishing the below objectives BPERNet will enable shared learning and research opportunities, establish new research projects, and facilitate joint applications for funding; thus, increasing the opportunity for peer review, especially if a cross-regional and multi-disciplinary team of authors is involved.

- Facilitate interdisciplinary relationships and collaboration to identify research goals and needs for bat-associated disease research and disease threat reduction; and

- Unify CBEP regions to create a common action plan that yields collaborative and sustainable projects that achieve the following end states:

  (1) better informed policy-makers;

  (2) better informed scientific community regarding funding targets and gaps in areas of research and development;

  (3) better defined threat to global health security from bat-associated pathogens; and

  (4) improved national, regional, and global capacity to detect and respond to pathogens of security concern; and

- Enable better communication, coordination, and outreach at the research and conservation interface.

OUTCOMES FROM RESEARCH FOCUS AREAS BREAKOUT SESSIONS

OPENING COMMENTS

Mr. Lance Books, Division Chief, DTRA CBEP and Professor Sutep Gonlachanvit, Deputy Director of Medicine and Research King Chulalongkorn Memorial Hospital, co-opened the BPERNet meeting by emphasizing the importance of continuing the RCN for the benefit of the One Health mission. The opening message conveyed the need for continuing infectious disease surveillance and providing opportunities to make new connections through research. Both agreed that the BPERNet ensures the future of interdisciplinary scientific research and provides a venue to address global issues.

MEETING FORMAT AND LESSONS LEARNED

The goals of this BPERNet meeting were:

(1) Define working group focus areas, resource needs, and outreach plans;

(2) Build strategy maps to identify, prioritize, and address BPERNet research gaps and needs; and

(3) Discuss short-term and long-term processes to collect and collate applications to the network

These objectives were set as the "true north" for this meeting, providing a target for participants to think about success from the beginning. General meeting instructions emphasized the importance of working collaboratively, but to also think about general limitations that have inhibited research goals. Emphasis was added that these objectives should be owned by the entire group.

Additionally, the SC worked to finalize the Terms of Reference for Trusted Agents (TORFTA). The SC agreed that the TORFTA will remain a living document and that will be reviewed annually.

Based on participant feedback and observations from event planners, the EC and SC chairs agree that future meetings should be longer, with more interactive portions for strategy building and collaboration exercises. One idea is to develop a scenario (based on a case-study) to engage a multi-disciplinary group through different phases or turns of response. Event organizers felt that presentations from members of the group on their current research interests or funded projects would help others to understand linkages and dependencies in their research. Event organizers have documented all lessons learned and changes will be implemented for future meetings.

AGENDA

The meeting agenda was designed to create two breakout sessions to guide working groups through a single strategy map. The morning session included a large group review of the working group research areas and creation of cross-cutting themes. Working groups then moved into their research areas to develop a mission statement, identify objectives, and highlight needs. The afternoon breakout group session had research areas developing initiatives for steps forward and identifying responsibility for these initiatives. After each session, the world café was used as a method to share the group's findings. Members of each group rotated to the other working groups to hear from a group representative and provide feedback on each topic. The second breakout group was followed by a short presentation of findings and a large group discussion on next steps. The full breakout of the agenda can be found in Annex B.

CROSS-CUTTING THEMES

Prior to breakout sessions, the SC worked to identify cross-cutting themes among all four working group areas. The SC agreed these themes were inclusive of the needs of all working groups and would help the RCN in developing outreach plans and strategy maps.

Cross-cutting themes from the focus area group discussion included:

- Communication, outreach, and advocacy of group goals to decision and policy makers;
- Standardizing common language;
- Optimizing database management and IT networks;
- Analyzing modeling; and
- Workforce development

Additionally, the objectives each working group identified highlight a need to research and publish knowledge gaps and identify the effects of spillover on human and animal health.

WORKING GROUP RESEARCH FOCUS AREA

Prior to breakouts; a whole group discussion outlined and defined the working group research focus areas. Below are the focuses of each group along with the research mentors for each group.

WORKING GROUP 1: HOST/PATHOGEN BIOLOGY AND INTERACTIONS

- Bat Physiology
- Bat Immunology
- Bat Pathology and pathophysiology
- Bat Pathogen Community Ecology (Co-infections and Co-morbidities)
- Distribution of Pathogens Among Species
- Develop Modeling Approaches for Host Dynamics and Epidemiology

WORKING GROUP 1 RESEARCH MENTORS

- Dr. Joram Buza, Nelson Mandela African Institute of Science and Technology, Tanzania
- Dr. Vivek Kapur, Penn State University, U.S.
- Dr. DeeAnn Reeder, Bucknell University, U.S.
- Dr. Gavin Smith, Duke-NUS, Singapore
- Dr. Mary Lancaster, DTRA CBEP, U.S.

WORKING GROUP 2: PATHOGEN SURVEILLANCE, DIAGNOSTIC CAPACITY, AND EPIDEMIOLOGY

- Molecular Epidemiology
- Distribution of Pathogens Geographically and Phylogenetically
- Detection, Diagnosis, and Reporting of Bat-associated Pathogens
- Establish Commonly Used Guidance on Sampling

WORKING GROUP 2 RESEARCH MENTORS

- Dr. Catalino Demetria, Research Institute for Tropical Medicine, Philippines
- Dr. Jon Epstein, EcoHealth Alliance, U.S.
- Dr. Tamar Kutateladze, National Center for Disease Control and Public Health, Georgia
- Dr. Abel Wade, National Veterinary Laboratory, Cameroon
- Dr. Keti Sidamonidze, National Center for Disease Control and Public Health, Georgia

WORKING GROUP 3: ECOLOGY SETTING (BAT, DOMESTICATED ANIMALS, AND WILDLIFE INTERFACE)

- Bat Behavior, Distribution, and Movement
- Domesticated Animals and Wildlife Behavior, Distribution, and Movement impact on Interaction with Bats
- Effect of Anthropogenic Disturbance and Modification on Pathogen Dynamics and Spillover Risk

WORKING GROUP 3 RESEARCH MENTORS

- Dr. Paul Cryan, United States Geological Survey Fort Collins Science Center, U.S.
- Dr. Tigga Kingston, Texas Tech University, U.S.
- Dr. Rebekah Kading, Colorado State University, U.S.
- Dr. Eiichi Hondo, Obihiro University of Agriculture and Veterinary Medicine, Japan

WORKING GROUP 4: HUMAN-BAT INTERACTIONS

- Human Behavioral Risk Characterization
- Hunting and Commodity Chain
- Ecotourism
- Interactions in Human Dwellings

WORKING GROUP 4 RESEARCH MENTORS

- Dr. Kevin Olival, EcoHealth Alliance, U.S.
- Dr. Ian Mendenhall, Duke-NUS, Singapore
- Dr. Supaporn Wacharapluesadee, King Chulalongkorn Memorial Hospital, Thailand
- Dr. Lela Urushadze, National Center for Disease Control and Public Health, Georgia
- Dr. Nesreen Alhmoud, Royal Scientific Society, Jordan
- Dr. Marty Stokes, DTRA CBEP, U.S.

OUTCOMES FROM RESEARCH FOCUS AREA BREAKOUT SESSIONS

BRIEF-OUT FROM WORKING GROUP SESSIONS

Working within their focus group areas, each develop mission statements, multi-year objectives, measurements for success, and identified overall challenges to success. In the table below, mission statements convey the group's long-term overarching goal while multi-year objectives are each outlined with a corresponding measure for success. Finally, the groups identified key challenges to the overall success of their work. The below table reflects a summary of the key findings from the breakout groups and world café. For the original working out-brief please reference Annex C.

Working Group 1 Mission: Explain the intrinsic and extrinsic characteristics that make certain bats susceptible and spread certain diseases and accurately assess the risk of spillover to another animal host.

Objectives	Measurements	Overall Challenges
Objective 1: Complete a systematic review of the knowledge gaps on modeling systems. **Objective 2:** Identify modeling systems that are representative of all geographic and phylogenetic areas. **Objective 3:** Evaluate the transmission risk and spillover of pathogens to another animal host.	**Objective 1:** Publish systematic review of modeling systems and knowledge gaps that were defined. **Objective 2:** Model system is defined, characterized, and validated. **Objective 3:** Intrinsic and extrinsic risk factors are identified for major diseases and geographic areas.	• Objectives require a multidisciplinary team. • Consortia would be needed for model systems review and validation.

Working Group 2 Mission: Form regional networks to establish a common methodology for surveillance and sustain the surveillance for both human and animal health. In addition to understanding spillover risk and epidemiology of bat pathogens.

Objectives	Measurements	Overall Challenges
Objective 1: Create gap analysis of diagnostic tools. **Objective 2:** Create outreach to various groups of researchers and create awareness among the public and science community. **Objective 3:** Establishing a common methodology for surveillance.	**Objective 1:** Publish systematic review understanding the epidemiology of bat pathogens. **Objective 2:** Formation of regional networks. **Objective 3:** Fully understanding the risk of spillover and developing a set of standards for surveillance.	• The logistics and bureaucracy of creating a multidisciplinary team. • Funding to support the efforts to standardize surveillance.

Working Group 3 Mission: Define how and to what extent the ecological context of bats, and human influence on that context, influence pathogen dynamics and spillover threats		
Objectives	**Measurements**	**Overall Challenges**
Objective 1: Engage the ecological community to define system uniqueness and interdependencies. **Objective 2:** Advocate for ecological design and analysis frameworks to pathogen research. **Objective 3:** Build capacity for disease researchers to gather ecological data to provide context for their studies. **Objective 4:** Define emerging ecological principles that could inform spillover threats. **Objective 5:** Establish key messages and conduct efforts to promote a culture of conservation among One Health researchers, practitioners, and stakeholders.	**Objective 1:** Pathogen research community acknowledges and integrates ecological systems and interdependencies. **Objective 2:** BPERNet research projects are designed using the framework for well-balanced outcomes. **Objective 3:** More studies return to ecological data. **Objective 4:** Emerging ecological principles become widely-accepted governing principles for practice. **Objective 5:** BPERNet establishes itself as a consistent and unbiased perspective from the community and its statements are widely accepted and distributed.	• Science communities have polarized and insular view of bats and diseases. • Lack of collaboration and communication efforts.

Working Group 4 Mission: Fully develop, understand, and communicate the bat and human interface to key stakeholders and communities.		
Objectives	**Measurements**	**Overall Challenges**
Objective 1: Develop and test policy interventions for specific human-bat interfaces. **Objective 2:** Communicate findings to key stakeholders. **Objective 3:** Develop global risk maps to assess existing data and validate risk maps. **Objective 4:** Identify high risk groups and develop education platforms to measure knowledge, attitudes, and practices.	**Objective 1:** Policy interventions for human bat interfaces are developed and put into place. **Objective 2:** Effectively communicate and publish findings of studies. **Objective 3:** Publish global risk maps highlighting geographic areas of risk. **Objective 4:** Getting community buy-in and understanding of concepts.	• Truthful responses in behavioral research on bat-human interactions. • Accuracy of risk map and models. • Cultural barriers and beliefs.

ACTION ITEMS

The following Action Items were recorded and compiled by the organizational and administrative support staff of CBEP / Executive Committee for the BPERN.

ACTION	APPROACH FOR COMPLETION WITH DATES	RESPONSIBLE AGENTS
Develop communication plan	(1) Themes and key messages (2) New name (3) Outreach (4) Social media (5) Recruitment and marketing	(1) Contingent on establishment of 5th working group; looking into Science Communication experts
Develop website plan	(1) Communication and outreach (2) Collaboration (3) Research mapping	(1) Contingent on establishment of 5th working group.
Publication of protocols and assays	(1)	(1)
Working Groups complete mission statements ***Change?*** Conduct System Reviews to Outline Knowledge Gaps	(1) ***	(1) ***Contingent on Working Group Leads
Conduct Series	(1) SEABCRU (2)	(1)
Publication of Perspectives and Policy piece	(1) Concept pitch (2) Outline (3) First Draft (4) Final Draft	(1) Perspectives Paper: Dr. Mary Lancaster, CBEP and Dr. Vivek Kapur, Penn State (2) Policy Forum: Dr. Marty Stokes, CBEP and Dr. Jon Epstein, EcoHealth Alliance
Conduct a 'funders meeting'	(1)	(1) CBEP

Star-Idaz

Economist debate-style forum

PARTICIPANT FEEDBACK

An after-event survey was sent to the SC to collect information on their progress and overall thoughts on the progress of the RCN. Members were asked to answer the following questions:

1. What did you like about the meeting?
2. Do you think the objectives for the 30 January BPERNet meeting were achieved? Please explain your answer.
3. What do you wish we did differently?
4. What does success of this network look like to you, for your field of study?
5. Will you be able to attend the next meeting in Saskatoon Saskatchewan (5th International One Health Congress) 22-25 June?
6. What do you wonder? As an example, “Do you wonder if this effort is worth your time?”
7. Additional comments.

Responses were collected from the majority of the attending SC and reflected a positive outlook on both the progress of the meeting and the future of BPERNet. The SC felt the 30 January meeting was well organized, with a clear agenda that increased the productivity of each working groups. Comments from members pointed to the formally developed themes and roles for each working group as the main reason for the meeting’s success. The SC agreed success of BPERNet will be achieved when the gaps identified are addressed, there is a standardization of data collection, and the completion of one or more research projects advancing the understanding of and response to emerging pathogen reservoirs in bats. Overall, the only change the group asked for was to extend the next BPERNet meeting to at least two full days. The majority of members will be present at the 5th International One Health Congress meeting and a longer side BPERNet meeting should be arranged during this time period.

ANNEX A – PARTICIPANTS

The following participants attended or were invited to attend the

STEERING COMMITTEE MEETING INVITEES, DID ATTEND		
Mendenhall	Ian	Duke-NUS, Singapore
Buza	Joram	Nelson Mandela African Institute of Science and Technology, Tanzania
Kapur	Vivek	Penn State University, U.S.
Olival	Kevin	EcoHealth Alliance, U.S.
Epstein	Jonathan	EcoHealth Alliance, U.S.
Kading	Rebekah	Colorado State University, U.S.
Urushadze	Lela	National Center for Disease Control and Public Health (NCDC), Georgia
Kutateladze	Tamar	National Center for Disease Control and Public Health (NCDC), Georgia
Sidamonidze	Keti	National Center for Disease Control and Public Health (NCDC), Georgia
Wacharapluesadee	Supaporn	WHO CC for Research and Training in Viral Zoonoses, King Chulalongkorn Memorial Hospital, Thailand
Wade	Abel	National Veterinary Laboratory of Cameroon (LANAVET)
Demetria	Catalino	RITM, Philippines
Kingston	Tigga	Texas Tech University, U.S.
Cryan	Paul	USGS Fort Collins Science Center, U.S.
Reeder	DeeAnn	Bucknell University, U.S.
Smith	Gavin	Duke-NUS, Singapore
Alhmoud	Nesreen	Royal Scientific Society, Jordan
Hondo	Eiichi	Obihiro University of Agriculture and Veterinary Medicine, Japan
STEERING COMMITTEE MEETING INVITEES, DID NOT ATTEND		
Kityo	Robert	Makerere University, Uganda
CBEP AND CBEP CONTRACTOR INVITEES, DID ATTEND		
Lancaster	Mary	DTRA CBEP
Stokes	Marty	DTRA CBEP
Brooks	Lance	DTRA CBEP
Newman	Carl	DTRA CBEP
Leahy	Katie	GSE
Hudson	Megan	GSE

ANNEX B – MEETING AGENDA

The following agenda was set for the meeting. The majority of discussions focused on administration, organization, and focus of the network. The group did not get to the topics to prioritize research gaps and set action plans with short and long-term milestones and deliverables. Event facilitators organized questions and prompts for those sessions, which they will use for the next BPERN meeting.

Time	Session	Notes
0830 - 0845	Introduction and Meeting Objectives	Lance Brooks and Sutep Gonlachanvit will welcome all participants and provide a brief overview of the meeting objectives for the week
0845 - 0900	Þ Review interim accomplishments since 27 June Þ Q&A on TORFTA changes Þ Call for votes to accept TORFTA	Executive Committee members will provide an overview of the TORFTA and mission areas; all participants will receive final version ahead of meeting
0900 - 1000	Working Group Focus Areas	Review WG focus areas that were outlined during the 27 June meeting Þ Review breakout group objectives and end goals Þ Review strategy map
1000 - 1015	Tea Break	
1015 - 1115	Breakout Group Session I	Breakout Group Session 1 Objectives: Þ Define WG research areas (sub-focus area definitions) Þ List and prioritize research questions and potential projects for each area Þ Identify internal and external research dependencies for each Working Group
1115 - 1200	Breakout Group Session I Interactive Feedback	Each group will participate in world café and rotate to review each group's findings
1200 – 1330	Working lunch / Open discussion	Open discussion objectives Þ Discuss group marketing campaign Þ Members should be prepared to introduce other network affiliations, conferences, and meeting opportunities to market the network, globally Þ Discuss long-term process to collect and collate applications to the network
1330 – 1430	Breakout Group Session II	Breakout Group Session 2 Objectives:

		⊳ List out WG research coverage (who is researching what and where) ⊳ Identify research gaps and needs ⊳ Identify WG resource and coverage needs (e.g., target environmentalists in Europe); identify critical POCs for membership ⊳ Begin drafting short and long timelines and work plans
1445 – 1530	Breakout Group Session II Interactive feedback and brief-out	Each group participated in the world café and then briefs out their discussions according to the objectives; brief-out 5 minutes / WG
1530-1545	Tea Break	
1545 – 1630	End of session	End of Session Objectives: ⊳ Review Strategy Map ⊳ Review Action Items ⊳ Discuss date, level of participation, and location for next meeting (all participants should come prepared to briefly discuss their ideas for this topic)

ANNEX C – GROUP BRIEF-OUT SLIDES

Each group was provided 10 minutes at the end of the day to present their strategic mapping work; below are the final slides that were presented.

Group 1

5 MINUTES

What must the Working Group achieve?	How will success be measured?
OBJECTIVES	MEASURE
• Almost all (ex. NIH, WT, WHO, France, Germany, India, China, Australia)	Almost all (ex. NIH, WT, WHO, France, Germany, India, China, Australia)

• Systematic review/knowledge gaps on model systems and transmission risk (short-term goal)
• RFP for model systems to answer:
  • Innate and adaptive immune response
  • Mechanisms of susceptibility
  • EnvironmentaL/I host conditions that are necessary for spillover
  • Resistance and susceptibility of certain bats species and certain pathogens
  • Co-infections and their role in pathogen ecology / spillover risk
	• SYSTEMATIC REVIEW / KNOWLEDGE GAPS DEFINED - PUBLISHED
	• RFPS ISSUED - TEAMS ASSEMBLED / ESTABLISHED
	• MODELS DEFINED / CHARACTERIZED / VALIDATED
	• KEY INTRINSIC/EXTRINSIC RISK FACTORS IDENTIFIED FOR MAJOR DISEASES / GEOGRAPHIES

1. Immunologist 2. Genomics 3. Cellular and molecular biologist • Ecologist /Trans Dynamic model • Systems biologist • Risk assessment • Bioinformatics • Microbiologist • Infectious disease	1. RESEARCHERS; FUNDING AGENCIES; POLICY MAKERS; OIE/WHO

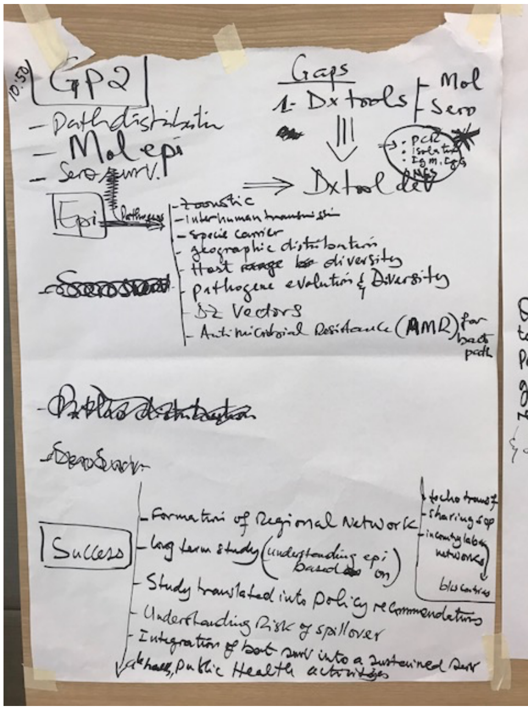
Investments, activities, and projects	Responsibility	Needs and risks
INITIATIVES	WHO	CHALLENGES
• BPERN / Multiple other	Almost all (ex. NIH, WT, BBSRC/DfId OTHER COUNTRY FUNDING AGENCIES)	• Multidisciplinary by nature there isn't a single funding source • Consortia would need to be created for model systems

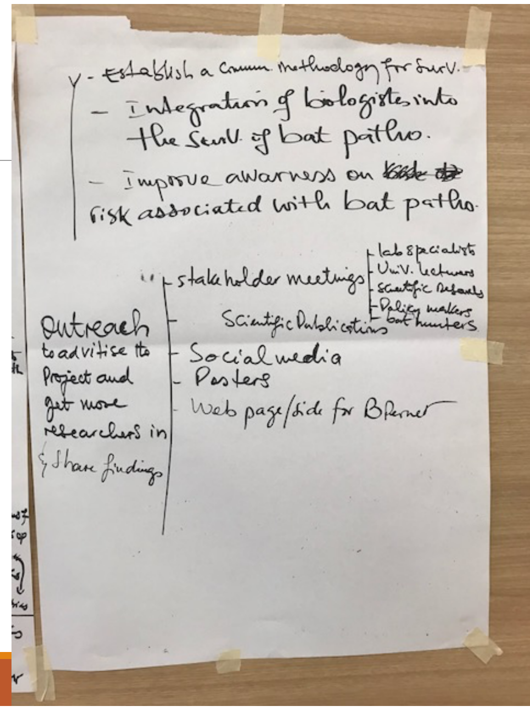
• Model Systems
  • Systematic review
  • RFP
• Natural and experimental disease transmission models
• Tool Kits
	Working Group 2 creates systematic review in which we identify gaps and lay out what would need to be in a RFP	• Quantifying and communicating Risk
		• Lack of baseline knowledge

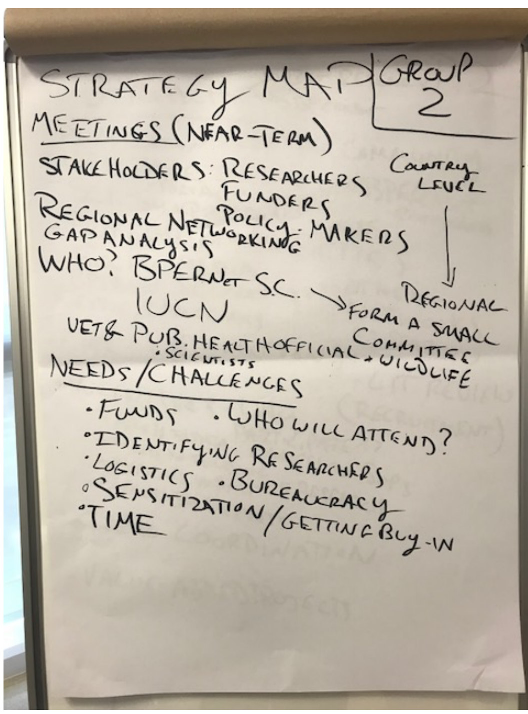
1. Immunologist 2. Genomics / bioinformatics 3. Cellular and molecular biologist • Ecologist /Disease transmission dynamic modelers • Systems biologists • Risk assessment • Microbiologists / Infectious disease specialists	Researchers; funding agencies; other stakeholders	• Quantifying and communicating Risk • Lack of baseline knowledge • Promoting collaboration

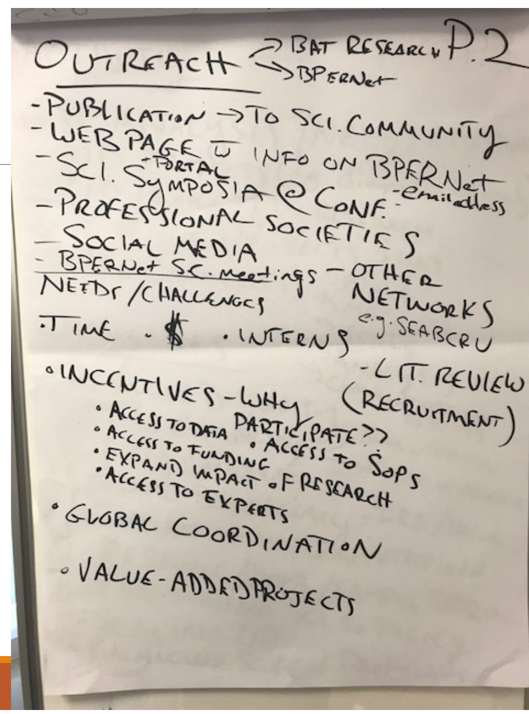
Group 2

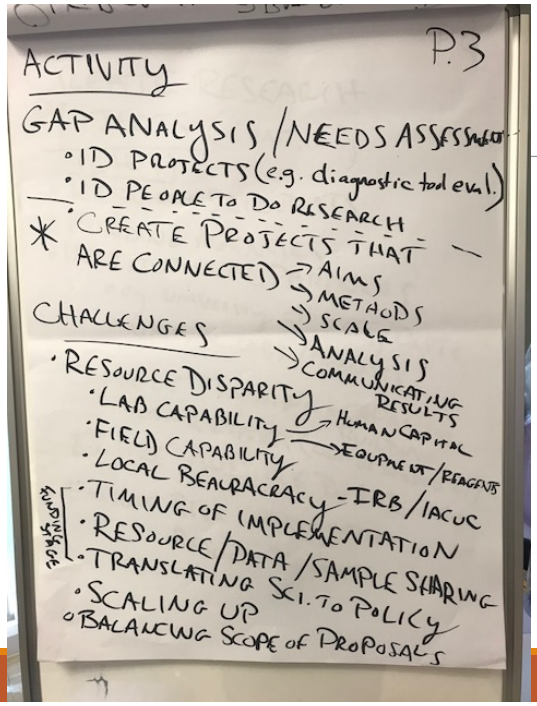
5 MINUTES

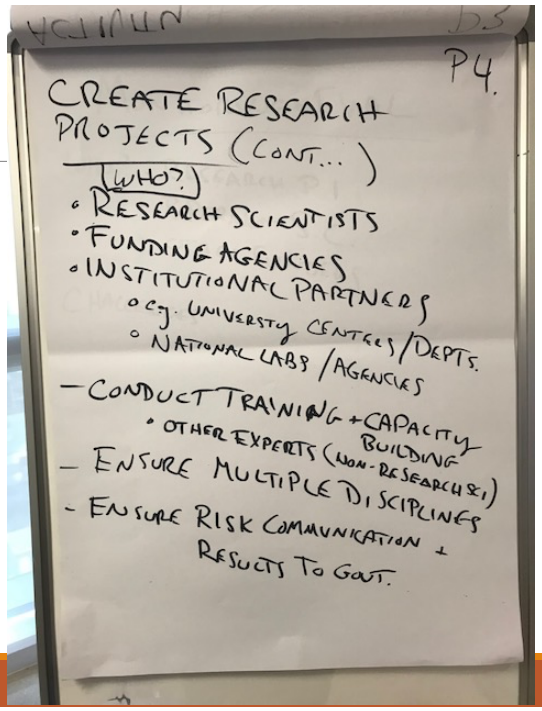

GP2
- Path distribution
- Mol epi
- Sero surv.
Gaps
1- Dx tools
Mol
Sero
Dx tool dev
Epi
- zoonotic
- inter human transmission
- specie carrier
- geographic distribution
- Host diversity
- pathogene evolution & Diversity
- Dz Vectors
- Anti-microbial Resistance (AMR)
Success
- Formation of Regional Network
- long term study (understanding epi)
- Study translated into Policy recommendations
- Understanding Risk of spillover
- Integration of
Public Health activities


- Establish a common methodology for surv.
- Integration of biologists into the surv. of bat patho.
- Improve awarness on risk associated with bat patho.
stakeholder meetings
lab specialists
Univ. lectures
Policy makers
bat hunters
Outreach to advitise the project and get more researchers in & share findings
Scientific Publications
- Social media
- Posters
- Web page/site for BPernet


STRATEGY MAP
GROUP 2
MEETINGS (NEAR-TERM)
STAKEHOLDERS: RESEARCHERS
FUNDERS
POLICY MAKERS
COUNTRY LEVEL
REGIONAL NETWORKING
GAP ANALYSIS
WHO? BPERNet SC.
IUCN
VET & PUB. HEALTH OFFICIAL
SCIENTISTS
REGIONAL
FORM A SMALL COMMITTEE
WILDLIFE
NEEDS/CHALLENGES
• FUNDS • WHO WILL ATTEND?
• IDENTIFYING RESEARCHERS
• LOGISTICS • BUREAUCRACY
• SENSITIZATION/GETTING BUY-IN
• TIME


OUTREACH
BAT RESEARCH
BPERNet
P. 2
- PUBLICATION → TO SCI. COMMUNITY
- WEB PAGE - PORTAL - INFO ON BPERNet
- email address
- SCI. SYMPOSIA @ CONF.
- PROFESSIONAL SOCIETIES
- SOCIAL MEDIA
- BPERNet SC. meetings - OTHER NETWORKS e.g. SEABCRU
NEEDS/CHALLENGES
• TIME • $ • INTERNS
- LIT. REVIEW (RECRUITMENT)
• INCENTIVES - WHY PARTICIPATE??
• ACCESS TO DATA • ACCESS TO SOPS
• ACCESS TO FUNDING
• EXPAND IMPACT OF RESEARCH
• ACCESS TO EXPERTS
• GLOBAL COORDINATION
• VALUE-ADDED PROJECTS





Group 3

5 MINUTES

Group 3 Mission: define how and to what extent the ecological context of bats, and human influence on that context, influence pathogen dynamics and spillover threats

What must the Working Group achieve?	How will success be measured?
OBJECTIVES	MEASURE
Objective 1: Engage the ecological community (including research groups, individuals, and networks) to define system uniqueness and interdependencies (movement, community, nutritional, physiological, social, reproductive, conservation, and population ecologies etc. **Objective 2:** Bring ecological design and analysis frameworks to pathogen research; advise the community of innovative and supportive technologies **Objective 3:** Build capacity for disease researchers to gather ecological data to provide context for their studies **Objective 4:** Define emerging ecological principles that could inform spillover threats **Objective 5:** Establish key messages and conduct efforts to promote a culture of conservation among One Health researchers, practioners, and stakeholders; BPERNet SC provides timely statements on potentially contentious research	**Objective 1 Measurement:** Pathogen research community acknowledges and integrates ecological system and interdependencies **Objective 2 Measurement:** BPERNet research projects are designed using the frame work for well-balanced outcomes **Objective 3 Measurement**: More studies are returning ecological data **Objective 4 Measurement:** Emerging ecological principles become widely-accepted governing principles for practice **Objective 5 Measurement:** BPERNet establishes itself as a consistent and unbiased perspective from the community and its statements are widely accepted, respected, and distributed

Group 3 Mission: define how and to what extent the ecological context of bats, and human influence on that context, influence pathogen dynamics and spillover threats

Investments, activities, and projects	Responsibility	Challenges, needs, and risks

1. Conduct a literature review of bat-associated papers to assess how many incorporated conservation principles and authorship
2. Conduct DTRA call for sampling opportunities associated with existing ecological research
  1. Demonstrate contribution to ecology of disease emergence
  2. Demonstrate existing funding (not associated with potential funding)
3. Ensure that any future solicitations include language that explicitly incorporates an ecology framework where relevant
4. Collect case studies for messaging
5. As part of a repository of 'tool kits', develop an ecology 'tool kit'; conduct tactical field activities to learn how to use and teach-back the tool kit
6. International Bat Research Conference (IBRC) 2019 – attend and participate (with 5-10 participants for discussion Q&A)
7. Convene a series of 'conservation awareness-building' workshops
8. FOR NEXT BPERNet MEETING: longer planning meeting, develop and work through a scenario that incorporates all the working group for future discussion-based training events
	1. WG
	2. CBEP / BPERNet
	3. CBEP (and other fudners)
	4. WG – 3
	5. WG – 3
	6. BPERNet
	7. WG – 3
	8. BPERNet
		• "The Great Divide" – solution: build awareness
		  • Vocal and polarized bat community
		  • Insular bat and disease communities
		  • Insensitive disease community
		• Lack of collaborative efforts
		• Communication issues

Group 4

5 MINUTES

What must the Working Group achieve?	How will success be measured?
OBJECTIVES	MEASURE
Identify other funding initiatives	Number of visits to website Number of proposals submitted and projects funded
Better understand bat/human interface Develop and test policy interventions for specific human-bat interfaces	Baseline knowledge and gaps identified Database development Maps and models developed Guidelines for human behaviroal risk characterization developed and used Intervention policies developed and tested
Communicate findings to key stakeholders • Policy makers • Community members (high risk groups)	Number of workshops and attendees (conventional metrics) Before and after surveys for KAPs

Investments, activities, and projects	Responsibility	Needs and risks
INITIATIVES	WHO	CHALLENGES
Create and curate web page with potential funding opportunities	BPERN; CBEP (to liaise w other USG funders); country governments	Lack of transparency and coordination among donors and recipients (=duplication) Silo'ing of funding Some countries (e.g. Singapore) doesn't fund outside of country Shaping national/country funding priorities
Develop global risk maps Assess existing data and literature review Research studies/support for ecol, social, and econ drivers Studies of seasonality Identify and model policy interventions Validate/ground-truth risk maps	BPERN, academics, research orgs, NGOs, and countries	Truthful responses in behavioral research Ensuring interventions developed will be acceptable and econ viable. Accuracy of risk maps/models
Identify target audience, and high risk groups Develop education platforms/materials Research to measure changes in knowledge, attitudes, and practices (KAP)	BPERN; SEABCRU; social behavioral scientists (needed); communication and PR specialists	Getting community buy-in and understand concepts Cultural barriers and beliefs (e.g. bats are medicinal to eat) Dissemination of info to larger group

From: Megan Hudson >
Sent: Friday, July 13, 2018 12:01 PM EDT
To: nisreen.hmoud >; joram.buza ;
cryanp <cryanp ; c demetria
epstein < >; Kading,Rebekah >;
vkapur >; tigga.kingston kityrob
>; tamar kutateladze ; ian.mendenhall -
nus.edu.sg >; olival ;
dreeder ; ksidamonidze ;
gavin.smith ; l.urushadze
>; abelwade ; raina.plowright
>
CC: Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) < Stokes, Martha M CIV
(US) >; Katie Leahy >; Becker, Stephen M CTR DTRA J3-7
(US) >
Subject: Draft Executive Summary and Website Materials
Attachment(s): "BOHRN Saskatoon_ExecutiveSumv.6.docx"

All,

Please find the draft report from our BOHRN meeting 20-21 June. This report includes an executive summary, action items, participant list, working group outcomes, and your research quad charts.

We ask that you provide constructive comments (e.g., content changes) no later than 18 July. It is our intent to adjudicate and incorporate any comments to then publish a final report.

In addition, you will find an updated version of the website map here (https://docs.google.com/document/d/1x5GdAKEPpKXTol9utZiYvaGoXNtOQsyTdlub1WvN0tk/edit?usp=sharing). Each page has the title of the website page and the content, make edits, as you see fit, to the language to help us better develop the website.

As a reminder, we will be adding individual bios to the website. If you have not already done so, you may submit your information here: https://www.surveymonkey.com/r/BPMTG2T

You will find the report contains softened language to add a more conservationist view point, please review the language within the report and on the website.

v/r,

Megan

Megan Hudson
Task Lead | Global Systems Engineering
6303 Little River Turnpike #208
Alexandria, VA 22312

http://globalsyseng.com

Executive Summary
Saskatoon June 2018

BOHRN

Bat One Health Research Network

BOHRN Saskatoon – Meeting Overview

Executive Summary

On 20-21 June 2018, the Bat One Health Research Network (BOHRN) Executive and Steering Committees gathered in Saskatoon, Saskatchewan (Canada) in advance of the 5th International One Health Congress. The two-day meeting was organized and hosted by the Defense Threat Reduction Agency (DTRA) Cooperative Threat Reduction Directorate, Biological Threat Reduction Department (CBEP) in its capacity as a sponsor of life sciences research-based Threat Reduction Networks (TRNs). The meeting served as a forum to advance the group's core agenda of enabling interdisciplinary collaboration at the interface of biological threat reduction, research, and conservation.

> *"Shifting priorities and budgets necessitate sustainable and enduring structures of knowledge and capability to meet the challenges of a complex, interconnected world."*
>
> Mr. Lance Brooks
> Biological Threat Reduction Department

The meeting began with introductions from Mr. Lance Brooks (Director), Dr. Martha Stokes (Southeast Asia Science Lead), and Dr. Mary Lancaster (Africa Science Lead) from CBEP. They welcomed the group and provided an update on their program's priority for supporting TRNs as opportunities to build and enhance local and regional expertise-based relationships that could identify, characterize, and mitigate biological threats sooner.

Based on the feedback and outcomes from previous meetings, event organizers designed an agenda to meet the following three objectives for the BOHRN meeting in Saskatoon:

- Better understand peer knowledge and interests through presentation of active research projects and other activities
- Continue work on focus area action plans that yield collaborative and sustainable projects
- Discuss challenges to and opportunities for increased network collaboration

The meeting was organized into three sessions. The first session provided time for members of the steering committee to outline their research activities via quad chart, which allowed the participants to better understand each other's research interests and funding sources. The quad chart format provided space for the presenters to outline challenges or questions pertaining to their research, which spurred discussions on comprehensive migration mapping, sustaining a cold chain for sample collection, transport, and preservation, and building consistencies in data collection.

The second session featured break-out group discussions on BOHRN's four focus areas: (1) Host-pathogen biology and interactions; (2) Pathogen surveillance, diagnostic capacity, and epidemiology; (3) Ecology setting; and (4) Human-bat interactions. The Breakout groups were asked to finalize the focus area mission statements, draft a list of short and long-term activities and projects for each objective and/or goal set during the Bangkok meeting, and create focus area workplans. The breakout groups presented their work to the larger group for discussion which emphasized the overarching needs for virtual communication and outreach.

The third and final session featured presentations from Los Alamos National Laboratory (LANL) on research network analysis, the National Public Health Laboratory in Tbilisi on its novel disease diagnostic capabilities, and a discussion about potential upcoming BOHRN events. The meeting concluded with a review of its action items and discussions. Members of BOHRN who were present agreed that the next meeting should take place in advance of the International Meeting on Emerging Diseases and Surveillance (IMED) 9-12 November 2018 in Vienna, Austria. Event organizers and participants felt they achieved the meeting's objectives and look forward to the next meeting tentatively scheduled for 8-9 November 2018.

BOHRN Background

In 2013, CBEP began leveraging, enhancing, and convening TRNs to accelerate its programmatic targets and end states. CBEP employs this approach as a way to connect its active funded research projects with other projects to improve global health security, building consistency in data sets, and facilitate more confident decision-making by policy makers. Relationship-based networks around the globe, made up of interdisciplinary researchers, allow for novel and transformative scientific solutions for the world's high-impact infectious disease threats.

BOHRN connects multidisciplinary and One Health expertise to address research-based capability gaps and threats posed by bat-associated pathogens of security concern. The group maintains the standards of all research networks that are supported by CBEP, in which members convene as a body of experts and researchers to: (1) share information, data, samples, and protocols; (2) coordinate research activities; (3) build training events and awareness-building workshops at all levels of decision-making authority; (4) develop community standards and best research practices; (5) create mentorship-based opportunities for students, trainees, and early-career researchers to convene, present, and share ideas; (6) establish a community of international research leaders and champions; and (7) reduce outbreak and disease transmission risks.

Why Bats?

Scientists hypothesize that some of the world's most deadly emerging zoonotic diseases are found in bats, including Nipah, Hendra, and Marburg viruses. However, because bats contribute significantly to the health and diversity of many environments around the world, a conservation-minded approach to their study is necessary. There are a number of factors which could make bats unique disease reservoirs, including their social behavior, distinct physiology and metabolism, ability to travel long distances, nocturnal activity, species diversity, and long life span (10-20 years, compared with a rat's average life of two years).[1] These special bat characteristics, coupled with the impact of human-mediated interactions and environmental changes, create research challenges to understanding the bat's role in the global zoonotic disease ecology, which is further complicated by being difficult animals to study within a typical laboratory setting.

BOHRN is a global network of conservationists, disease ecologists, and clinical virologists who have organized to better understand how bat-borne disease threats filter through ecological systems. BOHRN creates opportunities for policy makers, researchers, conservationists, funders, and students to identify community challenges, develop priority research lists and associated action plans that target needs and gaps, and work at all levels to build awareness of bat-associated disease burden and transmission risks to improve the prevention, detection, diagnosis, and reporting of pathogens of security concern.[2] This group, under sponsorship from CBEP, has established objectives to collaborate on multi-disciplinary research and establish standards for lab and field research practices.

BOHRN Mission and Vision

BOHRN convenes multi-disciplinary and One Health-focused scientists, policy makers, research scientists, and medical/veterinary practitioners with interests in bat-related research involving pathogens of security concern. The network builds on community standards and best practices for research. BOHRN identifies and shares information on research funding opportunities offered by multiple institutions. Most importantly, this network fosters international relationships among collaborators, agencies, and organizations, which can produce long-term, sustainable partnerships that withstand changes in government and organization budgets, priorities, postures, and policies.

All members play a role in operationalizing the objectives of BOHRN, strengthening linkages and reducing overlap in global research on high-priority pathogens of bats (especially zoonosis) to maximize

[1] Hayman, David T.S., "As the bat flies," *Science* 02 Dec 2016: Vol. 354, Issue 6316, pp. 1099-1100 http://science.sciencemag.org/content/354/6316/1099

[2] Schountz, Tony, "Immunology of Bats and Their Viruses; Challenges and Opportunities," *Viruses,* 2014 Dec; 6(12): 4880-4901. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4276934/

the efficient use of expertise and resources and accelerate the coordinated development of better disease surveillance and control methods.

BOHRN Objectives

This network will identify and connect interdisciplinary expertise, convening an agile group to adapt to a wide spectrum of emerging challenges and threats. By accomplishing the below objectives BOHRN will enable shared learning and research opportunities, establish new research projects, and facilitate joint applications for funding; thus, increasing the opportunity for peer review, especially if a cross-regional and multi-disciplinary team of authors is involved.

- Facilitate interdisciplinary relationships and collaboration to identify research goals and needs for bat-associated disease research and threat reduction; and
- Unify CBEP regions to create a common action plan that yields collaborative and sustainable projects that achieve the following end states:
    - Better informed policy-makers;
    - Better informed scientific community regarding funding targets and gaps in areas of research and development;
    - Better defined threat to global health security from bat-associated pathogens; and
    - Improved national, regional, and global capacity to detect and respond to pathogens of security concern; and
- Enable better communication, coordination, and outreach at the research and conservation interface.

Meeting Outcomes

Results from the Breakout Groups

On the first day of the meeting, following presentations from each of the participants on their research focus areas, meeting attendees "broke out" into four working groups. They were instructed to continue work on the objectives and goals set at previous meetings, creating workplans short and long-term intentions. Due to scheduling issues, all of the working groups were not fully represented, so other members were asked to fill-in for different groups. The following write-up describes the outcomes from the breakout group session.

Group 1: Host-Pathogen Biology and Interactions

Group 1: Host-Pathogen Biology and Interactions **Focus Area 1:** Bat physiology and immunology **Focus Area 2:** Bat pathogen community biology (e.g., coinfections and comorbidities) **Focus Area 3:** Distribution of pathogens amongst species **Focus Area 4:** Develop modeling approaches for host dynamics and epidemiology	
MISSION STATEMENT: Explain the determinants of tolerance, transmission, and spillover of pathogens by bats at individual and population levels.	
Objective 1	Complete a systematic review of the knowledge gaps on modeling systems
Objective 2	Identify model systems that are representative of all geographic and phylogenic areas
Objective 3	Evaluate the transmission risk and spillover of pathogens to other animal hosts
Projects or Activities	**Timeline / Responsible Authority / Needs (e.g., funding or other support**
Develop cell lines and bat animal models	Long-term lab study
IgM immunoassay	Long-term lab study
Develop methods for determining the age of bats	Long-term lab/field study
Determine the timing of viral shedding and the effects of environmental stresses	Long-term lab/field study
Determine co-infection in bat species	Long-term lab/field study
Determine temperate versus tropical variables associated with infection (hibernation periods / viral replication)	Long-term lab/field study; study species that live in both temperate and tropical locations; study climate change
Understand climate change in respect to physiology	Long-term lab/field study; study species that live in both temperate and tropical locations; study climate change
Map funding landscape / reach out to program officers from agencies	Short-term project (within 6-months) to map funders Long-term project (within 1-year) to host a funders meeting

	Need to identify funders with different interests in the same biological/ecological system to provide long-term funding
Develop heat stable preservatives	Long-term lab/field study
Develop smaller telemetry and physiology sensors	Long-term lab/field study

Group Notes

Group 1 discussed ways the need to mine existing studies for data, which could extend the longevity of data collection and the breadth of data sets. They additionally requested a funders' meeting to identify other program officers and tech companies that would be interested in BOHRN research projects. The group suggested providing opportunities for training, which could include EDGE at Los Alamos National Laboratory for bioinformatics and next generation sequencing. The group discussed the need to identify funders with different interest in the same biological/ecological system that can provide more longer-term funding and to also engage with biologists from regions that have expertise on bat ecology and history.

Group Research Mentors

Dr. Mary Lancaster, DTRA CBEP

Dr. Jon Epstein (EcoHealth Alliance) *– note: ordinarily works Group 2*

Dr. Lela Urushadze (NCDC, Georgia) *– note: ordinarily works Group 4*

Dr. Joram Buza (Nelson Mandela-African Institute of S&T, Tanzania) *– note: invited, could not attend*

Dr. Vivek Kapur (Penn State University) *– note: invited, could not attend*

Dr. DeeAnn Reeder (Bucknell University) *– note: invited, could not attend*

Dr. Gavin Smith (Duke NUS Medical School, Singapore) *– note: invited, could not attend*

Group 2: Host-Pathogen Biology Interactions

Group 2: Pathogen Surveillance, Diagnostic Capacity, and Epidemiology **Focus Area 1:** Molecular epidemiology **Focus Area 2:** Distribution of pathogens geographically and phylogenetically **Focus Area 3:** Detection, diagnosis, and reporting of bat-associated pathogens **Focus Area 4:** Establish commonly used guidance on sampling	
MISSION STATEMENT: Form regional networks to establish a common methodology for surveillance and sustain the surveillance for both human and animal health. In addition to understanding spillover risk and epidemiology of bats	
Objective 1	Fully establish a baseline of animal health and public health laboratories for equipment, staff, and diagnostic tools
Objective 2	Build awareness amongst the research, public health, and other science communities
Objective 3	Establish a common methodology for surveillance
Projects or Activities	**Timeline / Responsible Authority / Needs (e.g., funding or other support)**
Develop assessment tool and conduct capability assessments in laboratories to establish baseline requirements for conducting NGS and other diagnostic protocols for detecting novel and routine diseases from bats	Timeline: Immediate: identify laboratories to assess (likely National Reference Labs, Ministries or Departments of Public (human) and Animal Health) 1-9 Months: create, distribute, and receive feedback questionnaires from labs 9-12 Months: conduct lab visits (as necessary) to identify inconsistencies and fill in knowledge gaps 12-18 Months: assess data, send feedback to labs, and publish report on findings Needs: Technical support and funding
Conduct outreach through meetings with multisectoral stakeholders and social media	Timeline: Immediate: identify opportunities for side meetings at larger animal and public health events with topics related to diagnostic surveillance; identify POCs to serve on One Health committees 6 Months: present research findings and publications; form country-specific One Health committees to sustain awareness and serve as organizers for regional meetings (e.g., 2-3 Animal and Public Health researchers / university) 12 Months: form outreach teams that can network through social media, perform website updates, and survey additional information from other networks and associations Needs:

	Identify potential funders for logistics and planning support; need technical support for social media, web design, and communications
Establish a common methodology for diagnostic surveillance	Timeline: Long-term, after completion of needs assessment tool and implementation 2+ years to implement Needs: Funding for equipment and technical training; resources to develop EQA

Group Notes

Group 2 worked to emphasize the need for commonality (technique, tools, communication, and lexicon) and communication. They worked to offer a plan that identifies baseline tools for lab-based disease surveillance and sets up a system of multi-sectoral outreach and communication.

Group Research Mentors

Dr. Catalino Demetria (Research Institute for Tropical Medicine, Philippines)
Dr. Tamar Kutateladze (NCDC, Georgia)
Dr. Jon Epstein (EcoHealth Alliance) *– note: worked in Group 1*
Dr. Abel Wade (National Veterinary Laboratory, Cameroon) *– note: invited, could not attend*
Dr. Keti Sidamonidze (NCDC, Georgia) *– note: worked in Group 3*

Group 3: Ecology Setting (Bat, Domesticated Animals, and Wildlife Interface)

Group 3: Ecology Setting (Bat, Domesticated Animals, and Wildlife Interface) **Focus Area 1:** Bat behavior, distribution, and movement **Focus Area 2:** Domesticated animals and wildlife behavior, distribution, and movement and impact on interaction with bats **Focus Area 3:** Effect of anthropogenic disturbance and modification on pathogen dynamics and spillover risk	
MISSION STATEMENT: Define how and to what extent the ecological context of bats, and human influence on that context influence pathogen dynamics and spillover threats.	
Objective 1	Improve coordination at the One Health / conservation interface
Objective 2	Define ecological principles that could inform spillover threats
Objective 3	Conduct conservation-minded messaging and outreach
Projects or Activities	**Timeline / Responsible Authority /** **Needs (e.g., funding or other support)**
Quantify interdisciplinary relationship through assessment of publications that feature animal and/or public health, zoonotic disease focus and awareness	Timeline: 6-months post-identification of search parameters Needs: Require BOHRN help in defining search parameters (set as agenda item for next meeting) Research and lit review assistance
Define lit review search parameters for study	Timeline: 6-months Needs: Identify target journals for publication; research guidelines for conducting and publishing a lit review
Publish position paper advocating for improved relationships amongst conservation and One Health communities and suggesting collaborative research projects as a way to bridge differences	Timeline: 1-year (NLT summer 2019) Needs: Research assistance
Develop a repository of tool kits, safety and research guidelines for protecting human and bat health; publish available materials on the BOHRN website	Timeline: 6-months to collect information into training guides for use at field workshops

	Needs: Research assistance; meeting support
Conduct tactical field training activities and a “train the trainer” model	Timeline: 6-months (next BOHRN meeting) establish goals and objectives 9-months establish first training event (Uganda) Needs: Planning / funding / logistics support Funding support for implementation
Build case-control studies for training purposes in messaging	Timeline: 6-months for use during training events Needs: BOHRN group support for case-control study ideas
Participate in One Health / conservation conference panels	Timeline: International Bat Research Conference (IBRC) June 2019 Needs: Participation from BOHRN

Group Notes

Group 3 focused on engaging the ecological community and analyzing frameworks for pathogen research through assessing One Health interactions and developing workplans to include conferences for outreach. Their workplan offers the ability to establish key messages throughout the ecological community.

Group Research Mentors

Dr. Rebekah Kading (Colorado State University)
Dr. Keti Sidamonidze (NCDC, Georgia) *– note: ordinarily works in Group 2*
Dr. Paul Cryan (USGS Fort Collins Science Center) *– note: invited, could not attend*
Dr. Tigga Kingston (Texas Tech University) *– note: invited, could not attend*
Dr. Robert Kityo (Makerere University, Uganda) *– note: invited, could not attend*

Group 4: Human-Bat Interactions

Group 4: Human-Bat Interactions **Focus Area 1:** Human behavioral risk characterization **Focus Area 2:** Hunting and commodity chain (e.g. bushmeat, guano, and pet trade) **Focus Area 3:** Ecotourism **Focus Area 4:** Interactions in human dwellings	
MISSION STATEMENT: Characterize relationships and interactions between bats and humans and communicate findings to key stakeholders and communities.	
Objective 1	Identify and characterize high-risk interfaces
Objective 2	Develop risk maps to assess existing data and validate risks
Objective 3	Communicate findings to key stakeholders
Objective 4	Develop and test policy interventions for specific human bat interfaces
Projects or Activities	**Timeline / Responsible Authority / Needs (e.g., funding or other support)**
Convene a series of funders' meetings	Timeline: 12 months Needs: Assessment of available funders and timeline of BOHRN projects needing funding Funding platform on BOHRN website
Conduct survey that identifies risk groups and interfaces	Timeline: 12 months Needs: Literature assessment of current risk groups and interfaces
Develop risk map	Timeline: 12 – 36 months Needs: Literature review Research assistance
Conduct literature / research review	Timeline: 6 months Needs: Research assistance
Create a database of expertise, active research projects and activities	Timeline: 36 months Needs: Funding for database creation Development of platform on BOHRN website
Perform a seasonality study	Timeline: 36 months Needs: Research assistance Funding

Group Notes
Group 4 focused on a series of projects that would help assess the risk groups and characterize the interactions between bats and humans. Long-term the group's focus is to develop a way to effectively communicate these findings to stakeholders and the community

Group Research Mentors
Dr. Ian Mendenhall (Duke-NUS)
Dr. Supaporn Wacharapluesadee (WHO CC, King Chulalongkorn Medical Hospital, Thailand)
Dr. Nesreen Alhmoud (Royal Scientific Society, Jordan) *– note: worked in Group 3*
Dr. Lela Urushadze (NCDC, Georgia) *– note: worked in Group 1*
Dr. Kevin Olival (EcoHealth Alliance) *– note: invited, could not attend*

Participant Feedback

After the June BOHRN event, participants were asked to give feedback via SurveyMonkey to the following questions:

1. Do you think the objectives for the 20-21 June BOHRN meeting where achieved? Please explain your answer.
2. Do you wish we did anything differently?
3. What objectives do you think we should cover at our November meeting?
4. Are your working group's objectives and timelines clear? Do you think you will be able to accomplish the objectives outlined over the next year? Please explain why or why not.
5. Will you be able to attend the BOHRN and International Meeting on Emerging Disease and Surveillance in Vienna, Austria on 9 – 12 November?

Of the participants who responded, there was an overwhelmingly positive response to the two-day BOHRN meeting. All participants answered that they felt the meeting met its set objectives and nothing was noted to change for future meetings. Participants are able to attend the November IMED and BOHRN meetings. For the November meeting, responses indicated that the steering committee would like to review progress updates, readouts from the September event, and design an approach for outreach and communication. In addition, responses indicated the need to engage with other donors prior to IMED. It was suggested to hold "a side meeting with key steering committee members and funders to discuss needs and interest in joint activities with DTRA." To facilitate this discussion, it was suggested that a survey of U.S. and International donors be summarized prior to the November meeting.

Annotated Action Items

The following Action Items were recorded and compiled by the organization and administrative support staff of CBEP / Executive Committee for BOHRN.

Description		Approach for Completion (with suspense dates)	Responsible Point of Contact
Action 1	Collect information on BOHRN SC bios and ideas on BOHRN messaging for website	July 2018	GSE
Action 2	Create task list for each working group	July 2018	GSE
Action 3	Update BOHRN website messaging and tools	August 2018	GSE
Action 4	Literature review scoping	October 2018	BOHRN working groups led by Rebekah Kading, Kevin Olival, Paul Cryan and Tigga Kingston
Action 5	Collect status and assessments of Working Group action items prior to November meeting	October 2018	GSE
Action 6	Develop action items and agenda using suggestions from BOHRN SC for November IMED conference and BOHRN meeting	October 2018	DTRA and GSE
Action 7	Begin messaging and outlining Uganda BTCD	October / November 2018	DTRA, GSE, Rebekah Kading and Robert Kityo

BOHRN – International Meeting on Emerging Diseases and Surveillance

During the BOHRN meeting, the steering committee voted on options for the next full BOHRN meeting. Several conferences in October – December 2018 were suggested. The group decided that the objectives for the International Meeting on Emerging Diseases and Surveillance (IMED) best met the overall goals of BOHRN. IMED is organized by the International Society for Infectious Diseases and will take place in Vienna, Austria from 9 – 12 November 2018. The conference draft agenda reviews the following objectives: methods and models of disease surveillance, detection and prediction, lessons from epidemic emerging zoonoses, animal health threats biosecurity, agents of bioterrorism and biological warfare infections, and migration of human and animal vector borne diseases. The meeting aims to unite human, veterinary, and environmental specialists on approaches to pathogens in a broad ecological context. These goals align directly to the BOHRN objectives and provide opportunities for the steering committee to socialize the network while gaining tools and information from the interdisciplinary collaboration to aid in accomplishing the working group actions

The BORHN steering committee agreed upon a two-day meeting around IMED. The following objectives are suggested:

1. Prioritizes funding needs based on working groups' characterization of gaps and needs, to help organize and develop funding initiatives; and
2. Analyze progress of action plans and their yields establishing collaborate and sustainable projects

The following items are topics for discussion during the meeting:

- Draft initial Request for Approvals
- Develop initiatives for a funding discussion
- Review and begin developing abstracts for working group actions
- Discuss literature review scoping
- Plan and draft agenda for Uganda Training Event
- Read out from Georgia Biological Threat Characterization Discussion (BTCD)
- Identify and catalog existing tool kits for website database
- Develop an approach to outreach and populating working groups
- Report out of working group progress
- Strategy session for future International bat meeting and conferences

Annex A: BOHRN Saskatoon Meeting Agenda

Day 1 – 20 June 2018 (Wednesday)

- 1000 – 1045 Welcoming Remarks
- 1045 – 1100 House Keeping and Admin
- 1100 – 1130 Updates on BOHRN
- 1130 – 1145 Working Break
- 1145 – 1300 Current Research and Interest – Quad Chart Presentations
- 1300 – 1400 Lunch
- 1400 – 1600 Breakout Sessions
- 1500 – 1530 Working Break
- 1600 – 1630 Brief-out of Breakout Sessions
- 1630 – 1645 Close-out Discussion

Day 2 – 21 June 2018 (Thursday)

- 0900 – 1000 Review of Day 1 / BOHRN timeline
- 1000 – 1030 Large Group Discussion – BOHRN Website
- 1030 – 1045 Working Break
- 1045 – 1145 Network Analysis
- 1145 – 1215 Lunch
- 1215 – 1315 Biological Threat Characterization Discussion
- 1315 – 1345 Lugar Center Presentation
- 1345 – 1415 Large Group BTCD Q&A
- 1415 – 1430 Working Break
- 1430 – 1500 Build Next Meeting Agenda
- 1500 – 1600 Next Steps

Annex B: BOHRN Saskatoon Meeting Participants

STEERING COMMITTEE MEETING INVITEES, DID ATTEND		
Mendenhall	Ian	Duke-NUS, Singapore
Epstein	Jonathan	EcoHealth Alliance, U.S.
Kading	Rebekah	Colorado State University, U.S.
Urushadze	Lela	National Center for Disease Control and Public Health (NCDC), Georgia
Kutateladze	Tamar	National Center for Disease Control and Public Health (NCDC), Georgia
Sidamonidze	Keti	National Center for Disease Control and Public Health (NCDC), Georgia
Wacharapluesadee	Supaporn	WHO CC for Research and Training in Viral Zoonoses, King Chulalongkorn Medical Hospital, Thailand
Demetria	Catalino	Research Institute for Tropical Medicine (RITM), Philippines
Alhmoud	Nesreen	Royal Scientific Society, Jordan
STEERING COMMITTEE MEETING INVITEES, DID NOT ATTEND		
Buza	Joram	Nelson Mandela African Institute of Science and Technology, Tanzania
Kapur	Vivek	Penn State University, U.S.
Wade	Abel	National Veterinary Laboratory of Cameroon (LANAVET)
Kingston	Tigga	Texas Tech University
Cryan	Paul	USGS Fort Collins Science Center, U.S.
Reeder	DeeAnn	Bucknell University, U.S.
Smith	Gavin	Duke-NUS, Singapore
Kityo	Robert	Makerere University, Uganda
Plowright	Raina	Montana State University, U.S.

CBEP AND CBEP CONTACTORS ATTENDEES		
Brooks	Lance	DTRA CBEP
Lancaster	Mary	DTRA CBEP
Stokes	Marty	DTRA CBEP
Fair	Jeanne	Los Alamos National Laboratory (LANL)
Bartlow	Andrew	Los Alamos National Laboratory (LANL)
Becker	Stephen	DTRA A&AS
Russell	Chris	GSE
Leahy	Katie	GSE
Devaney	Caitlin	GSE
Hudson	Megan	GSE

Annex C: Research Quad Charts

EcoHealth Alliance

Dr. Jon Epstein presented on pandemic prevention and disease ecology. Stating there is very little to our current understanding about host-pathogen relationships and the species involved in maintaining zoonotic viruses in nature. However, studying viral pathogens in wildlife is logistically challenging therefore, they are taking a multidisciplinary approach in study locations. PREDICT's impact has helped strengthen lab networks and regional surveillance networks for disease detection.

TECHNICAL DESCRIPTION AND OBJECTIVES

Pandemic prevention / Disease Ecology
Challenges: Most emerging viral pathogens come from wildlife - especially bats. Studying viral pathogens in wildlife is logistically challenging and requires intensive, long-term efforts and specific technical expertise to obtain meaningful data and conduct analyses.
Current state of understanding: Very little is understood about the host-pathogen relationship and the species involved in maintaining zoonotic viruses in nature.

APPROACH

- Multidisciplinary, collaborative teams including local experts in the study location, coupled with capacity building has been an effective approach to conducting research on zoonotic pathogens *in situ*.
- Identifying strong scientific partners and relevant govt agencies with whom to partner is essential. Local scientists lead the research, with collaborative input and support from EHA's core staff scientists. Consistent communication with partners, and updates to govt. entities maintains positive relationships and validates the work.
- The most important tool, and often least available is technical expertise to safely and effectively work with wildlife. This requires specialized training. Lab capacity to safely detect pathogens and antibodies is also essential.

MILESTONES, SCHEDULE, AND STATUS

Research is ongoing and reflects several major projects:
e.g. USAID PREDICT (through Oct 2019)
DTRA CBEP project in Malaysia (through 2022)
PREDICT began in 2009, and is led by a consortium of institutions operating in 26 countries. To date, it has detected more than 1,000 new viruses and trained members of the human and animal workforce to use a One Health approach to detect viruses in wildlife, livestock, and humans and focus surveillance activities in locations of high risk for spillover.
SARS-CoV in China – studying risk of SARS and SARS-related CoVs In rural and urban China. (through 2019).

IMPACT

PREDICT has trained thousands of scientists and govt officials in 30 countries to be better able to detect and respond to potential pandemic threats. Laboratory capacity has been enhanced in more than 30 labs, field expertise developed, and policies impacted by PREDICT activities. EHA has been part of the development of the One Health Secretariat in Bangladesh – an official body that includes representation from the ministries of health, agriculture, and environment as well as additional stakeholders and that convenes regularly to discuss and implement surveillance and outbreak response activities for zoonoses.
Globally and regionally, PREDICT has helped strengthen lab networks and regional surveillance networks for disease detection. Example: ebola host project (PREDICT) in Liberia, Sierra Leone, and Guinea - coordinated surveillance for Ebola reservoirs.

Duke-National University Singapore

Dr. Ian Mendenhall presented on his research to inform and improve biosurveillance to more effectively use resources. Through surveying bats and small mammals across Cambodia and India the study aims to increase the understanding of disease ecology and detect evidence of spillover to humans, characterize parasite communities, and develop predictive host, ectoparasites and virus/bacteria. The study aims to help detect spillover from bats to humans in India and develop predictive maps in Cambodia.

TECHNICAL DESCRIPTION AND OBJECTIVES

The research I conduct is to inform and improve biosurveillance to more efficaciously use resources. We are surveying bats and small mammals across Cambodia and in India to understand the disease ecology of these systems and detect evidence of spillover to humans, characterize parasite communities, and develop predictive host, ectoparasite and virus/bacteria.

This work is labor intensive and often is performed in difficult to reach areas. The coordination with local agencies is key for obtaining permission. We don't have a great way to age a bat or determine if a bat is sick.

On a global scale, we understand what variables are associated expected presence and emergence. Shedding appears locally influenced (age/ gender, partuition peaks)

APPROACH

India: Studying an annual bat harvest in a remote part of India to understand risk of spillover
Difficulty reaching site and maintaining cold chain (car breakdowns)
Obtain permission from village council
Building capacity in a conservation genetics lab
Difficulty in timely ordering of reagents
Permits to ship samples overseas
Cambodia: Develop predictive maps for bat/small mammal/ectoparasite/virus & bacteria
As this is a randomly selected model, some points are difficult to access
Pseudoreplicate
Acoustic call library
Difficulty in timely ordering of reagents
Landscape change & access to maps

MILESTONES, SCHEDULE, AND STATUS

All delayed due to legal contracts, transfer of funds, and delays in purchasing reagents
India: Two year project. Originally wanted to sample before and after harvest, but logistically unfeasible

- Visited for 2 harvests. Have large sample bank. Serology complete. NGS logistics is difficult
- Plan to visit this harvest in 2018

Cambodia: Sampled in every province. Running preliminary models to tell us how many sites we need to visit. Setting up lab in July where we will begin testing samples (delays in ordering)

IMPACT

India: If we can detect spillover to humans directly from bats (same population of humans and same species of bats)

- Develop lab tools to see if these are occurring in other sites (specifically Cambodia and Singapore)
- Provide information campaign and PPE for bat harvesters, in addition to using harp trap for more sustainable harvest

Cambodia: Develop predictive maps and see if these can be validated. If this approach works, it would be beneficial to beta-test in the greater Mekong. Can we determine mappable attributes associated with the presence of absence of organisms of interest

Colorado State University

Dr. Rebekah Kading presented her labs work on investigating the role of bats as reservoirs in arbovirus transmission cycles. Through a multidisciplinary approach this study includes work on viral disease pathogenesis, molecular characterization, ecology, and biosurveillance. The study aims to characterize novel molecular, virological, and field data on bat associated orbiviruses and bat disease response to foreign pathogens.

TECHNICAL DESCRIPTION AND OBJECTIVES

My lab is investigating the role of bats as reservoirs in arbovirus transmission cycles. Our multidisciplinary approach includes studies on viral disease pathogenesis, molecular characterization, ecology, and biosurveillance. Currently we are studying bat-associated orbiviruses, including Bukakata orbivirus, isolated from an Egyptian rousette bat in Uganda.

1. Underlying challenges
   - Reagent and assay development for studying new viruses; need *in vitro* and *in vivo* model systems
2. Current state of understanding (=poor)
   - Mosquitoes feed on bats
   - Arboviruses isolated from naturally-infected bats
   - Some seroprevalence data available
   - Overall: field and experimental data are sparse

APPROACH

Specific aims:
1. Characterize clinical disease manifestations, virus shedding patterns, and immune kinetics of Bukakata orbivirus infection in Jamaican fruit bats (*Artibeus jamaicensis*)
2. Assess the reassortment potential of tick-borne orbiviruses in vector and vertebrate cell lines
3. Investigate the prevalence of Bukakata orbivirus exposure in bat, tick, and human populations in Uganda

Challenges: assay development and positive controls; tick cell line establishment; high-throughput assessment of reassortment among 10-segmented viruses
Key steps: model system development; reagents and approvals; sample collection and testing; analysis and interpretation
Tools and technology: IHC, qRT-PCR, ddPCR, cell culture, IFA, NGS

MILESTONES, SCHEDULE, AND STATUS

1. Timeline for delivery
   - Aim 1: Spring 2019
   - Aim 2: Fall 2019
   - Aim 3: Spring 2020 or earlier
2. Project status
   - Aim 1: infections completed; samples still to be tested
   - Aim 2: to begin this summer
   - Aim 3: additional bat, tick, and human samples available but not yet tested; qRT-PCR assay optimized

Colorado State University
Rebekah Kading, PhD

IMPACT

1. Quantitative
   - Publications: at least 1 manuscript per aim; another on Bukakata virus discovery and molecular and *in vitro* characterization
   - Grant proposals
     - Bat disease response observed for Bukakata virus in JFBs – continued studies planned on pathogenesis
     - Role of orbivirus reassortment on emergence and zoonotic potential
     - Continued field studies and biosurveillance capacity building efforts
2. Regional and global – novel molecular, virological and field data on bat-associated orbiviruses. Bat disease response to a foreign pathogen.

National Center for Disease Control and Public Health, Georgia

Dr. Lela Urushadze, Dr. Tamar Kutateladze, and Dr. Keti Sidamonidze presented on their research of understanding the risk of bat borne zoonotic disease emergence in Western Asia, molecular epidemiology and phylogenetic analysis of zoonotic pathogens in Georgian bats, and the assessment of emerging pathogens from bats in Ukraine and Georgia. The research highlights several key points to include that bats in Georgia are vulnerable to several bacterial pathogens and may play an important role in maintaining those agents in nature. The research aims to help assess the pathogen diversity in bat populations and their role in the transmission of zoonotic infections to humans.

TECHNICAL DESCRIPTION AND OBJECTIVES

1. I am Key person of Project "Understanding the Risk of Bat-Borne Zoonotic Disease Emergence in Western Asia" from Georgian side.
2. My PHD is about, "Molecular epidemiology and phylogenetic analyze zoonotic pathogens in Georgian bats"
3. Working on project "Assessment of Emerging Pathogens From Bats in Ukraine and Georgia"
4. Working on project "Risk of infection from insectivorous bat borne viruses in incidental hosts: comparative phylogeography of filoviruses, coronaviruses, and paramyxoviruses in the Philippines and the Country of Georgia"

APPROACH

1. Workshops for bats sampling, Trap and collection non-lethal specimens from bats and associated ecological data, Test specimens for CoVs via PCR at regional labs; sequence positive specimens in Georgia.
2. Collection, description and analyses all data what was done from 2012 till today for bat borne pathogens research in Georgia.
3. According the reviewers comments we are working on new version for abstract, because It is would be first study for bat borne pathogens in Ukraine. For Georgia project would be beneficial according the data what we have under preliminary research, but further studies need to be carried out to understand the importance of these agents in both public health and animal health.
4. Due to reviewer's suggestions, we are participating for rewriting abstract for the DTRA BAA. Ten roosts in the Georgia will be monitored every month, including human structures and caves in both countries that are permanently occupied by insectivorous bat species

MILESTONES, SCHEDULE, AND STATUS

1. Characterization of bat coronaviruses (CoV) across Western Asia

   Analyze and map bat pathogen spillover risk by including broader, regional ecological data- ongoing project, first year
2. Day of Dissertation defense July 5th 2018.
3. Working on new version of abstract for resubmission for DTRA BAA- for September 2018
4. Resubmission process of abstract for DTRA BAA- for September 2018

IMPACT

1. Participation for establishment Western Asia Bat Research Network (WAB-Net) Improvement local capacity for zoonotic disease investigations and early detection from Georgian side
2. I concluded, that bats from Georgia are vulnerable to several bacterial pathogens. These data highlighted that bats may play important role in maintaining those agents in nature.
3. Project will help to assessment of the pathogen diversity in bat populations of Ukraine and Georgia, to determine their role on the transmission of potentially zoonotic infectious diseases to humans; characterization of the novel viruses and bacteria from Insectivorous Bats in Ukraine and Georgia; development of a risk assessment framework for both countries.
4. Due to the fact that these countries share many of the same genera of insectivorous bats and are species rich. This project will provide data on bat-borne virus epidemiology in tropical (Philippines) and temperate sites (Georgia) drivers .

WHO CC for Research and Training in Viral Zoonoses, King Chulalongkorn Memorial Hospital

Dr. Supaporn Wacharapluesadee explained her work to assess and mitigate the risk of bat borne pathogens to communities. By conducting a systemic and longitudinal surveillance to address the internal and external factors that enhance infectivity in bats and conducting serosurveillance in multiple bat borne pathogens and bat species, the study will be able to better understand the risk of bat borne pathogens and educate communities.

TECHNICAL DESCRIPTION AND OBJECTIVES

Underlying Challenge

- Seasonal prevalence of Coronavirus (CoV) in Wrinkle-lipped free-tailed bat (*Chaerephon plicata*)
- Bat borne viral pathogens and risk to the communities; people in the community are unaware (PREDICT project)
- Serology study of bat borne pathogens in Thailand needed

Current State of Understanding

- MERS-related CoV was found in *C. plicata* in certain months in Thailand
- There is a relationship between virus and host species and/or geography
- No education of villagers at-risk from infection of bat viruses; no tools in place to help prevention of infection
- Lack of serology data on new bat borne viral pathogens in Thailand; only Nipah and Ebola have been studied

APPROACH

What can be done to address the challenges?

- Conduct a systemic and longitudinal surveillance to address the internal and external factors that enhance infectivity in bats
- Educate communities with continued workshops and evaluation
- Conduct serosurveillance in multiple bat borne pathogens and bat species

What are the key steps along the way

- Identify and prioritize pathogens of interest and its reservoir
- Identify the key factors involved in the viral infection
- Create tools (education and prevention tools) for implementing in the communities at-risk from bat infection

What tools and technologies are needed to address the challenges?

- Diagnostic tools: serology, molecular, NGS, viral isolation
- Prevention tools: guidebook, innovative instrument

MILESTONES, SCHEDULE, AND STATUS

Delivery	Q3Y 18	Q1Y 19	Q2Y 19	Q3Y 19
Knowledge of CoV's seasonal prevalence	x			
Finding bat borne viral pathogens	x	x	x	x
Identify preliminary factor(s) that facilitate infection		x	x	x
Risk behaviors/ culture of community	x	x	x	x
Serological data			x	x
Deeper viral characterizations such as NGS and isolation		x	x	x

Project name	Status
CoV seasonal prevalence	Collection and Testing completed
PREDICT project	Sample collection will be completed in July 2018, testing to continue
Serology	Project will start July 2018

IMPACT

Define the quantitative impact of project.

- New knowledge that will be lead to the development of a guideline to detect, control, and prevent an outbreak of bat borne pathogens
- Implementation tool or strategy to help prevent infection from bats at the community level
- Community levels to learn how to prevent infection and spread of bat borne pathogens

Define the regional and global impact.

- Regional networking to share and support training and knowledge acquired
- Knowledge to prevent spread and identify hot spots globally

Will this lead to the need for future studies?

Yes, several factors related to the infectivity of virus in bats are unclear and needs more studies, both natural infection and an animal model studies.

Research Institute for Tropical Medicine, Philippines

Dr. Catalino Demetria presented on his proposed research on bat assay development. He then presented on his current research on the Dengue vaccine to improve the surveillance data of other Flaviruese that are mistaken for Dengue and to provide tools to determine if the vaccine have seroconverted and to determine the serostatus of the population.

TECHNICAL DESCRIPTION AND OBJECTIVES

The research is about development of new serological test in the light of CYD dengue vaccine controversy in the Philippines. The new test aims to distinguish between vaccine induced antibodies from wild type strain. One of the challenges is having around 80% seroprevalence of dengue IgG in the Population. Previous research shows that vaccine induced antibodies are not reactive to ELISAs using NS1 antigens since this is not a component of the chimeric vaccine. The vaccine has gene encoding NS1 from yellow fever virus which served as the backbone of the chimeric vaccine.

APPROACH

Develop a multiplex bead -based assay that will be able to differentiate between naturally acquired antibodies from vaccine induced. The research will make use of Luminex technology's strength which is multiplexing. The panel will include Dengue serotypes 1-4 for both envelope protein and NS1, Zika virus, Jap E., Yellow Fever Virus and Chikungunya virus. This will also improve surveillance data for the other Flaviviruses.

MILESTONES, SCHEDULE, AND STATUS

The project is expected to be finished in 30 months. Deliverables include a working assay.

IMPACT

The research will be able try to accomplish the following;
- Provide a tool to determine if vaccinees have seroconverted or not
- Improve surveillance data of other Flaviruese and Chikungunya virus which is often clinically mistaken for Dengue
- Provide a tool to determine the serostatus of the population

Royal Scientific Society, Jordan

Dr. Nesreen Alhmoud presented on understanding the risk of bat-borne zoonotic diseases emergence in Western Asia. This research project is in collaboration with the National Center for Disease Control and Public Health in Georgia. The research aims to characterize bat coronaviruses across Western Asia, analyze and map bat borne pathogen spillover risk, and create a collaborative Western Asia Bat Research Network.

TECHNICAL DESCRIPTION AND OBJECTIVES

Understanding the Risk of Bat-Borne Zoonotic Disease Emergence in Western Asia

Current research on the distribution of bats, diversity of their viruses, and potential for zoonotic disease emergence in Western Asia is severely limited.

To fill this gap and contribute to biological threat reduction, the project proposes a hypothesis-driven One Health research project focused on *characterizing bat coronavirus diversity and the risk of bat-borne zoonotic disease emergence*.

APPROACH

Objective 1: Characterize bat coronaviruses (CoV) across Western Asia; this will include

- extensive nonlethal field sampling of bats,
- screening and characterization of viruses from bat specimens (Jordan, Georgia Pakistan & Turkey)

Objective 2: Analyze and map bat pathogen spillover risk by including broader, regional ecological data

Objective 3: Creation of a collaborative Western Asia Bat Research Network (WAB-Net) – including key researchers and public health representatives from >12 countries

- Annual workshop
- Hands on Training – Research Exchanges

MILESTONES, SCHEDULE, AND STATUS

Timeline

October 2017 – January 2022

Year 1 (October 2017-September 2018)

- Task 1: Establish robust scientific research platform to understand zoonotic disease risk in Western Asia.
- Task 2: Bat specimen and disease ecology field data collection.
- Task 3: Regional bat coronavirus characterization.
- Task 4: Compile and disseminate research results and reports to stakeholders.

Jordan:

Field Sampling: July 2018

IMPACT

Regionally:

- The RSS Center will act as a liaison between WAB-Net and other regional networks.
- The RSS Center will serve as a regional hub for laboratory research and training.

Globally:

The integrated approach of the project presents a coordinated strategy to advance scientific knowledge around transboundary zoonotic disease emergence risk in Western Asia to inform early detection, diagnosis, and response to support the Global Health Security Agenda and CBEP goals.

Annex D: Recommendations for CBEP

The BOHRN meeting in Saskatoon provided a forum for productive discussions regarding potential research activities and projects; however, it also highlighted the need to expand the network to include other sources of funding for its sustainment. GSE submits the following recommendations to CBEP to both broaden the network and ensure it meets its objectives. These recommendations are designed to provide a roadmap to develop enduring capabilities for BOHRN.

Recommendation 1: Engage Other Interested Funding Sources

GSE proposes a step-wise approach to engaging other interested funding sources. This approach aims to provide a forum for collaboration within and across DoD agencies. By taking this approach, CBEP and the steering committee will be able to align projected projects and research within DoD interest.

Step 1: Convene a meeting for USG Funding Sources, including the following departments and organizations (at a minimum):

- RD CB (JSTO)
- USAMRIID
- AFHSB
- NIH NIAID
- DARPA

This meeting could include the following objectives (1) gain buy-in on BOHRN objectives and end states; (2) outline funding departments' equities and trends, mechanisms, timelines, and active projects; and (3) discuss alignment opportunities (mechanisms) and challenges.

Step 2: Convene a meeting for both USG funders and International Funders. To further BOHRN's capabilities, projects and overall outreach, an additional group of funders outside of DoD need to be included. This should include the following (at a minimum):

Convene Funders / Researchers Meeting

- BOHRN Members
- USG Funding Sources
- NGOs

A funders meeting could include the following objectives (1) gain buy-in on BOHRN objectives and end states; (2) outline funding departments' equities and trends, mechanisms, timelines, and active projects; and (3) discuss alignment opportunities (mechanisms) and challenges.

Recommendation 2: CBEP Coordinate on an Request for Information or Proposal with other Partners

GSE suggest that CBEP encourage BOHRN SC members to develop abstracts in-line with Focus Areas to support the development of program Unfunded Requirements (UFRs), Requests for Information, or Request for Proposals. In addition to fulfilling objectives of BOHRN, CBEP should shape these documents to answer force protection benefits for bat research, coordination with DTRA RD CB and/or global capability gaps for bat-borne pathogen threats assigned by other USG and NGO funding sources. By developing these requirements, CBEP will be able to assess its ability to commit to the working group projects within the scope of the DTRA mission. Requirements developed by CBEP will help outline the needs for additional funders for specific focus areas.

Recommendation 2 requirements:

- Analyze fund mapping application for bat migration patterns and overlays for human populations, pro-med data for fevers of unknown origin

- Write a STEP TD for BOHRN

Recommendation 3: Support Attendance to Relevant Training Events

GSE recommends the continual support of BOHRN members to attend relevant training events. By increasing the experience through training, BOHRN members will be able to improve and develop skills to better aid in the working group task. This will help BOHRN to meet its overall objectives. In addition, these trainings and conferences help socialize BOHRN to a new individuals and bat networks. This will help BOHRN develop its regional working groups and connect with existing networks.

GSE recommends the following workshops as examples of training events. In addition, partnerships with universities for developing and participating in future trainings should be considered:

- US Davis Galaxy Training Workshop http://bioinformatics.ucdavis.edu/training/
- Harvard Bioinformatics Workshops https://catalyst.harvard.edu/services/bioinformatics-workshops/

From: Grant, Evan H >
Sent: Thursday, April 09, 2020 5:39 PM EDT
To: castlekl >; O'Shea, Thomas ; raina.plowright >; dreeder Daniel.Streicker ; sja ; epstein >; kate.e.jones < >; ckjohnson wfrick ; linfa.wang < jit8@ a.peel ; rbaric >; Kading,Rebekah >; Amy.T.Gilbert >; Lorch, Jeffrey M >
CC: Runge, Michael C >; Cryan, Paul >; olival >; Sleeman, Jonathan M < ; Coleman, Jeremy T ; Gibbs, Samantha ; Hopkins, Maria-Richetta (Camille) C >
Subject: Expert judgement for SARS-CoV-2 risk assessment for North American bats
Attachment(s): "Assessing the Risks Posed by SARS CoV. intro Elicitation v2.docx","BatEE Practice Questions v2.xlsx"

Hello experts,

Thank you for volunteering your time and expertise to help estimate the risk of SARS-CoV-2 to North American bats. Mike Runge and I (Evan Grant), with the U.S. Geological Survey Patuxent Wildlife Research Center, are facilitating this effort in collaboration with the USGS National Wildlife Health Center, USGS Fort Collins Science Center, USFWS, and EcoHealth Alliance. We are conducting a rapid assessment of the risks for transmission of SARS-CoV-2 from humans to bats. The goal is to provide scientific information that will guide wildlife management agency response to this potential risk, including development of management recommendations and mitigation strategies.

Attached please find two documents: (1) an introduction to expert elicitation with some background on the issue we are addressing, and (2) a spreadsheet <BatEE Practice Questions v2.xlsx> with calibration questions. There are three tabs (corresponding to the three questions) in the accompanying spreadsheet, and a fourth tab that summarizes the responses and the calculated mean and standard deviation for each question.

We have a very tight timeline to provide guidance to U.S. management agencies, so we thank you for your participation along the following timeline:

i. Respond to ehgrant with your responses to the calibration questions in the attached spreadsheet (due by 12 PM ET 10 Apr)
ii. Review the background information and elicitation questions (we will send these additional documents to you by 6 pm ET 10 Apr)
iii. Respond with your initial responses to the questions (due by 6 PM ET 13 Apr)
iv. Be available for a 2-hr conference call to discuss initial responses and share insights (4 PM ET 14 Apr – and/or – 4 PM ET 15 Apr)
v. Revise and send your second-round responses to the questions (due 24 hours after the last conference call)

Thank you in advance for your participation. If you have questions – please contact Evan .

Kindest regards,
Evan and Mike

Assessing the Risks Posed by SARS CoV-2 in and via North American Bats
A Rapid Decision and Risk Assessment

Introduction to Expert Elicitation for an Expert Panel

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U.S. Geological Survey Patuxent Wildlife Research Center
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09 April 2020

Introduction

The novel betacoronavirus, SARS-CoV-2, that has caused a pandemic disease in humans, arose from a mammalian host, possibly Old-World bats in the family *Rhinolophidae*; the closest known virus discovered in wildlife was found in a horseshoe bat (*Rhinolopus affinis*) from Yunnan province in China (Zhou et al. 2000). No SARS-related betacoronaviruses have yet been identified in New-World bats, but a different type of betacoronavirus has been identified in a New-World bat from Mexico (Anthony et al. 2013). This raises an important question about whether North and South American bats could be vulnerable to infection with SARS-CoV-2, via contact with humans, which in turn raises questions about whether there may be reciprocal spread to humans via a bat reservoir. This inquiry is designed to be a rapid assessment of the risk of transmission of SARS-CoV-2 from humans to North American bats, the management contexts in which this risk might be relevant, and an assessment of possible mitigation actions that may be implemented by those who come into contact with bats or their habitats.

Justification for an expert elicitation

Ideally, we would obtain parameter estimates from empirical data and associated mathematical models. Because these information are unavailable and time is of the essence for decision makers, we aim to use an expert panel to elicit parameter values with associated uncertainty, using techniques of expert judgment that utilize best available scientific information, account for uncertainty, and reduce bias (Morgan 2014, Sutherland and Burgman 2015).

Expert elicitation is a formal, structured process of obtaining expert judgment for specific questions. An expert is someone who possesses substantive information on a particular topic that is not widely known by others. We know that experts have knowledge, often privileged knowledge, that accrues as a result of their research and experience, even about processes for which data have not been collected. The question is how to extract that knowledge accurately and precisely. Expert judgment is a quantitative expression of an expert's belief based on knowledge and experience; it is an informed belief. Expert elicitation can provide improved information over single-expert inquiry when a diverse group of experts is asked to provide estimates, using a facilitated approach with discrete opportunities for information sharing, provision of estimates, and review of summarized information (Martin et al. 2012). Expert elicitation, when conducted with the same level of rigor as the collection and use of empirical data, can result in reliable predictions (e.g., O'Hagan et al. 2006, Speirs-Bridge et al. 2010, Runge et al. 2011, Martin et al. 2012, Adams-Hosking et al. 2016).

An expert elicitation is governed by specific protocols to avoid inherent biases resulting from cognitive traps. These cognitive traps are shortcuts, or heuristics, that serve us well for simple decisions but result in biased estimates for more complex tasks (O'Hagan 2019). These biases include:

- Availability bias (experts will be influenced by evidence or events that are easily recalled)
- Anchoring bias (experts fail to consider possible values far from an initial estimate)
- Overconfidence (experts tend to underestimate their uncertainty, and make forecasts that are too narrow)
- Representativeness bias (a tendency to think of probabilities related to readily-available examples)
- Motivational bias (an innate desire to further our own interests)

When the number of experts is limited, we would additionally be concerned about small-sample bias.

There are additional biases that arise through the behavior of groups. To some extent, these can be collectively referred to as "groupthink", the tendency for groups to converge too quickly on consensus estimates or decisions and to ignore or forget divergent views that are held my members of the group. In this way, groups of experts can be collectively overconfident, or even biased.

So, the methodological challenge of expert judgment is to reliably extract the desired information from each member of a group of experts, without falling into the cognitive and behavioral biases that can undermine such an exercise. The best practices in an expert judgment approach have evolved by considering this challenge, testing approaches via experiments, and recommending a set of protocols for conducting an expert elicitation.

Steps in an elicitation

We are using a protocol based on a modified Delphi method called the IDEA protocol (Hanea et al. 2017), with the four-point elicitation method (Speirs-Bridge et al. 2010). There are six steps in the process:

1) Select experts
2) Calibrate experts (seed questions and sharing available information)
3) Elicitation of parameter values (4-point method)
4) Summary, review, and discussion (aimed at reducing linguistic uncertainty – relating to the instructions – and sharing insights, not to reach consensus)
5) Experts revise their initial values (if desired)
6) Aggregate information across experts

Steps 3-6 comprise a modified Delphi approach (described below).

Selection of experts

Experts are individuals with specific subject-matter experience and knowledge. Experts should have relevant expertise which may come from formal training and be demonstrated by

professional accomplishments such as peer-reviewed publications, familiarity with and knowledge of the system or related systems, willingness to participate fully and impartially in an elicitation process, and good interpersonal and communication skills (Ayyub 2001, Fazey et al., 2006).

Groups of experts have been found to perform as well (in terms of providing information close to the true empirically observed data) as more specific experts (e.g., Burgman et al. 2011). The expert panel should be diverse – possessing knowledge of North American bats, zoonotic disease, and possible mitigation strategies; representing multiple institutions, specialization, and gender. The optimal number of experts for a structured elicitation is between 5 and 12, with decreasing marginal benefit after 12 experts (Hogarth 1978, Hemming et al. 2018).

Calibration questions

Before starting the elicitation concerning the questions of interest, we will provide the expert panel a chance to practice the elicitation methods. We will provide questions that are known (i.e., we have identified values from the literature, but are unlikely to be known precisely by experts). We use these questions to ensure that the instructions are understood by experts, and to allow experts a chance to calibrate their estimates of uncertainty.

Three questions are listed below (see accompanying spreadsheet < BatEE Practice Questions v2.xlsx>). For each question, we ask experts to provide four responses: an estimate that represents your view of the lowest reasonable value; an estimate of the highest reasonable value; an estimate that represents the best central value; and your confidence that the true value lies within the low and high values that you have provided. We have attached a spreadsheet in which you can enter these values; the spreadsheet automatically calculates a probability distribution that represents your uncertainty, as immediate feedback about whether your responses reflect your expert belief. This is a "closed book" exercise (we ask that you do not check this information in books or online). Please return your answers to us; we will use them to provide feedback to the group about your individual and collective accuracy and precision; as a means of allowing you to calibrate your thinking process prior to the elicitation for the questions of central importance.

The calibration questions are:

1) What is the mean forearm length (in centimeters) of an adult little brown bat (*Myotis lucifugus*)?

2) What is the average number of subsequent white-nose syndrome infections resulting from a single infected little brown bat (i.e., R_0)?

3) In a population that has already experienced decline due to WNS, out of 100 adult female little brown bats, how many would you expect to breed in a given year?

Elicitation of parameters using a modified Delphi approach

To generate empirical estimates of each parameter, we use a '4-point' elicitation method. This approach has been shown to reduce overconfidence in experts (Speirs-Bridge et al. 2010) and can generate a quantitative estimate from experts who may be uncomfortable providing

estimates. We derive a median and credible interval for each parameter from the following four questions:

1) Realistically, what is the lowest reasonable value for the parameter?
2) Realistically, what is the highest reasonable value for the parameter?
3) Realistically, what is the most likely reasonable value (i.e., your best estimate) for the parameter?
4) How confident are you that the true value is between the lowest and highest values you provided?

We then assume that the most likely value is the median value, and combine the upper and lower estimates and the reported confidence to generate a credible interval.

Experts provide their estimates anonymously, and summaries are provided that maintain anonymity, to avoid biases associated with group thinking and dominant personalities. Experts are encouraged to discuss the information during a facilitated discussion of the summarized data, after which experts have the opportunity to revise any of their estimates.

The modified Delphi sequence (independent-group-independent) is important to preserve the unique insights help by individuals while at the same time allowing the benefit of wisdom to be shared. By asking experts to perform the first estimate independently, their own personal views are captured. By allowing the expert to share and discuss their initial estimates, we can explore whether there is residual linguistic uncertainty that needs to be corrected and we can allow insights to be shared across experts. By allowing the final estimates to be made independently, we guard against dominant voices in the group and retain the diversity of insights among the experts.

Aggregation of information across experts

Following the elicitation, we will aggregate the results to produce a single probability distribution that represents an estimate, with uncertainty, for each parameter. To do this, we will first transform the four-point elicitation results into a probability distribution for each expert. We will then average these probability distributions across experts, with equal weighting. (There are involved methods for weighting experts based on sets of calibration questions, but we are both skeptical of these methods and limited on time).

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	A	B	C	D	E	F
1						
2		1. What is the mean forearm length (in centimeters) of an adult little brown bat (*Myotis lucifugus*)?				
3						Assume: no
4						Quantile
5		What is the lowest reasonable estimate?				0.5
6		What is the highest reasonable estimate?				0.5
7		What is your central estimate?				0.5
8		How confidence are you that the true mean is between your low and high estimates?		Error: Confidence should be >50		
9		(Confidence should be a number greater than 50 and less than 100)				
10						x
11						#N/A
12						#N/A
13						#N/A
14						#N/A
15						#N/A
16						#N/A
17						#N/A
18						#N/A
19						#N/A
20						#N/A
21						#N/A
22						#N/A
23						#N/A
24						#N/A
25						#N/A
26						#N/A
27						#N/A
28						#N/A
29						#N/A
30						#N/A
31						#N/A
32						#N/A
33						#N/A
34						#N/A
35						#N/A
36						#N/A

	G	H	I	J
1				
2				
3	mal uncertainty distribution			
4	IPDF			
5	0	#N/A	mean	#N/A
6	0	#N/A	sd	#N/A
7	0			
8				
9				
10	pdf			
11	#N/A			
12	#N/A			
13	#N/A			
14	#N/A			
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16	#N/A			
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31	#N/A			
32	#N/A			
33	#N/A			
34	#N/A			
35	#N/A			
36	#N/A			

	A	B	C	D	E	F
1						
2		2. What is the average number of subsequent white-nose syndrome infections resulting from a single infected little brown bat (i.e., R_0)?				
3						Assume: log
4				ln(x)		Quantile
5		What is the lowest reasonable estimate?		Error: R0 must be >0		0.5
6		What is the highest reasonable estimate?		Error: R0 must be >0		0.5
7		What is your central estimate?		Error: R0 must be >0		0.5
8		How confidence are you that the true mean is between your low and high estimates?		Error: Confidence should be >50		
9		(Confidence should be a number between 50 and 100)				
10					x	ln(x)
11					#N/A	#N/A
12			Based on your responses:		#N/A	#N/A
13			$p(R_0>1)$	#N/A	#N/A	#N/A
14					#N/A	#N/A
15					#N/A	#N/A
16					#N/A	#N/A
17					#N/A	#N/A
18					#N/A	#N/A
19					#N/A	#N/A
20					#N/A	#N/A
21					#N/A	#N/A
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33					#N/A	#N/A
34					#N/A	#N/A
35					#N/A	#N/A
36					#N/A	#N/A

	G	H	I	J
1				
2				
3	-normal uncertainty distribution			
4	IPDF			
5	0	#N/A	mean	#N/A
6	0	#N/A	sd	#N/A
7	0		min	#N/A
8			max	#N/A
9			delta	#N/A
10	pdf			
11	#N/A			
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31	#N/A			
32	#N/A			
33	#N/A			
34	#N/A			
35	#N/A			
36	#N/A			

	A	B	C	D	E	F
1						
2		3. In a population that has already experienced decline due to WNS, out of 100 adult female little brown bats, how many would you expect to breed in a given year?				
3						Assume: logi
4				logit(x)		Quantile
5		What is the lowest reasonable estimate?		Error: must be between 0 and 100		0.5
6		What is the highest reasonable estimate?		Error: must be between 0 and 100		0.5
7		What is your central estimate?		Error: must be between 0 and 100		0.5
8		How confidence are you that the true mean is between your low and high estimates?		Error: Confidence should be >50		
9		(Confidence should be a number between 50 and 100)				
10					x	logit(x)
11					#N/A	#N/A
12					#N/A	#N/A
13					#N/A	#N/A
14					#N/A	#N/A
15					#N/A	#N/A
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33					#N/A	#N/A
34					#N/A	#N/A
35					#N/A	#N/A
36					#N/A	#N/A

	G	H	I	J
1				
2				
3	it-normal uncertainty distribution			
4	IPDF			
5	0	#N/A	mean	#N/A
6	0	#N/A	sd	#N/A
7	0		min	#N/A
8			max	#N/A
9			delta	#N/A
10	pdf			
11	#N/A			
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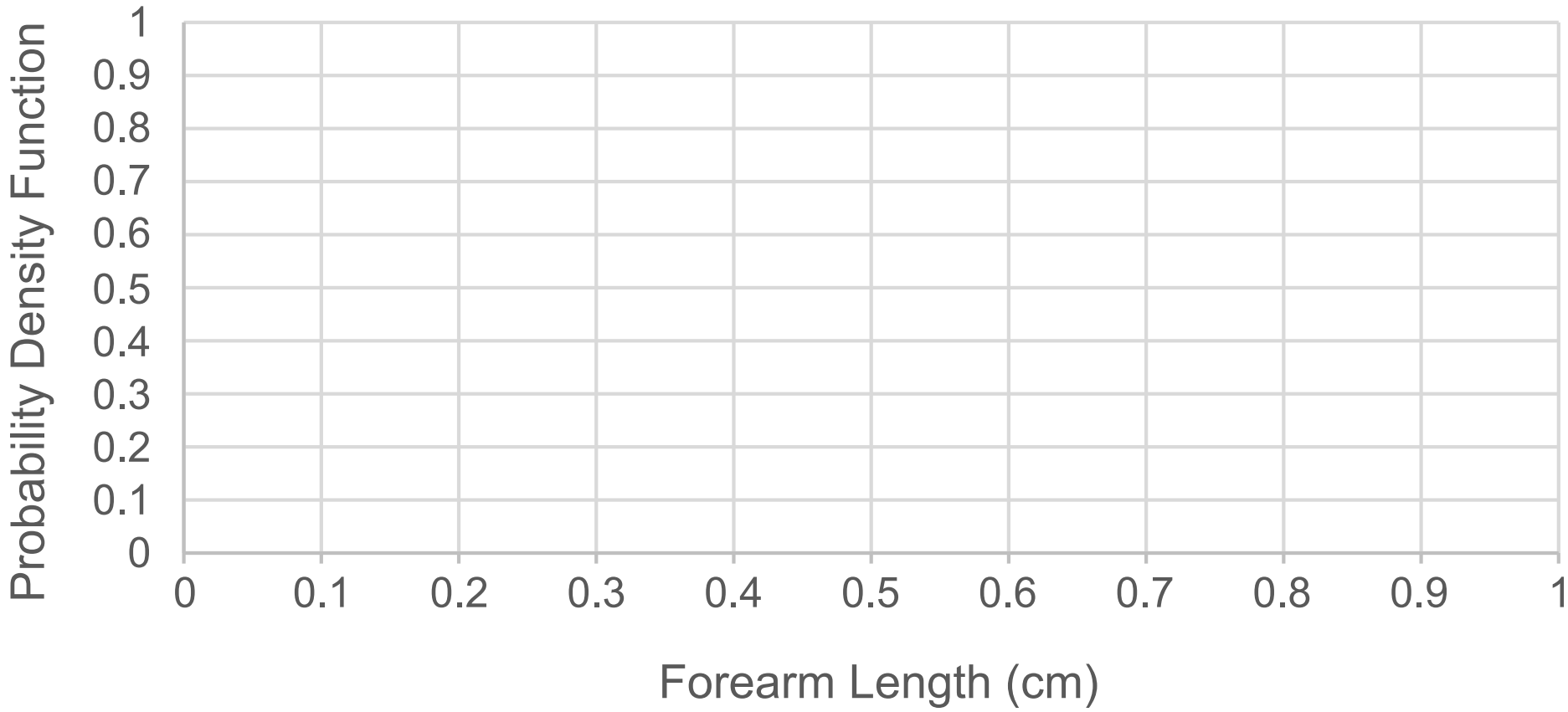
31	#N/A			
32	#N/A			
33	#N/A			
34	#N/A			
35	#N/A			
36	#N/A			

	A	B	C	D	E	F	G	H	I
1									
2									
3			lo	hi	best	CI	distn	mean	sd
4		Question 1	0	0	0	0	normal	#N/A	#N/A
5		Question 2	0	0	0	0	log-normal	#N/A	#N/A
6		Question 3	0	0	0	0	logit-normal	#N/A	#N/A


Best-fit Probability Distribution for Your Responses
Probability Density Function
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0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
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0.3
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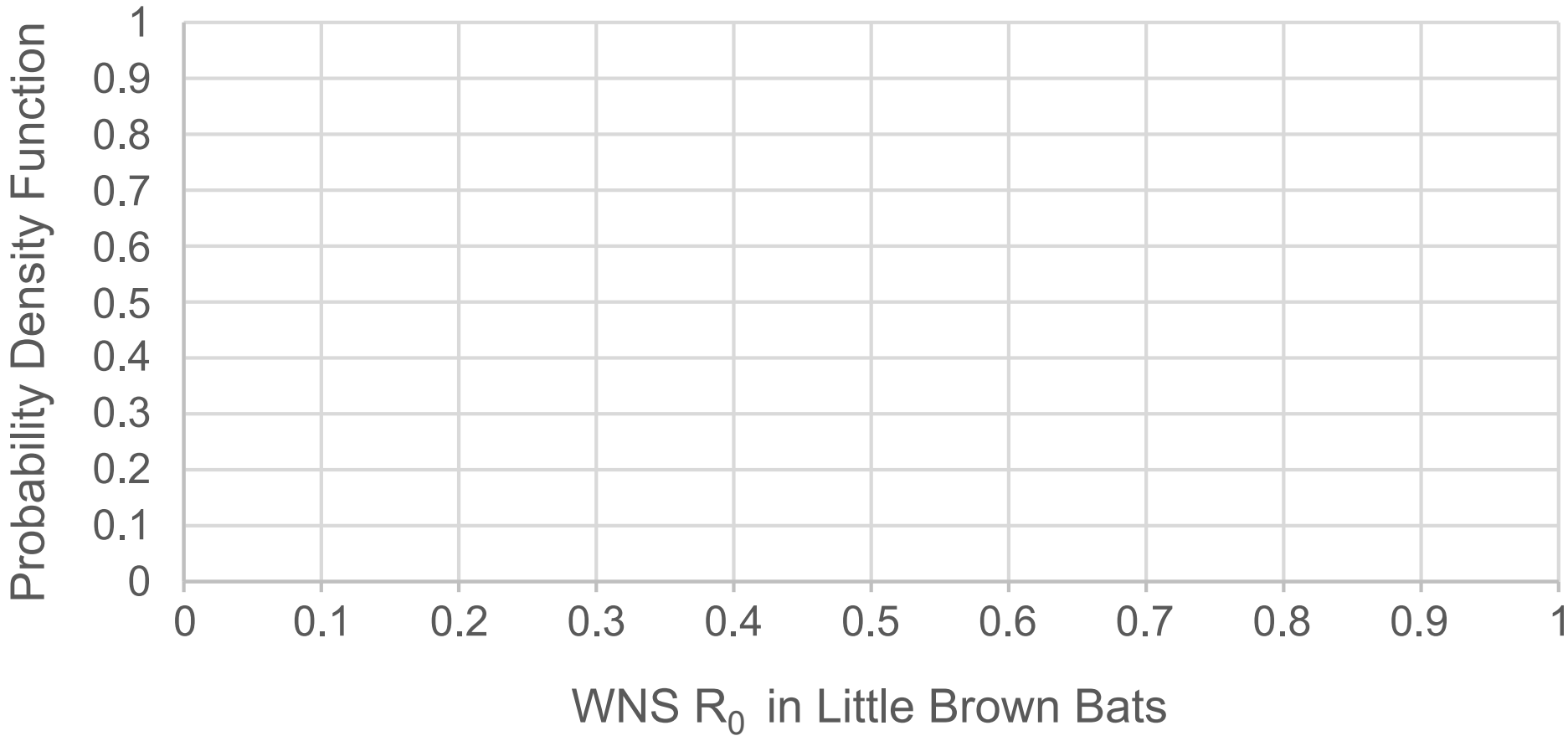
0.9
1
Forearm Length (cm)


Best-fit Probability Distribution for Your Responses
Probability Density Function
1
0.9
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0.6
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0.4
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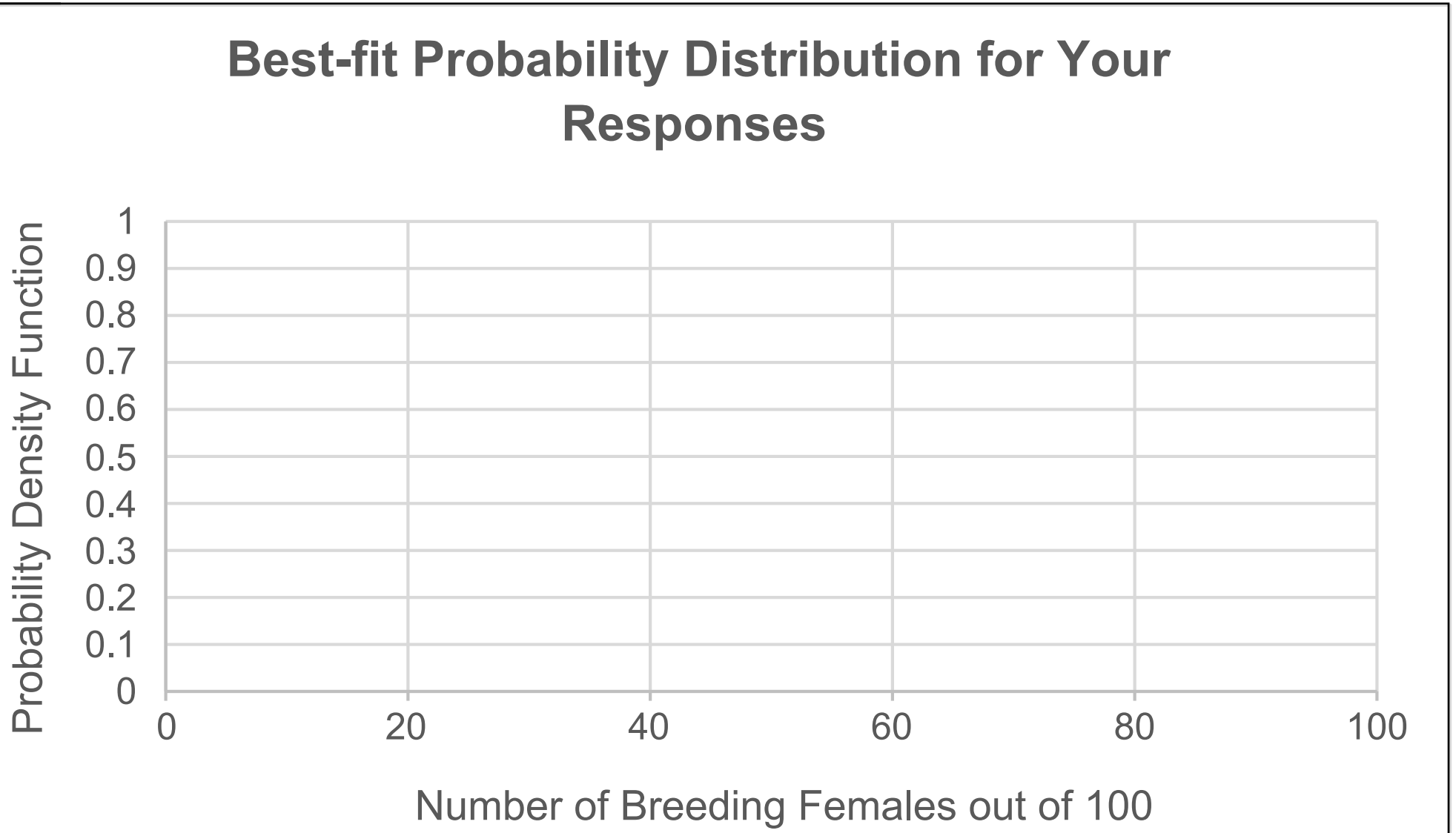
0.2
0.1
0
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
WNS R_0 in Little Brown Bats


Best-fit Probability Distribution for Your Responses
Probability Density Function
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
20
40
60
80
100
Number of Breeding Females out of 100

Assessing the Risks Posed by SARS-CoV-2 in and via North American Bats

Expert Elicitation, Discussion after Round 1

16 April 2020

Key insights/clarifications from discussion:

Questions 1-3, regarding research, survey, monitoring, and management (RSM):

Consider the number exposed by each member of a research team, but we're looking at individual (per-human) exposure while conducting each of the activities. We assume that individuals conducting research are: asymptomatic, but actively shedding a sufficient amount of virus that may lead to infection of a little brown bat

Q1: The description of typical handling procedures for researchers working with bats (handling of LBB typical of other species: LBB occur in colonies with other species) includes:

1) Duration of contact 1-2 min per bat
2) Holding bat within 12 inches of face
3) Take measurements
4) Sexing (blowing on bats)
5) Discouraging biting (blowing on bats)

Q2: the definition of enclosed space:

1) Includes caves, mines
2) Various sizes and morphologies – variation among sites in airflow
3) Activity in enclosed space may be 1hr+
4) Mixture of bats that are stationary (roosting) and in flight

Q3: Typical activities that are within 6 ft but **not** in an enclosed space:

1) Typically, the management agency conducting emergence counts
2) May occur at cave and mine entrances, bridges

Questions 4-5 (regarding Wildlife Rehabilitation, WR) & Questions 6-7 (regarding Wildlife Control Operators)

WR – typical activities

1) In general, WR have repeated contact with small number of bats
    a. Hand feeding (especially LBB), rehab injuries
    b. Duration of contact: weeks to months
2) Typically dedicate an enclosed room in house, garage, shed
3) Repeated activity within room over weeks-months
4) Those that don't handle bats might nevertheless be in close proximity, feeding bats, recording data for someone who is handling the bats, etc.
5)

Q7: WCO typical activities (3:15 pm conference call).

1) Most activity does not involve handling the bats. Typically, the WCO will do an exterior visual inspection to find where the bats are coming and going from. May involve ascending a ladder and being within 6 feet of the bats (which might be in eaves, or under siding). Typically, the idea is to set up excluders at entrances (one-way devices that allow bats out but not in). Such work is typically not done during the maternity season. Unlike that WCO will be wearing a mask.
2) If bats are in an enclosed space, like an attic, the best management practices do **not** involve entering the space and trying to remove the bats. Instead, educate the client, the use exclusion devices once the maternity season is over. But there are operators (perhaps as many as half) who might be willing to remove such bats if the homeowner insists.
3) If bats are in the living space, WCOs will catch them, usually with a net and gloves. Handling is brief, but might be several minutes while they educate the homeowners (who will often want to see the bat). Place the bat in some container, then release outside. But this will vary by state depending on the rabies guidelines.

Question 8. Again, focus on little brown bats (LBB). We are asking for the most likely range. There is some evidence that the probability of infection is low (based on sequence matching ACE-2 receptor), but other evidence that infection is possible; we don't have infection trials which would be the most useful information. SARS-CoV-2 is a member of a group of viruses that is prone to host switching and recombination. Clarification: the question is asking about the probability of viral replication within the bat tissue, which may or may not lead to shedding virus. (The probability of shedding virus is embedded as part of Question 13).

Questions 9-11: Mitigation

Consider the same scenario as Q1-3 – person is asymptomatic, actively shedding virus. The change here is that now management agencies have provided training and compliance oversight in the use of enhanced PPE. This includes the training and use of N95 respirators, as well as training in the use of PPE already in place under current WNS recommendations. Note that training may or may not change compliance either in the mean compliance or the variance in compliance within each user group.

From: S Wacharapluesadee <
Sent: Wednesday, January 31, 2018 7:50 AM EST
To: Katie Leahy >; lance.r.brooks < ; Newman, Carl I CIV DTRA J3-7 (US) l>; Lancaster, Mary J CIV (US) >; christopher.r.lewis ; Kading,Rebekah ; DeeAnn Reeder Cryan, Paul >; Vivek Kapur ; Gavin James Smith >; Tigga Kingston >; abelwade Ian Mendenhall tamar_kutateladze Keti Sidamonidze >; Lela Urushadze >; joram.buza <joram.buza@ c_demetria >; Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; cryan.paul >
CC: Stokes, Martha M CIV (US)
Subject: Field trip
Attachment(s): "1517399433493.jpg"

For your memory!

Thank you,
Supaporn

ส่งจากสมาร์ทโฟน Samsung Galaxy ของฉัน

-------- ข้อความดั้งเดิม --------
จาก: Katie Leahy >
วันที่: 30/1/18 13:15 (GMT+07:00)
ถึง: lance.r.brooks "Newman, Carl I CIV DTRA J3-7 (US)" >, "Lancaster, Mary J CIV (US)" , christopher.r.lewis , "Kading,Rebekah" >, DeeAnn Reeder , "Cryan, Paul" , Vivek Kapur >, Gavin James Smith Tigga Kingston >, abelwade , Ian Mendenhall tamar_kutateladze , Keti Sidamonidze , Lela Urushadze >, joram.buza c_demetria , Kevin Olival ecohealthalliance.org>, Jon Epstein ecohealthalliance.org>, cryan.paul
Cc: "Stokes, Martha M CIV (US)" , Simmi Ghai >, S Wacharapluesadee >
เรื่อง: Afternoon Session

All,

Here are slides to start filling out for the afternoon session.

V/r,

Katie Leahy

From: Katie Leahy >
Date: Tuesday, January 30, 2018 at 10:30 AM
To: "lance.r.brooks , "Newman, Carl I CIV DTRA J3-7 (US)" , "Lancaster, Mary J CIV (US)" >, "christopher.r.lewis " , "Kading,Rebekah" , DeeAnn Reeder >, "Cryan, Paul" , Vivek Kapur >, Gavin James Smith , Tigga Kingston < >, "abelwade " >, Ian Mendenhall "tamar_kutateladze < >, Keti Sidamonidze >, Lela Urushadze "joram.buza " "c_demetria , Kevin Olival ecohealthalliance.org>, Jon Epstein ecohealthalliance.org>, Jason Rao >, "cryan.paul " >
Cc: "Stokes, Martha M CIV (US)" l>, Simmi Ghai >, S Wacharapluesadee >
Subject: NEW SLIDES

Here are the working group slides that were live-edited for your use in break-out groups.

V/r,

Katie Leahy

From: Katie Leahy
Date: Monday, January 29, 2018 at 9:01 PM
To: "lance.r.brooks " >, "Newman, Carl I CIV DTRA J3-7 (US)" >, "Lancaster, Mary J CIV (US)" < "christopher.r.lewis < >, "Kading,Rebekah" >, DeeAnn Reeder , "Cryan, Paul" >, Vivek Kapur >, Gavin James Smith >, Tigga Kingston >, "abelwade " < >, Ian Mendenhall "tamar_kutateladze " < >, Keti Sidamonidze >, Lela Urushadze "joram.buza " "c_demetria " , Kevin Olival ecohealthalliance.org>, Jon Epstein cohealthalliance.org>, Jason Rao "cryan.paul " >
Cc: "Stokes, Martha M CIV (US)" >, Simmi Ghai >, S Wacharapluesadee >
Subject: Update to the BPERNet Slides

Hi, everyone! We made a couple changes to the slides for tomorrow. Nothing substantive, just our approach to conducting the brief-out discussions and the order of a couple of the initial slides.

A reminder again to please be in the lobby at 0745, the bus will depart for Chulalongkorn promptly at 0800.

V/r,

Katie Leahy

From: Katie Leahy >
Date: Monday, January 29, 2018 at 10:28 AM
To: "lance.r.brooks , "Newman, Carl I CIV DTRA J3-7 (US)" , "Lancaster, Mary J CIV (US)" >, "christopher.r.lewis "Kading,Rebekah" >, DeeAnn Reeder , "Cryan, Paul" >, Vivek Kapur < >, Gavin James Smith , Tigga Kingston >, "abelwade " , Ian Mendenhall "tamar_kutateladze " >, Keti Sidamonidze , Lela Urushadze , "joram.buza "c_demetria " Kevin Olival ecohealthalliance.org>, Jon Epstein ecohealthalliance.org>
Cc: "Stokes, Martha M CIV (US)" <m , Simmi Ghai , S Wacharapluesadee >
Subject: BPERNet: Transportation Times and Other Useful Information (30 and 31 January 2017)

Hello, everyone! Welcome to Bangkok. On behalf of the Executive Committee (Dr. Martha Stokes and Dr. Mary Lancaster), we are so pleased that you are able to join us this week for our BPERNet planning meeting and other PMAC activities.

Please use this email as your resource for information regarding transportation, logistics, and other coordinating information for 30 January – 31 January.

30 January – BPERNet Meeting at Chulalongkorn Hospital

1. **The bus will depart from the Renaissance Hotel promptly at 0800** ; please be in the lobby for head count at 0745
2. We will provide coffee and light refreshment during the meeting; you will take lunch at one of the many canteen options at the hotel; please bring about 200 - 300 thai baht (~10 USD) for lunch

31 January – PMAC / BPERNet Field Trip

1. **The bus will depart from the Renaissance Hotel promptly at 0630** ; please be in the lobby for head count at 0615; please make sure that you are on time, as we are caravanning with a delegation from the Centara Hotel and will receive a police escort to move us quickly through traffic
2. We will provide a box breakfast for the bus ride
3. Please make sure that you dress appropriately for this field trip; we strongly suggest covered shoes and loose, comfortable clothing; in addition to this mode of dress we also suggest that you bring accompaniments for spending a day outdoors amongst bat roosts; such as:
    a. Hat
    b. Sunscreen
    c. Sunglasses
    d. Bug spray
    e. Water bottle

We will provide information regarding the Ambassador's reception at the close of tomorrow's meeting.

Again, we are so excited to have you all here. Please do not hesitate to reach out to me or Megan Hudson (copied) if you have any questions.

V/r,

Katie Leahy

Katie Leahy
Program Manager | Global Systems Engineering
6303 Little River Turnpike, Suite 208
Alexandria, VA 22305

http://globalsyseng.com


A
B

From: Katie Leahy
Sent: Wednesday, February 21, 2018 2:23 PM EST
To: Tamar Kutateladze >; Kading,Rebekah ; DeeAnn Reeder ; Cryan, Paul < Vivek Kapur ; Gavin James Smith ; abelwade ; Ian Mendenhall Keti Sidamonidze ; Lela Urushadze ; c_demetria >; Jon Epstein ecohealthalliance.org>; cryan.paul < ; Kingston, Tigga ; S Wacharapluesadee ; Kevin Olival ecohealthalliance.org>
CC: Stokes, Martha M CIV (US) ; Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) ; Megan Hudson >
Subject: Final BPERNet Read-out
Attachment(s): "Bangkok BPERNet ExecSum_Final.pdf"

All,

Please find the final BPERNet read-out for your files. To everyone who provided feedback, we thank you very much for your responses.

A couple housekeeping items:

1. In the next several weeks, we will begin making plans for our next meeting to take place around the One Health Congress in Saskatoon, Canada. The event feedback you provided will help shape this event and that we anticipate building a 2-day program that includes a scenario-based exercise and presentations.

2. One action item from our Bangkok meeting was to begin discussion about a new name for the network; **please participate in this survey monkey poll to find our new name https://www.surveymonkey.com/r/PQXTHCV**. Please note that the group's will assist the group with establishing a web presence for better communications and outreach, so we depend on your feedback to meet these goals. Please let us know through the survey if you do not feel we are using the right words to communicate the group's core mission.

Thank you again for your participation in these polls and feedback on the report. Please let us know if you have any questions or concerns.

Katie Leahy
Program Manager | Global Systems Engineering
6303 Little River Turnpike, Suite 208
Alexandria, VA 22305

http://globalsyseng.com

Bangkok Meeting Final Report

BPERNET

BAT-ASSOCIATED PATHOGEN AND ECOLOGY RESEARCH NETWORK

TABLE OF CONTENTS

MEETING OVERVIEW

EXECUTIVE SUMMARY

The Bat-associated Pathogen and Ecology Research Network (BPERNet) Executive and Steering Committees met as a side meeting to the Prince Mahidol Award Conference (PMAC) on 30 January 2018 at the Chulalongkorn Hospital and University in Bangkok, Thailand. This meeting served as a follow-up to its kick-off meeting in Fort Collins, CO in June 2017, where the group chartered research objectives and terms of agreement. Members of the Executive Committee (EC) and the Steering Committee (SC) chairmen developed an agenda to meet the following objectives: (1) define working group focus areas, resource needs, and outreach plans; (2) build strategy maps to identify, prioritize, and address BPERNet research gaps and needs; and (3) discuss short and long-term processes to collect and collate applications to the network. A complete agenda from the meeting in addition to a list of its participants may be found in Annex A and Annex B, respectively.

Figure 1Members of the Executive and Steering Committee at the BPERNet Meeting in Bangkok on 30 January 2018.

The meeting began with remarks from Professor Sutep Gonlachanvit from Chulalongkorn Hospital and University and Mr. Lance Brooks from the Cooperative Biological Engagement Program and followed with a review of the interim progress towards finalizing the group's research Terms of Reference. The Executive Committee leads, Dr. Martha Stokes (CBEP SEA Science Lead) and Dr. Mary Lancaster (CBEP Africa Science Lead) facilitated a review of the network objectives, outlined progress since its last meeting, and set the guidelines for the meeting. Participants then broke out into the research focus areas that were established in Fort Collins to develop strategic maps for each working group, consisting of objectives, metrics, challenges, and potential investments, projects, and activities.

Ultimately, meeting organizers and facilitators agreed that the meeting achieved its objectives. Working within their focus group areas, and then interactively using the World Café Method, they were able to develop ambitious multi-year strategies and characterize associated challenges and risks to achieving their goals. The group agreed on the importance of its momentum to develop supportive structures for communication and outreach both internally and externally to firmly establish itself as a unique global network of multi-disciplined researchers who aim to answer complex questions at the nexus of One Health.

The meeting's success is evident in the responses from the SC. The SC was given an opportunity to provide feedback via an anonymous survey shortly after the conclusion of meeting. Unanimously the group agreed that the meeting was productive and outlined a path forward for BPERNet. All members noted that their contributions were beneficial and there is consensus about taking steps to moving forward with research and publications. The survey was sent to all participants via email and a summary of the responses can be found in the Participant Feedback section.

BACKGROUND

In 2014, the Defense Threat Reduction Agency (DTRA) Cooperative Biological Engagement Program (CBEP) began leveraging, enhancing, and convening research networks to accelerate its programmatic and research driven targets and end states. CBEP uses this approach as a way to connect its active funded research projects with other projects to help influence effective change for global health security; translating data into policy. Further, by using relationship-based research networks around the globe, made up of interdisciplinary relationships, it will allow for novel and transformative scientific solutions for the world's largest infectious disease threats.

The Bat-associated Pathogen Ecology and Research Network (BPERNet) is a CBEP research network that connects multidisciplinary and One Health expertise to address challenges and threats posed by bat-associated pathogens of security concern. The BPERNet maintains the standards of all research networks that are supported by CBEP, in which members convene as a body of experts and researchers to: (1) share information, data, samples, and protocols; (2) coordinate research activities; (3) build training events and awareness-building workshops at all levels of decision-making authority; (4) develop community standards and best research practices; (5) create mentorship-based opportunities for students, trainees, and early-career researchers to convene, present, and share ideas; (6) establish a community of international research leaders and champions; and (7) reduce outbreak / transmission risk.

Some of the world's most deadly emerging zoonotic diseases are found in bats, including Nipah, Hendra, and Marburg viruses. There are a number of factors which make bats unique disease reservoirs, including their social behavior, distinct physiology and metabolism, ability to travel long distances, nocturnal activity, species diversity, and long life span (10-20 years, compared with a rat's average life of two years).[1] These special bat characteristics, coupled with the impact of human mediated interactions and environmental changes, create research challenges to understanding the bat's role in the global zoonotic disease ecology, which is further complicated by being difficult animals to control within a typical laboratory setting. The BPERNet creates opportunities for policy makers, researchers, conservationists, funders, and students to identify community challenges, develop priority research lists and associated action plans that target needs and gaps, and work at all levels to build awareness of bat-associated disease burden and transmission risks to improve the prevention, detection, diagnosis, and reporting of pathogens of security concern.[2]

MISSION AND VISION

The BPERNet brings together a multidisciplinary and One Health-focused group of scientists, policy makers, research scientists, and medical/veterinary practitioners with interests in bat-related research

[1] Hayman, David T.S., "As the bat flies," *Science* 02 Dec 2016: Vol. 354, Issue 6316, pp. 1099-1100 http://science.sciencemag.org/content/354/6316/1099

[2] Schountz, Tony, "Immunology of Bats and Their Viruses; Challenges and Opportunities," *Viruses,* 2014 Dec; 6(12): 4880-4901. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4276934/

involving pathogens of security concern. The network builds on community standards and best practices for research. The BPERNet identifies and shares information on research funding opportunities offered by multiple institutions. Most importantly, this network fosters international relationships among collaborators, agencies, and organizations, which can produce long-term, sustainable partnerships that withstand changes in government and organization budgets, priorities, postures, and policies.

All members play a role in operationalizing the objectives of the BPERNet, strengthening linkages and reducing overlap in global research on high-priority pathogens of bats (especially zoonosis) to maximize the efficient use of expertise and resources and accelerate the coordinated development of better disease surveillance and control methods.

NETWORK OBJECTIVES

This network will identify and connect interdisciplinary expertise, convening an agile group to adapt to a wide spectrum of arising challenges and threats. By accomplishing the below objectives BPERNet will enable shared learning and research opportunities, establish new research projects, and facilitate joint applications for funding; thus, increasing the opportunity for peer review, especially if a cross-regional and multi-disciplinary team of authors is involved.

- Facilitate interdisciplinary relationships and collaboration to identify research goals and needs for bat-associated disease research and threat reduction; and

- Unify CBEP regions to create a common action plan that yields collaborative and sustainable projects that achieve the following end states:

  (1) better informed policy-makers;

  (2) better informed scientific community regarding funding targets and gaps in areas of research and development;

  (3) better defined threat to global health security from bat-associated pathogens; and

  (4) improved national, regional, and global capacity to detect and respond to pathogens of security concern; and

- Enable better communication, coordination, and outreach at the research and conservation interface.

OUTCOMES FROM RESEARCH FOCUS AREAS BREAKOUT SESSIONS

OPENING COMMENTS

Mr. Lance Books, Division Chief, DTRA CBEP and Professor Sutep Gonlachanvit, Deputy Director of Medicine and Research King Chulalongkorn Memorial Hospital, co-opened the BPERNet meeting by emphasizing the importance of continuing the Research Coordination Network (RCN) for the benefit of the One Health mission. The opening message conveyed the need for continuing infectious disease surveillance and providing opportunities to make new connections through research. Both agreed that the BPERNet ensures the future of interdisciplinary scientific research and provides a venue to address global issues.

MEETING FORMAT AND LESSONS LEARNED

The goals of this BPERNet meeting were:

(1) Define working group focus areas, resource needs, and outreach plans;

(2) Build strategy maps to identify, prioritize, and address BPERNet research gaps and needs; and

(3) Discuss short-term and long-term processes to collect and collate applications to the network

These objectives were set as the "true north" for this meeting, providing a target for participants to think about success from the beginning. General meeting instructions emphasized the importance of working collaboratively, but to also think about general limitations that have inhibited research goals. Emphasis was added that these objectives should be owned by the entire group.

Additionally, the SC worked to finalize the Terms of Reference for Trusted Agents (TORFTA). The SC agreed that the TORFTA will remain a living document and that will be reviewed annually.

Based on participant feedback and observations from event planners, the EC and SC chairs agree that future meetings should be longer, with more interactive portions for strategy building and collaboration exercises. One idea is to develop a scenario (based on a case-study) to engage a multi-disciplinary group through different phases or turns of response. Event organizers felt that presentations from members of the group on their current research interests or funded projects would help others to understand linkages and dependencies in their research. Event organizers have documented all lessons learned and changes will be implemented for future meetings.

AGENDA

The meeting agenda was designed to create two breakout sessions to guide working groups through a single strategy map. The morning session included a large group review of the working group research areas and creation of cross-cutting themes. Working groups then moved into their research areas to develop a mission statement, identify objectives, and highlight needs. The afternoon breakout group session had research areas developing initiatives for steps forward and identifying responsibility for these initiatives. After each session, the world café was used as a method to share the group's findings. Members of each group rotated to the other working groups to hear from a group representative and provide feedback on each topic. The second breakout group was followed by a short presentation of findings and a large group discussion on next steps. The full breakout of the agenda can be found in Annex B.

CROSS-CUTTING THEMES

Prior to breakout sessions, the SC worked to identify cross-cutting themes among all four working group areas. The SC agreed these themes were inclusive of the needs of all working groups and would help the RCN in developing outreach plans and strategy maps.

Cross-cutting themes from the focus area group discussion included:

- Communication, outreach, and advocacy of group goals to decision and policy makers;
- Standardizing common language;
- Optimizing database management and IT networks;
- Analyzing modeling; and
- Workforce development

Additionally, the objectives each working group identified highlight a need to research and publish knowledge gaps and identify the effects of spillover on human and animal health.

WORKING GROUP RESEARCH FOCUS AREA

Prior to breakouts; a whole group discussion outlined and defined the working group research focus areas. Below are the focuses of each group along with the research mentors for each group.

WORKING GROUP 1: HOST/PATHOGEN BIOLOGY AND INTERACTIONS

- Bat Physiology
- Bat Immunology
- Bat Pathology and pathophysiology
- Bat Pathogen Community Ecology (Co-infections and Co-morbidities)
- Distribution of Pathogens Among Species
- Develop Modeling Approaches for Host Dynamics and Epidemiology

WORKING GROUP 1 RESEARCH MENTORS

- Dr. Joram Buza, Nelson Mandela African Institute of Science and Technology, Tanzania
- Dr. Vivek Kapur, Penn State University, U.S.
- Dr. DeeAnn Reeder, Bucknell University, U.S.
- Dr. Gavin Smith, Duke-NUS, Singapore
- Dr. Mary Lancaster, DTRA CBEP, U.S.

WORKING GROUP 2: PATHOGEN SURVEILLANCE, DIAGNOSTIC CAPACITY, AND EPIDEMIOLOGY

- Molecular Epidemiology
- Distribution of Pathogens Geographically and Phylogenetically
- Detection, Diagnosis, and Reporting of Bat-associated Pathogens
- Establish Commonly Used Guidance on Sampling

WORKING GROUP 2 RESEARCH MENTORS

- Dr. Catalino Demetria, Research Institute for Tropical Medicine, Philippines
- Dr. Jon Epstein, EcoHealth Alliance, U.S.
- Dr. Tamar Kutateladze, National Center for Disease Control and Public Health, Georgia
- Dr. Abel Wade, National Veterinary Laboratory, Cameroon
- Dr. Keti Sidamonidze, National Center for Disease Control and Public Health, Georgia

WORKING GROUP 3: ECOLOGY SETTING (BAT, DOMESTICATED ANIMALS, AND WILDLIFE INTERFACE)

- Bat Behavior, Distribution, and Movement
- Domesticated Animals and Wildlife Behavior, Distribution, and Movement impact on Interaction with Bats
- Effect of Anthropogenic Disturbance and Modification on Pathogen Dynamics and Spillover Risk

WORKING GROUP 3 RESEARCH MENTORS

- Dr. Paul Cryan, United States Geological Survey Fort Collins Science Center, U.S.
- Dr. Tigga Kingston, Texas Tech University, U.S.
- Dr. Rebekah Kading, Colorado State University, U.S.
- Dr. Eiichi Hondo, Obihiro University of Agriculture and Veterinary Medicine, Japan
- Dr. Robert Kityo, Makerere University, Kampala, Uganda *

*Was not present at 30 Jan 2018 Meeting

WORKING GROUP 4: HUMAN-BAT INTERACTIONS

- Human Behavioral Risk Characterization
- Hunting and Commodity Chain
- Ecotourism
- Interactions in Human Dwellings

WORKING GROUP 4 RESEARCH MENTORS

- Dr. Kevin Olival, EcoHealth Alliance, U.S.
- Dr. Ian Mendenhall, Duke-NUS, Singapore
- Dr. Supaporn Wacharapluesadee, King Chulalongkorn Memorial Hospital, Thailand
- Dr. Lela Urushadze, National Center for Disease Control and Public Health, Georgia
- Dr. Nesreen Alhmoud, Royal Scientific Society, Jordan
- Dr. Marty Stokes, DTRA CBEP, U.S.

OUTCOMES FROM RESEARCH FOCUS AREA BREAKOUT SESSIONS

BRIEF-OUT FROM WORKING GROUP SESSIONS

Working within their focus group areas, each develop mission statements, multi-year objectives, measurements for success, and identified overall challenges to success. In the table below, mission statements convey the group's long-term overarching goal while multi-year objectives are each outlined with a corresponding measure for success. Finally, the groups identified key challenges to the overall success of their work. The below table reflects a summary of the key findings from the breakout groups and world café. For the original working out-brief please reference Annex C.

Working Group 1 Mission: Explain the intrinsic and extrinsic characteristics that make certain bats susceptible and spread certain diseases and accurately assess the risk of spillover to another animal host.		
Objectives	**Measurements**	**Overall Challenges**
Objective 1: Complete a systematic review of the knowledge gaps on modeling systems. **Objective 2:** Identify modeling systems that are representative of all phylogeographic and phylogenetic areas. **Objective 3:** Evaluate the transmission risk and spillover of pathogens to another animal host.	**Objective 1:** Publish systematic review of modeling systems and knowledge gaps that were defined. **Objective 2:** Model system is defined, characterized, and validated. **Objective 3:** Intrinsic and extrinsic risk factors are identified for major diseases and geographic areas.	• Objectives require a multidisciplinary team. • Consortia would be needed for model systems review and validation.

Working Group 2 Mission: Form regional networks to establish a common methodology for surveillance and sustain the surveillance for both human and animal health. In addition to understanding spillover risk and epidemiology of bat associated pathogens.		
Objectives	**Measurements**	**Overall Challenges**
Objective 1: Create gap analysis of diagnostic tools. **Objective 2:** Create outreach to various groups of researchers and create awareness among the public and science community. **Objective 3:** Establishing a common methodology for surveillance.	**Objective 1:** Publish systematic review understanding the epidemiology of bat pathogens. **Objective 2:** Formation of regional networks. **Objective 3:** Fully understanding the risk of spillover and developing a set of standards for surveillance.	• The logistics and bureaucracy of creating a multidisciplinary team. • Funding to support the efforts to standardize surveillance.

Working Group 3 Mission: Define how and to what extent the ecological context of bats, and human influence on that context, influence pathogen dynamics and spillover threats		
Objectives	**Measurements**	**Overall Challenges**
Objective 1: Engage the ecological community to define system uniqueness and interdependencies. **Objective 2:** Advocate for ecological design and analysis frameworks to pathogen research. **Objective 3:** Build capacity for disease researchers to gather ecological data to provide context for their studies. **Objective 4:** Define emerging ecological principles that could inform spillover threats. **Objective 5:** Establish key messages and conduct efforts to promote a culture of conservation among One Health researchers, practitioners, and stakeholders.	**Objective 1:** Pathogen research community acknowledges and integrates ecological systems and interdependencies. **Objective 2:** BPERNet research projects are designed using the framework for well-balanced outcomes. **Objective 3:** More studies return to ecological data. **Objective 4:** Emerging ecological principles become widely-accepted governing principles for practice. **Objective 5:** BPERNet establishes itself as a consistent and unbiased perspective from the community and its statements are widely accepted and distributed.	• Science communities have polarized and insular view of bats and diseases. • Lack of collaboration and communication efforts.

Working Group 4 Mission: Fully develop, understand, and communicate the bat and human interface to key stakeholders and communities.		
Objectives	**Measurements**	**Overall Challenges**
Objective 1: Develop and test policy interventions for specific human-bat interfaces. **Objective 2:** Communicate findings to key stakeholders. **Objective 3:** Develop global risk maps to assess existing data and validate risk maps. **Objective 4:** Identify high risk groups and develop education platforms to measure knowledge, attitudes, and practices.	**Objective 1:** Policy interventions for human bat interfaces are developed and put into place. **Objective 2:** Effectively communicate and publish findings of studies. **Objective 3:** Publish global risk maps highlighting geographic areas of risk. **Objective 4:** Getting community buy-in and understanding of concepts.	• Truthful responses in behavioral research on bat-human interactions. • Accuracy of risk map and models. • Cultural barriers and beliefs.

ACTION ITEMS

The following Action Items were recorded and compiled by the organizational and administrative support staff of CBEP / Executive Committee for the BPERNet.

ACTION	APPROACH FOR COMPLETION WITH DATES	RESPONSIBLE AGENTS
Develop communication plan	(1) Themes and key messages (2) New name (3) Outreach (4) Social media (5) Recruitment and marketing	(1) Contingent on establishment of 5th working group; looking into Science Communication experts
Develop website plan	(1) Communication and outreach (2) Collaboration (3) Research mapping	(1) Contingent on establishment of 5th working group.
Publication of protocols and assays	(1)	(1)
Working Groups complete mission statements ***Change?*** Conduct System Reviews to Outline Knowledge Gaps	(1) ***	(1) ***Contingent on Working Group Leads
Conduct Series	(1) SEABCRU (2)	(1)
Publication of Perspectives and Policy piece	(1) Concept pitch (2) Outline (3) First Draft (4) Final Draft	(1) Perspectives Paper: Dr. Mary Lancaster, CBEP and Dr. Vivek Kapur, Penn State (2) Policy Forum: Dr. Marty Stokes, CBEP and Dr. Jon Epstein, EcoHealth Alliance
Conduct a 'funders meeting'	(1)	(1) CBEP

Star-Idaz

Economist debate-style forum

PARTICIPANT FEEDBACK

An after-event survey was sent to the SC to collect information on their progress and overall thoughts on the progress of the RCN. Members were asked to answer the following questions:

1. What did you like about the meeting?
2. Do you think the objectives for the 30 January BPERNet meeting were achieved? Please explain your answer.
3. What do you wish we did differently?
4. What does success of this network look like to you, for your field of study?
5. Will you be able to attend the next meeting in Saskatoon Saskatchewan (5th International One Health Congress) 22-25 June?
6. What do you wonder? As an example, "Do you wonder if this effort is worth your time?"
7. Additional comments.

Responses were collected from the majority of the attending SC and reflected a positive outlook on both the progress of the meeting and the future of BPERNet. The SC felt the 30 January meeting was well organized, with a clear agenda that increased the productivity of each working groups. Comments from members pointed to the formally developed themes and roles for each working group as the main reason for the meeting's success. The SC agreed success of BPERNet will be achieved when the gaps identified are addressed, there is a standardization of data collection, and the completion of one or more research projects advancing the understanding of and response to emerging pathogen reservoirs in bats. Overall, the only change the group asked for was to extend the next BPERNet meeting to at least two full days. The majority of members will be present at the 5th International One Health Congress meeting and a longer side BPERNet meeting should be arranged during this time period.

ANNEX A – PARTICIPANTS

The following participants attended or were invited to attend the

STEERING COMMITTEE MEETING INVITEES, DID ATTEND		
Mendenhall	Ian	Duke-NUS, Singapore
Buza	Joram	Nelson Mandela African Institute of Science and Technology, Tanzania
Kapur	Vivek	Penn State University, U.S.
Olival	Kevin	EcoHealth Alliance, U.S.
Epstein	Jonathan	EcoHealth Alliance, U.S.
Kading	Rebekah	Colorado State University, U.S.
Urushadze	Lela	National Center for Disease Control and Public Health (NCDC), Georgia
Kutateladze	Tamar	National Center for Disease Control and Public Health (NCDC), Georgia
Sidamonidze	Keti	National Center for Disease Control and Public Health (NCDC), Georgia
Wacharapluesadee	Supaporn	WHO CC for Research and Training in Viral Zoonoses, King Chulalongkorn Memorial Hospital, Thailand
Wade	Abel	National Veterinary Laboratory of Cameroon (LANAVET)
Demetria	Catalino	RITM, Philippines
Kingston	Tigga	Texas Tech University, U.S.
Cryan	Paul	USGS Fort Collins Science Center, U.S.
Reeder	DeeAnn	Bucknell University, U.S.
Smith	Gavin	Duke-NUS, Singapore
Alhmoud	Nesreen	Royal Scientific Society, Jordan
Hondo	Eiichi	Obihiro University of Agriculture and Veterinary Medicine, Japan
STEERING COMMITTEE MEETING INVITEES, DID NOT ATTEND		
Kityo	Robert	Makerere University, Uganda
CBEP AND CBEP CONTRACTOR INVITEES, DID ATTEND		
Lancaster	Mary	DTRA CBEP
Stokes	Marty	DTRA CBEP
Brooks	Lance	DTRA CBEP
Newman	Carl	DTRA CBEP
Leahy	Katie	GSE
Hudson	Megan	GSE

ANNEX B – MEETING AGENDA

The following agenda was set for the meeting. The majority of discussions focused on administration, organization, and focus of the network. The group did not get to the topics to prioritize research gaps and set action plans with short and long-term milestones and deliverables. Event facilitators organized questions and prompts for those sessions, which they will use for the next BPERNet meeting.

Time	Session	Notes
0830 - 0845	Introduction and Meeting Objectives	Lance Brooks and Sutep Gonlachanvit will welcome all participants and provide a brief overview of the meeting objectives for the week
0845 - 0900	⇒ Review interim accomplishments since 27 June ⇒ Q&A on TORFTA changes ⇒ Call for votes to accept TORFTA	Executive Committee members will provide an overview of the TORFTA and mission areas; all participants will receive final version ahead of meeting
0900 - 1000	Working Group Focus Areas	Review WG focus areas that were outlined during the 27 June meeting ⇒ Review breakout group objectives and end goals ⇒ Review strategy map
1000 - 1015	Tea Break	
1015 - 1115	Breakout Group Session I	Breakout Group Session 1 Objectives: ⇒ Define WG research areas (sub-focus area definitions) ⇒ List and prioritize research questions and potential projects for each area ⇒ Identify internal and external research dependencies for each Working Group
1115 - 1200	Breakout Group Session I Interactive Feedback	Each group will participate in world café and rotate to review each group's findings
1200 – 1330	Working lunch / Open discussion	Open discussion objectives ⇒ Discuss group marketing campaign ⇒ Members should be prepared to introduce other network affiliations, conferences, and meeting opportunities to market the network, globally ⇒ Discuss long-term process to collect and collate applications to the network
1330 – 1430	Breakout Group Session II	Breakout Group Session 2 Objectives: ⇒ List out WG research coverage (who is researching what and where)

		⇒ Identify research gaps and needs ⇒ Identify WG resource and coverage needs (e.g., target environmentalists in Europe); identify critical POCs for membership ⇒ Begin drafting short and long timelines and work plans
1445 – 1530	Breakout Group Session II Interactive feedback and brief-out	Each group participated in the world café and then briefs out their discussions according to the objectives; brief-out 5 minutes / WG
1530-1545	Tea Break	
1545 – 1630	End of session	End of Session Objectives: ⇒ Review Strategy Map ⇒ Review Action Items ⇒ Discuss date, level of participation, and location for next meeting (all participants should come prepared to briefly discuss their ideas for this topic)

ANNEX C – GROUP BRIEF-OUT SLIDES

Each group was provided 10 minutes at the end of the day to present their strategic mapping work; below are the final slides that were presented.

Group 1

5 MINUTES

What must the Working Group achieve?	How will success be measured?
OBJECTIVES	MEASURE
• Almost all (ex. NIH, WT, WHO, France, Germany, India, China, Australia)	Almost all (ex. NIH, WT, WHO, France, Germany, India, China, Australia)

• Systematic review/knowledge gaps on model systems and transmission risk (short-term goal)
• RFP for model systems to answer:
  • Innate and adaptive immune response
  • Mechanisms of susceptibility
  • EnvironmentaL/l host conditions that are necessary for spillover
  • Resistance and susceptibility of certain bats species and certain pathogens
  • Co-infections and their role in pathogen ecology / spillover risk
	• SYSTEMATIC REVIEW / KNOWLEDGE GAPS DEFINED - PUBLISHED
	• RFPS ISSUED - TEAMS ASSEMBLED / ESTABLISHED
	• MODELS DEFINED / CHARACTERIZED / VALIDATED
	• KEY INTRINSIC/EXTRINSIC RISK FACTORS IDENTIFIED FOR MAJOR DISEASES / GEOGRAPHIES

1. Immunologist 2. Genomics 3. Cellular and molecular biologist • Ecologist /Trans Dynamic model • Systems biologist • Risk assessment • Bioinformatics • Microbiologist • Infectious disease	1. RESEARCHERS; FUNDING AGENCIES; POLICY MAKERS; OIE/WHO

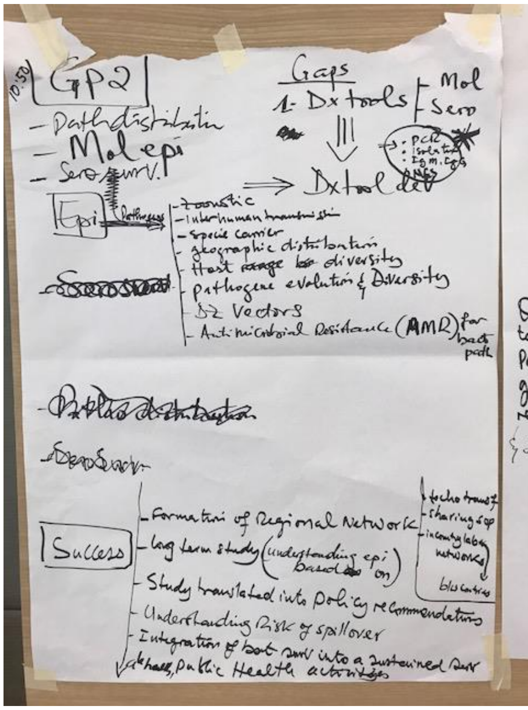
Investments, activities, and projects	Responsibility	Needs and risks
INITIATIVES	WHO	CHALLENGES
• BPERN / Multiple other	Almost all (ex. NIH, WT, BBSRC/DfId OTHER COUNTRY FUNDING AGENCIES)	• Multidisciplinary by nature there isn't a single funding source • Consortia would need to be created for model systems

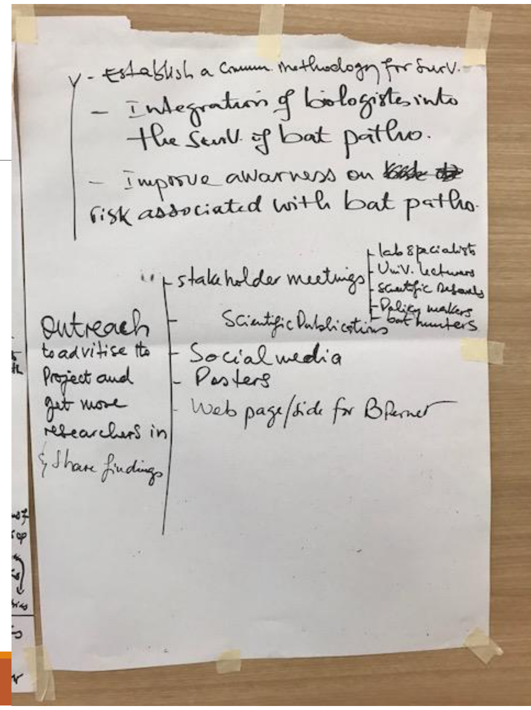
• Model Systems
  • Systematic review
  • RFP
• Natural and experimental disease transmission models
• Tool Kits
	Working Group 2 creates systematic review in which we identify gaps and lay out what would need to be in a RFP	• Quantifying and communicating Risk
		• Lack of baseline knowledge

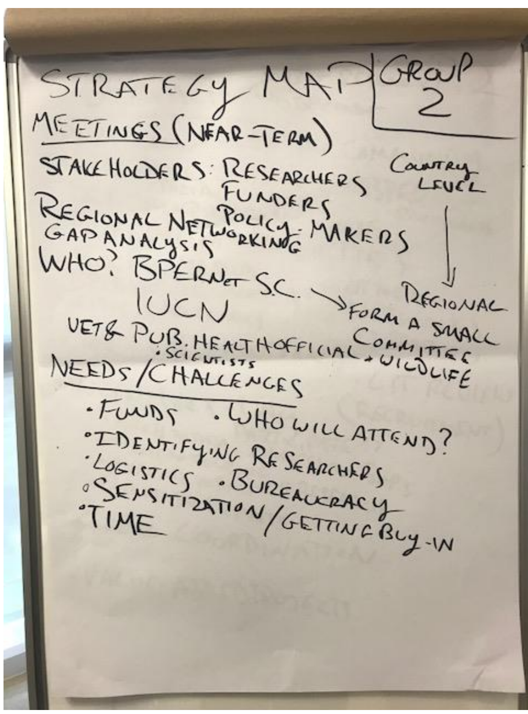
1. Immunologist 2. Genomics / bioinformatics 3. Cellular and molecular biologist • Ecologist /Disease transmission dynamic modelers • Systems biologists • Risk assessment • Microbiologists / Infectious disease specialists	Researchers; funding agencies; other stakeholders	• Quantifying and communicating Risk • Lack of baseline knowledge • Promoting collaboration

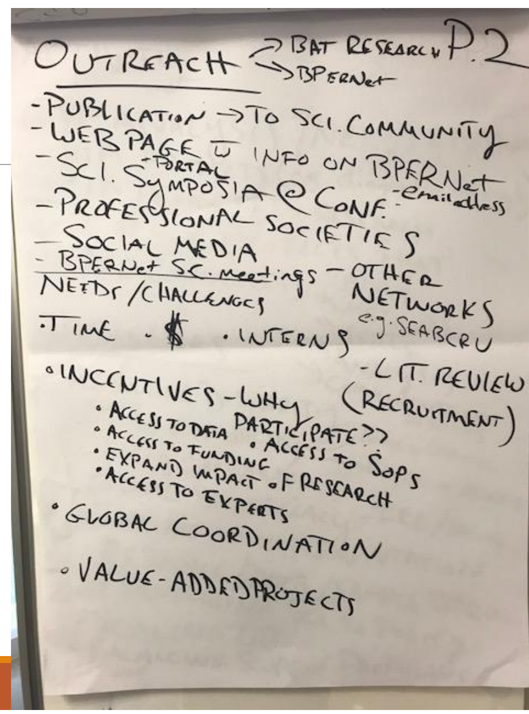
Group 2

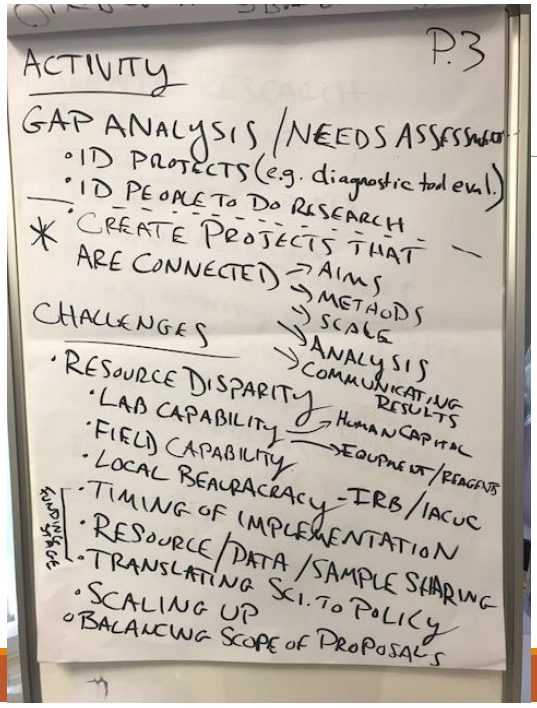
5 MINUTES

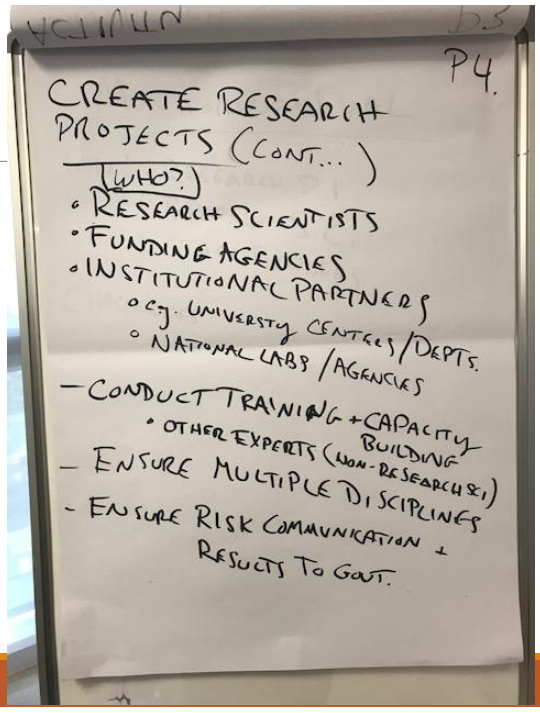

GP2
Gaps
1- Dx tools
Mol
Sero
- Path distribution
- Mol epi
- Sero surv.
PCR
Dx tool dev
Epi
- Zoonotic
- Inter human transmission
- Specie carrier
- Geographic distribution
- Host diversity
- Pathogene evolution & Diversity
- Dz Vectors
- Anti-microbial Resistance (AMR) for bact path
Success
- Formation of Regional Network
- Long term study (understanding epi)
- Study translated into Policy recommendations
- Understanding Risk of spillover
- Integration of surv into a sustained surv Public Health activities
techno transf
sharing sop
in-country lab networks


- Establish a comm. methodology for surv.
- Integration of biologists into the surv. of bat patho.
- Improve awarness on risk associated with bat patho.
Outreach to advitise the project and get more researchers in & share findings
stakeholder meetings
lab specialists
Univ. lecturers
Policy makers
bat hunters
Scientific Publications
Social media
Posters
Web page/site for BPernet


STRATEGY MAP
GROUP 2
MEETINGS (NEAR-TERM)
STAKEHOLDERS: RESEARCHERS
FUNDERS
POLICY MAKERS
COUNTRY LEVEL
REGIONAL
REGIONAL NETWORKING
GAP ANALYSIS
WHO? BPERNet SC. → FORM A SMALL COMMITTEE
IUCN
VET & PUB. HEALTH OFFICIAL, WILDLIFE
• SCIENTISTS
NEEDS/CHALLENGES
• FUNDS • WHO WILL ATTEND?
• IDENTIFYING RESEARCHERS
• LOGISTICS • BUREAUCRACY
• SENSITIZATION/GETTING BUY-IN
• TIME


OUTREACH
BAT RESEARCH
BPERNet
P.2
- PUBLICATION → TO SCI. COMMUNITY
- WEBPAGE - PORTAL INFO ON BPERNet - email address
- SCI. SYMPOSIA @ CONF.
- PROFESSIONAL SOCIETIES
- SOCIAL MEDIA
- BPERNet SC. meetings - OTHER NETWORKS e.g. SEABCRU
NEEDS/CHALLENGES
• TIME • $ • INTERNS
- LIT. REVIEW (RECRUITMENT)
• INCENTIVES - WHY PARTICIPATE??
• ACCESS TO DATA • ACCESS TO SOPS
• ACCESS TO FUNDING
• EXPAND IMPACT OF RESEARCH
• ACCESS TO EXPERTS
• GLOBAL COORDINATION
• VALUE-ADDED PROJECTS





Group 3

5 MINUTES

Group 3 Mission: define how and to what extent the ecological context of bats, and human influence on that context, influence pathogen dynamics and spillover threats

What must the Working Group achieve?	How will success be measured?
OBJECTIVES	MEASURE
Objective 1: Engage the ecological community (including research groups, individuals, and networks) to define system uniqueness and interdependencies (movement, community, nutritional, physiological, social, reproductive, conservation, and population ecologies etc. **Objective 2:** Bring ecological design and analysis frameworks to pathogen research; advise the community of innovative and supportive technologies **Objective 3:** Build capacity for disease researchers to gather ecological data to provide context for their studies **Objective 4:** Define emerging ecological principles that could inform spillover threats **Objective 5:** Establish key messages and conduct efforts to promote a culture of conservation among One Health researchers, practioners, and stakeholders; BPERNet SC provides timely statements on potentially contentious research	**Objective 1 Measurement:** Pathogen research community acknowledges and integrates ecological system and interdependencies **Objective 2 Measurement:** BPERNet research projects are designed using the frame work for well-balanced outcomes **Objective 3 Measurement**: More studies are returning ecological data **Objective 4 Measurement:** Emerging ecological principles become widely-accepted governing principles for practice **Objective 5 Measurement:** BPERNet establishes itself as a consistent and unbiased perspective from the community and its statements are widely accepted, respected, and distributed

Group 3 Mission: define how and to what extent the ecological context of bats, and human influence on that context, influence pathogen dynamics and spillover threats

Investments, activities, and projects	Responsibility	Challenges, needs, and risks

1. Conduct a literature review of bat-associated papers to assess how many incorporated conservation principles and authorship
2. Conduct DTRA call for sampling opportunities associated with existing ecological research
  1. Demonstrate contribution to ecology of disease emergence
  2. Demonstrate existing funding (not associated with potential funding)
3. Ensure that any future solicitations include language that explicitly incorporates an ecology framework where relevant
4. Collect case studies for messaging
5. As part of a repository of 'tool kits', develop an ecology 'tool kit'; conduct tactical field activities to learn how to use and teach-back the tool kit
6. International Bat Research Conference (IBRC) 2019 – attend and participate (with 5-10 participants for discussion Q&A)
7. Convene a series of 'conservation awareness-building' workshops
8. FOR NEXT BPERNet MEETING: longer planning meeting, develop and work through a scenario that incorporates all the working group for future discussion-based training events
	1. WG
	2. CBEP / BPERNet
	3. CBEP (and other fudners)
	4. WG – 3
	5. WG – 3
	6. BPERNet
	7. WG – 3
	8. BPERNet
		• "The Great Divide" – solution: build awareness
		  • Vocal and polarized bat community
		  • Insular bat and disease communities
		  • Insensitive disease community
		• Lack of collaborative efforts
		• Communication issues

Group 4

5 MINUTES

What must the Working Group achieve?	How will success be measured?
OBJECTIVES	MEASURE
Identify other funding initiatives	Number of visits to website Number of proposals submitted and projects funded
Better understand bat/human interface Develop and test policy interventions for specific human-bat interfaces	Baseline knowledge and gaps identified Database development Maps and models developed Guidelines for human behaviroal risk characterization developed and used Intervention policies developed and tested
Communicate findings to key stakeholders • Policy makers • Community members (high risk groups)	Number of workshops and attendees (conventional metrics) Before and after surveys for KAPs

Investments, activities, and projects	Responsibility	Needs and risks
INITIATIVES	WHO	CHALLENGES
Create and curate web page with potential funding opportunities	BPERN; CBEP (to liaise w other USG funders); country governments	Lack of transparency and coordination among donors and recipients (=duplication) Silo'ing of funding Some countries (e.g. Singapore) doesn't fund outside of country Shaping national/country funding priorities
Develop global risk maps Assess existing data and literature review Research studies/support for ecol, social, and econ drivers Studies of seasonality Identify and model policy interventions Validate/ground-truth risk maps	BPERN, academics, research orgs, NGOs, and countries	Truthful responses in behavioral research Ensuring interventions developed will be acceptable and econ viable. Accuracy of risk maps/models
Identify target audience, and high risk groups Develop education platforms/materials Research to measure changes in knowledge, attitudes, and practices (KAP)	BPERN; SEABCRU; social behavioral scientists (needed); communication and PR specialists	Getting community buy-in and understand concepts Cultural barriers and beliefs (e.g. bats are medicinal to eat) Dissemination of info to larger group

From: Kevin Olival ecohealthalliance.org>
Sent: Monday, April 27, 2020 12:11 AM EDT
To: Paul Cryan ; Brian R. Amman < Ralph S. Baric David S Blehert >; Cara Brook ; Charles H Calisher ; Kevin Castle Jeremy Coleman Peter Daszak ecohealthalliance.org>; epstein ecohealthalliance.org>; Hume Field ecohealthalliance.org>; Winifred F Frick, Ph.D. >; Gilbert, Amy T - APHIS >; David Hayman < >; Hon S Ip >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah >; Tigga Kingston >; Lorch, Jeffrey M ; Ian Mendenhall ; alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina >; DeeAnn Reeder ; Jonathan D Reichard >; Jonathan M Sleeman ; Daniel Streicker < Jonathan S. Towner
Subject: Final version of North American bat/SARS2 ms - PLEASE REVIEW
Attachment(s): "Table S1 for Olival et al. bat CoVs_V5.xlsx","Olival et al. bat CoVs 20200425_V6.1.docx","References cited Table S1_V5.docx"

Dear Esteemed Colleagues,

Please review the attached penultimate draft of our manuscript (now entitled: **'Possible risks of SARS-CoV-2 spillover to free-ranging wildlife: a case study of bats")**, together with the supplementary table and refs. Our plan is to submit to *Lancet Infectious Diseases* as a review article (correct length and they allow 150 refs) in the next week - references are currently formatted for that journal. We would also like to post it on bioRxiv as a pre-print once we get it submitted to *Lancet ID*. Please let me know if you have any concerns with that plan.

Thank you all for your excellent comments and edits on the previous draft. Paul and I have gone back and forth on several rounds of revisions since then (and multiple late night texts), aiming to take each and every suggestion into account, and we believe it's a much better manuscript now! Very excited about this one, and looking forward to getting it published!

By Thursday April 30th (or ASAP), could you each please:

1. Confirm that you agree to be a co-author.
2. Double check your name and affiliation, and send me your ORCID number if you have one.
3. Read through the ms and send any important, last minute changes or edits you feel are necessary. Please use track changes. If you're okay with the ms as is, please just confirm so.
4. For my Federal US Gov't friends (USFWS, USGS, CDC, USDA) - please let us know what we need to do for approval on your end. I know Paul is working with USGS now to hopefully get rapid clearance.

No need to cc all if you don't want, but please include both me and Paul on your response.

Looking forward to hearing from you all soon!

Cheers,
Kevin and Paul

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
460 West 34th Street, Suite 1701
New York, NY 10001

www.ecohealthalliance.org

Possible risks of SARS-CoV-2 spillover to free-ranging wildlife: a case study of bats

Kevin J. Olival*[1†], Paul M. Cryan*[†2], Brian R. Amman[3], Ralph S. Baric[4], David S. Blehert[5], Cara E. Brook[6], Charles H. Calisher[7], Kevin T. Castle[8], Jeremy T. H. Coleman[9], Peter Daszak[1], Jonathan H. Epstein[1], Hume Field[1], Winifred F. Frick[10], Amy T. Gilbert[11], David T.H. Hayman[12], Hon S. Ip[5], William B. Karesh[1], Christine Kreuder Johnson[13], Rebekah C. Kading[7], Tigga Kingston[14], Jeffery M. Lorch[5], Ian H. Mendenhall[15], Alison J. Peel[16], Kendra L. Phelps[1], Raina K. Plowright[17], DeeAnn M. Reeder[18], Jonathan D. Reichard[8], Jonathan M. Sleeman[5], Daniel G. Streiker[19], and Jonathan S. Towner[3]

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[2] U.S. Geological Survey, Fort Collins Science Center, Ft. Collins, CO, USA
[3] U.S. Centers for Disease Control and Prevention, Atlanta, GA, USA
[4] University of North Carolina, Chapel Hill, NC, USA
[5] U.S. Geological Survey National Wildlife Health Center, Madison, WI, USA
[6] University of California Berkeley, Berkeley, CA, USA
[7] Colorado State University, Ft. Collins, CO, USA
[8] Wildlife Veterinary Consulting, Livermore, CO, USA
[9] U.S. Fish and Wildlife Service, Hadley, MA, USA
[10] Bat Conservation International, Austin, TX, USA
[11] U.S. Department of Agriculture, National Wildlife Research Center, Ft. Collins, CO, USA
[12] Massey University, Palmerston North, New Zealand
[13] University of California Davis, Davis, CA, USA
[14] Texas Tech University, Lubbock, TX, USA
[15] Duke-National University of Singapore Medical School, Singapore
[16] Griffith University, QLD, Australia
[17] Montana State University, Boseman, MT, USA
[18] Bucknell University, Lewisburg, PA, USA
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*These authors contributed equally

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Spillover of pandemic viruses

The threat of emerging infectious diseases (EIDs) to wildlife health and biodiversity conservation is recognized,[1] but cross-species transmission of novel pathogens, or spillover, is typically viewed in the narrow context of originating *from* a wildlife reservoir and transmitting *to* humans.[2] Research assessing EID risk has typically focused on identifying geographic regions[3,4] and wildlife species[5-7] whereby spillover of zoonotic diseases into humans is most likely. Among recent pandemic zoonotic viruses, some have no evidence of transmission back to wildlife or domestic animal populations after establishment in people (e.g., human immunodeficiency virus, which causes acquired immunodeficiency syndrome), while others have crossed species boundaries with fluidity (e.g., pandemic H1N1 influenza A virus).[8-10] Evidence of 'reverse zoonoses' transmitting from people to wildlife and domestic animals is widespread[10], however systematic surveys to determine the proportion of EIDs that spill back into novel wildlife hosts are lacking. Evidence of humans infecting bats with any virus is limited to a single observation,[11] and onward transmission[12], or viral spread from an initial infected individual to an entire bat population, has not been recorded. Bats rank among the most ecologically important, but underappreciated, mammals that play varied roles in most of Earth's ecosystems; bats are primary nocturnal predators of invertebrates and small vertebrates, as well as pollinators and seed dispersers of many tropical plants.[13,14]

In December 2019, a novel coronavirus was detected from a cluster of 41 atypical pneumonia cases in Wuhan, China, and has since spread to cause a pandemic.[15] As of late April 2020, the virus had reached over 185 countries, infected >2.7 M people, and killed >195,000. Phylogenetic evidence suggests that this virus, now named severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), along with the entire clade of SARS-related coronaviruses (SARSr-CoVs), evolved in Old-World bats of the family Rhinolophidae.[16-18] There is no epidemiological evidence of direct or indirect transmission of SARS-CoV-2 from bats to people, but the closest known virus to SARS-CoV-2, with 96% sequence similarity across the virus' genome, was discovered in an intermediate horseshoe bat (*Rhinolophus affinis*) sampled from Yunnan province, China in 2013.[19] The timing of SARS-CoV-2 spillover from bats to humans, and whether an intermediate host species was involved, remain undetermined.[20,21] The United States (U.S.) currently has the highest number of confirmed human cases of COVID-19, the disease caused by SARS-CoV-2, with transmission reported in all 50 states. The unintended consequences of this pandemic are many and include the possibility of SARS-CoV-2 transmission from humans to free-ranging wildlife populations. Given the likely bat origin of SARS-CoV-2, bats are a group of primary concern for spillover from humans. Anticipating the need for similar risk assessments across many potentially vulnerable species of wildlife and domesticated mammals globally, here we assess the possibility of humans inadvertently infecting free-ranging North American bats with SARS-CoV-2. We further discuss the possible public health and wildlife conservation consequences of SARS-CoV-2 becoming endemic in bats outside its natural host range.

The triple threat of SARS-CoV-2 to North American bats

The pandemic human spread of SARS-CoV-2 may directly or indirectly threaten North American bat populations in at least three different ways. First, SARS-CoV-2 might infect the diverse and historically isolated 40+ endemic species of temperate-zone North American bats, with or without causing disease. Second, SARS-CoV-2 might infect and then become established

in one or more North American species, creating novel wildlife disease reservoirs capable of causing future human infections. Third, if SARS-CoV-2 infection persists in North American bats of one or more species, it could potentially evolve, or recombine with endemic viruses, to become more pathogenic or infectious to humans or other animals. In addition to new public health challenges, the latter outcomes could quickly shift public perception of bats from mostly beneficial wildlife with manageable associated disease risks, to bats posing unacceptable disease risks to human health. Such shifts could increase the likelihood of harmful human-bat interactions, as well as undermine decades of concerted science, conservation, and education efforts aimed at protecting these important animals.[22] The potential threats outlined above apply to many species of wildlife and domesticated mammals, but the likely bat origin of SARS-CoV-2 and the current state of disease-ravaged bat populations in North America influenced us focus this review on bats.

Lessons from an epizootic -- susceptibility of North American bats to an introduced pathogen

SARS-CoV-2 is not be the first pathogen with the potential for inadvertent spread from people to North American bats. The COVID-19 pandemic follows the arrival of a fungal pathogen (*Pseudogymnoascus destructans*) that in 2007 began infecting hibernating bat populations in North America, crossing species barriers, spreading among, and altering the evolutionary trajectory of the continent's bats.[23-25] White-nose syndrome (WNS) -- the disease caused by *P. destructans* remains the first and only documented bat epizootic to cause multi-year, spreading mass mortality,[26] although short-term bat die-offs were linked to Lloviu virus in Europe.[27] WNS has killed millions of North American bats, affected populations of at least 12 species of 3 genera, and has already spread across half of the U.S. and Canada. Effective methods to mitigate WNS spread and impacts remain elusive despite substantial research effort, and targeted mitigation actions have had limited success against the disease impacts of WNS.[28] It took years of concerted international scientific effort to identify the cold-growing fungus, determine that it likely originated somewhere in the temperate zones of Europe or Asia, understand its mechanisms of infection and pathogenicity, and track its rapid spread through an immunologically naïve continental assemblage of hibernating bats that largely lacked robust defenses against it.[29-31] The devastating impact of WNS on a diverse group of North American bats likely resulted from evolutionary isolation of the continent's bat fauna from other parts of the world for millions of years, despite other species of *Pseudogymnoascus* being present. No extant species of bat in the Americas also occurs outside of the Americas,[32,33] and no bats migrate or likely survive natural flights across the Pacific or Atlantic oceans.[34,35] Bats in both Europe and Asia can become infected by *P. destructans*, but do not suffer mass mortality from WNS.[36,37] The bat fauna spanning the higher latitudes of North America (in U.S. and Canada) is composed almost entirely of species belonging to the world's largest bat family -- Vespertilionidae with at least 500 described species. Vespertilionid bats occur all over the world, but likely originated and diversified in North America tens of millions of years ago -- this second-largest family of mammals is the only bat family to increase in diversity northward out of the tropics and consistently reach high latitudes (50ºN).[38,39] The WNS epizootic taught us that a large proportion of these historically isolated bats can be vulnerable to a pathogen introduced from another continent during a single event. Additionally, bats already in a physiologically stressed condition due to WNS or other pressures may have increased susceptibility to viral infection, experience exacerbated disease outcomes, and/or increased viral shedding.[40,41] The COVID-19 pandemic invokes the specter of WNS with respect to potential for pathogen spread

through interconnected, multi-species populations that might be immunologically naïve, and highlighs deficits in our understanding of temperate-zone bat pathogens in North America.

Gaps in understanding global patterns of bat-CoV diversity, evolution, and host range

Bats are among the world's most diverse mammals (approximately 1,400 species), and the global distribution and diversity of CoVs in bats proportionally reflects that of their hosts.[42,43] Available evidence indicates that bats are natural reservoirs of CoVs, some of which have the potential to cause diseases in humans, livestock, and other types of domestic animals and wildlife.[19,42,44-56] Coronaviruses appear to have ancient and ancestral relationships with bats, diversifying globally through a process of within-host evolution and cross-taxonomic host-switching events.[42,56-58] Indeed, bats are the likely mammalian progenitor hosts of all alpha (α-) and beta (β-) CoVs[59] and potentially all coronaviruses.[60-62] Alpha-CoVs of likely bat origin include the causative agent of swine acute diarrheal syndrome (SADS) that caused mass mortality of piglets on farms in Guangdong province, China,[53] and a variant strain of porcine epidemic diarrhea virus (PEDV) that spread rapidly from China in recent decades and caused mass piglet mortality in multiple U.S. states.[63,64] Human CoVs NL63 and 229E also likely had their evolutionary origins in bats.[56,65] Two recent human disease epidemics (severe acute respiratory syndrome [SARS], Middle East respiratory syndrome [MERS]) and now the current COVID-19 pandemic were caused by viruses that probably originated from β-CoVs circulating in bat populations in regions where the outbreak occurred.[19,21,45-50,54,55,66]

Emergence of diseases like SADS, PEDV, SARS, MERS, and now COVID-19 from the same general region strongly indicates a close association between CoVs that are likely to evolve into pathogens and the wildlife reservoirs from which they originate.[19,45-50] The evolutionary relationships of CoVs within bats are consistent with geographically structured transmission cycles, with occasional transmission among related bat species.[42,54,67] These phylogeographic factors are also universal determinates of viral sharing among all mammals.[68] However, bat-virus association patterns can be particularly difficult to discern because bats often roost together in multi-species aggregations that can facilitate viral sharing, with each capable of asymptomatically harboring multiple CoV lineages.[42,54,55,69,70] Host shifts to more divergent, non-bat hosts (i.e., that lead to spillover) are more difficult to predict -- firstly, because the potential host breadth for many CoVs is broad,[51,52,57,71,72] and, secondly, because host susceptibility and onward transmission involve complex, multi-stage processes.[2,12] Bat-CoV associations remain woefully under-sampled and understudied in temperate-zone North America, despite the large number of bat biologists and virologists working in the U.S., Mexico, and Canada.[42,69,73,74]

Are viruses like SARS-CoV-2 already present in North American bats?

Our examination of CoV evolutionary lineages and global distribution patterns of the diverse bats they infect suggests that temperate-zone North American bats could be immunologically naïve to infection by viruses like SARS-CoV-2. Alpha and β-CoVs have been detected in bats on most continents, sometimes with both types occurring in bats of the same species.[54,55,75] However, an exception to this pattern is the apparent lack of evidence that β-CoVs infect bats of temperate-zone North America, despite methods suitable to detect both α- and β-CoVs.[56,69,74,76] Multiple novel α-CoVs have been detected and described in vespertilionid bats of the U.S. and Canada, infecting species both living in close contact with humans and in remote wild areas.[56,69,74,76,77] However, SARSr-CoVs and β-CoVs of the viral subgenus *Sarbecovirus* have

thus far been detected almost exclusively in species of the Old-World Chiropteran suborder Yinpterochiroptera (figure 1A, table S1).[42,54,67] The few exceptions to this pattern were detection of novel Clade 3 and Clade 1 *Sarbecovirus* (*sensu*[48]) in the wrinkle-lipped bat (*Mops plicatus*, family Molossidae) in China[78] and the vespertilionid lesser noctule (*Nyctalus leisleri*) cohabiting a Bulgarian cave during autumn with several species of rhinolophids in which other SARSr β-CoVs were concurrently detected, suggesting cross-species infections (figure 1A).[79] Putative detections of a Clade 1 *Sarbecovirus* were also reported from guano samples of the vespertilionid brown long-eared bat (*Plecotus auritus*) and the molossid European free-tailed bat (*Tadarida teniotis*) on Sardinia, where the same novel β-CoV was described from greater horseshoe bats (*R. ferrumequinum*).[80]

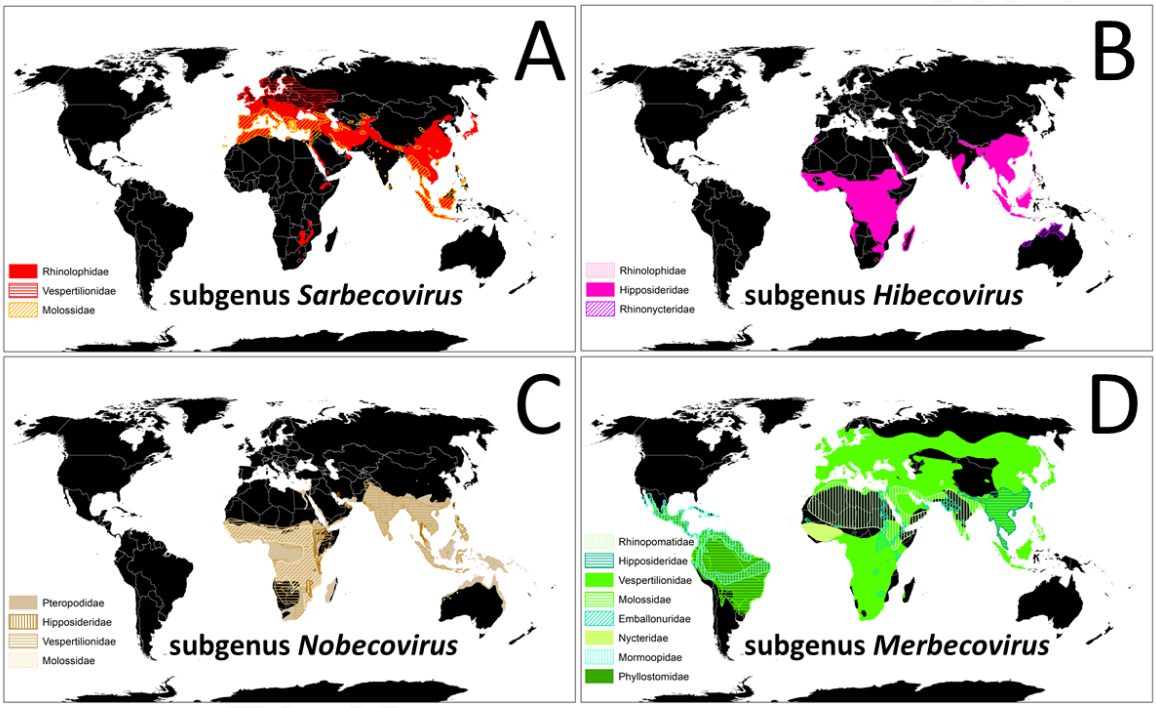

Figure 1. Global patterns of bats and associated beta-coronaviruses (β-CoVs). A) red-shaded distributions of bat species in which SARS-related β-CoVs of the subgenus *Sarbecovirus* have been detected; B) pink-shaded distributions of bat species known to host β-CoVs of the subgenus *Hibecovirus*; C) brown-shaded distributions of bats in which β-CoVs of the *Nobecovirus* lineage have been detected; and D) green-shaded distributions of bats known to host MERS-related β-CoVs of the subgenus *Merbecovirus*. Different colors and shade styles within each panel represent different families of bats. See table S1 for species lists and data sources. Maps created using ArcMap (ESRI, Redlands, California, USA) and bat ranges derived from spatial data on terrestrial mammals from the International Union for the Conservation of Nature (IUCN 2020. The IUCN Red List of Threatened Species. January 2019 [version 6.2]. https://www.iucnredlist.org; Downloaded on 11 April 2020).

Viruses in the β-CoVs subgenera *Hibecovirus* and *Nobecovirus*, also tend to associate mostly with Old-World bat families, except for novel viruses of the latter subgenus detected in four species of the vespertilionid genus *Scotophilus* in Asia and Africa (figure 1B, C; table S1).[42,54,67]

Bat β-CoVs of the subgenus *Merbecovirus* (MERS-related lineage) occur in a greater diversity of bat families and across more global regions than the other subgenera (figure 1D).[42,54,67] These widely distributed MERS-like viruses can cause disease in humans (e.g., MERS) and notably appear to be the only bat β-CoVs to diversify among several families of the globally distributed suborder Yangochiroptera (figure 1D, table S1).[42,54,67]

Lack of evidence for β-CoVs in temperate-zone North American bats

The several hundred species of extant bats spanning the Americas all belong to the suborder Yangochiroptera, which likely diverged from the Old-World suborder Yinpterochiroptera more than 50 million years ago (figure 2).[81] The only β-CoVs detected in the Americas to date belong to the subgenus *Merbecovirus*, and appear restricted to two exclusively Neotropical bat families (Phyllostomidae and Mormoopidae) and one that is globally distributed (Molossidae). Distinct CoV lineages in the subgenus *Merbecovirus* were described from three species of *Pteronotus* (family Mormoopidae) and four species of *Artibeus* and Seba's short-tailed bat (*Carollia perspicillata*; family Phyllostomidae) from tropical regions of Mexico (table S1).[42,82,83] Another novel β-CoV of the subgenus *Merbecovirus* was detected in broad-eared bats (*Nyctinomops laticaudatus*, family Molossidae) in southern Mexico.[82] It was subsequently shown *in vitro* that primary kidney cells from the Neotropical bat *Artibeus jamaicensis* could become infected with MERS-CoV, and experimental infection trials demonstrated virus replication and shedding in individual bats of this species but without obvious clinical signs of disease.[84] Available evidence suggests β-CoVs may have arrived to the New World through South America and have long been evolving in Neotropical bats. Although some bat hosts of *Merbecoviruses* overlap geographically with species of temperate-zone North American bats, none occur outside of the Neotropics. Sampling has been limited, but we are not aware of any published detections of *Merbecoviruses* or any other β-CoVs in temperate-zone North American vespertilionid bats.

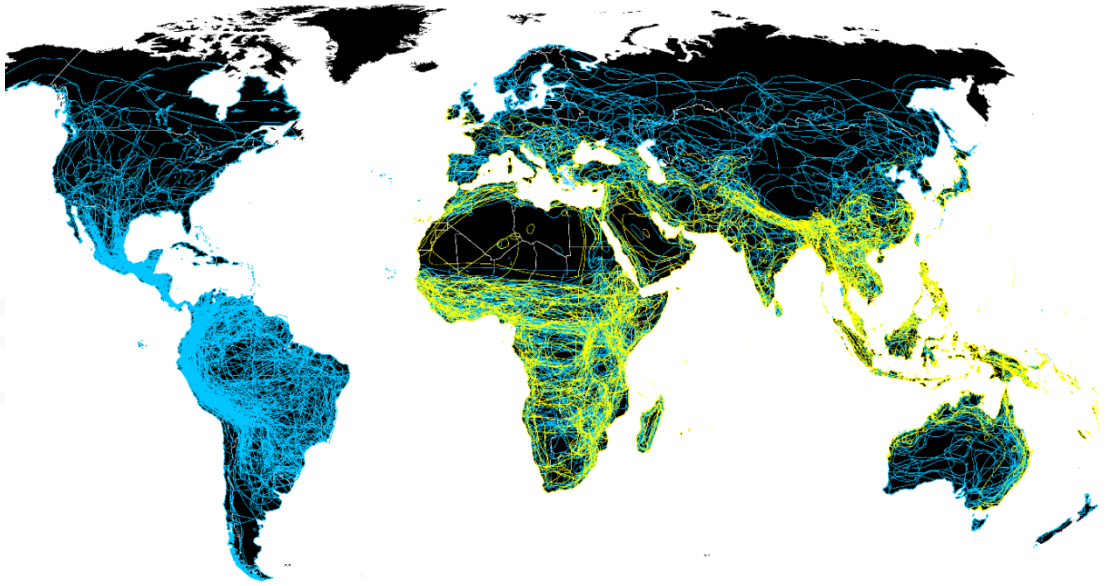

Figure 2. Old-World and New-World bats. Overlapping species distribution outlines of bats in the globally distributed suborder Yangochiroptera (blue) and Old-World Yinpterochiroptera (yellow). Maps

created using ArcMap (ESRI, Redlands, California, USA) and bat ranges derived from spatial data on terrestrial mammals from the IUCN (International Union for the Conservation of Nature (IUCN 2020. The IUCN Red List of Threatened Species. January 2019 [version 6.2]. https://www.iucnredlist.org; Downloaded on 11 April 2020).

Globally, only a fraction of the approximately 1,400 species of bats have been robustly sampled and tested for CoVs. This sampling deficit limits our inference of North American bat host susceptibility to SARS-CoV-2 through examination of known patterns of bat-CoV occurrence and distribution. To our knowledge, the only SARSr-CoVs (*Sarbecovirus* spp)[48,85] documented in the ultra-diverse and globally distributed bat family Vespertilionidae were from Bulgaria[79] and Sardinia,[80] likely transmissions from co-occurring *Rhinolophus* sp. bats. This absence of evidence for β-CoVs in vespertilionid bats in general, and in temperate-zone vespertilionid bats of North America in particular, may represent a sampling deficit or, more likely, a unique biogeographic pattern driven by underlying factors of host susceptibility or life history.

More than half of bats in the U.S. and Canada hibernate,[86] which might have an influence on their susceptibility to viruses, as was postulated for common vespertilionids infected with α-CoVs and rabies virus.[40,87-89] Body temperatures of hibernating bats can remain consistently below 10ºC for periods lasting 7-9 months per year,[90] providing a potential mechanism to limit viral replication and spread. Experimental studies to assess the ability of SARS-CoV-2 or other β-CoV to survive and replicate in bats (cell lines and individuals) at low temperatures would provide additional insight into risk of reverse zoonosis. However, we may currently lack appropriate tools for studying such possibilities, such as immortalized cell lines from several hibernating, vespertilionid bats.[56] Scientists did not discover and isolate the fungus that causes WNS until they prepared samples in bat hibernation sites and moved culture dishes from laboratory benches into refrigerators.[23] Similar innovative explorations outside the typical temperature conditions of laboratory experimentation could help assess risk of SARS-CoV-2 infecting the more than two dozen species of bats in the U.S. and Canada that hibernate to survive harsh temperate-zone winters.

Proactively connecting the wellbeing of human and bat populations

Scientists have long recognized the risk of disease spillover from humans to bats,[91-93] but bat researchers in North America did not systematically address such risk prior to WNS. Outside of reservoir host studies, few bat researchers studied infectious diseases in bats before WNS emerged in 2007,[73] and proportionally few disease researchers studied bat pathogens before bats were retrospectively connected to the SARS epidemic.[17,66,94] An often unstated duality that can inhibit bat disease research is the potential conflict created from the fact that bats are unequivocally ecologically important,[13,14] yet also a source of diverse emerging infectious diseases.[7,94,95] Possible explanations for why bats might host particularly pathogenic viruses include characteristics of their life history (e.g., long-lived, wide ranging, multi-species aggregations, daily and seasonal heterothermy),[94] unique physiology for repairing their damaged DNA,[96] unique ability to regulate immune responses,[97-102] high species diversity,[43] and unmatched metabolic range and high body temperatures during flight.[103] Bats also cryptically come into close contact with humans, increasingly in urban and per-urban settings as a result of native habitat loss, often crossing human-wildlife interfaces.[104-110]

Except for *Lyssavirus* infections, bats rarely show signs of sickness from the same dangerous pathogens that cause virulent disease in humans. Bats cope with viral infections in ways that we do not yet fully comprehend but learning how they do so may reveal important insights to develop therapeutics and ultimately to protect human health.[100-102] *In vitro* and laboratory studies demonstrate that bats can specifically regulate immune response to effectively cope with pathogenic viruses.[111] For example, dendritic cells generated from the bone marrow of the Egyptian rousette bat (*Rousettus aegyptiacus*) infected with Marburg virus downregulate immune-stimulatory pathways and maturation of cells targeted by the virus, while upregulating pathogen-sensing pathways.[112] Unique bat immune regulation may occur with MERS-CoV and SARS-CoV-2 infection, at least under experimental conditions.[98,113] Lack of clear signs of illness in bats and the cryptic habits of many species also generally inhibit our ability to easily detect spillover of pathogens from human to bat populations, further adding to uncertainty about cross-species transmission and dispersal of CoVs among human and animal communities. Laboratory findings suggest human viruses that likely originated in bats, such as HCoV-NL63, seem capable of infecting bat cells, at least *in vitro*.[56] Despite having specialized RNA proofreading machinery, the replicating RNA genomes of SARS-CoV-2 and other CoVs rank among the largest known,[114,115] making them prone to recombination and copy errors in bats with resulting functional adaptations (e.g., altered receptor binding capacity or temperature adaptation of enzymes).[116] CoVs can even recombine with functional fragments of other virus families, such as when a bat-derived CoV gained a functional gene from a reovirus.[117] Spillover of SARS-CoV-2 into North American bats could lead to the virus becoming either less or more pathogenic to bats, domestic animals, or humans through genetic mixing in a new reservoir host. The public-health and conservation consequences of a more virulent virus could be severe, whereas genetic mixing in a bat host that resulted in a less virulent virus might go unnoticed.

Need for an interdisciplinary response

Effectively managing risks of human disease caused by emerging zoonotic pathogens *and* ensuring the health and conservation of wildlife species that are potential reservoirs of those disease agents can be synergistic goals under a One Health framework. Research has shown that spillover risk (from or to wildlife) may be highest in disturbed ecosystems where there is an elevated frequency of human-wildlife interactions or disruption of ecological patterns.[3,118-122] Thus, effective bat conservation and management requires understanding both pathogens that cause disease in bats, as well as human activities and ecological contexts that increase direct and indirect interactions with bats that could present health risks.[2] Furthermore, fear-based reactions to disease risk from wildlife, such as culling infected bat populations or indiscriminate killing, often have negative unintended consequences for the interconnected health of both humans and bats (e.g., culling of bats in a Uganda mine led to a more than doubling of Marburg virus prevalence in the bats living there).[26,123-125] Temperate-zone vespertilionid bats inhabiting human dwellings in the U.S. and Canada represent a particularly relevant human-wildlife interface where conservation and management actions to proactively address the potential consequences for disease spillover may be particularly worth careful consideration.[73]

Conservation-minded surveillance of bat viruses has demonstrated the potential for mutual beneficial collaboration between public health scientists and conservation stakeholders.[91,110,123,126,127] Disease-focused studies that integrate ecological principles into a

rigorous study design provide the most ecologically relevant context to the bat pathogen findings.[128,129] Assessing the risks of SARS-CoV-2 spillback into North American bats presents a timely opportunity to form multidisciplinary scientific teams that include experts on emerging infectious diseases and bat ecologists with expertise on North American bat species.[126] Scientists researching emerging infectious diseases can benefit from methods bat researchers have developed for observing, counting, and non-invasively sampling bats.[73,130] Bat researchers can learn important biosafety, health monitoring, laboratory techniques, safe and secure handling/storage of CoV-positive samples, and training in the proper use of personal protective equipment (PPE) from researchers with expertise in veterinary and medical sciences.[110,129,131] All investigators can work together to develop mutually beneficial goals, such as joint risk communications to the public with effective and balanced messaging about bat populations, especially regarding higher risk areas or activities of human and bat contacts.

The emergence of WNS in 2007 prompted changes to guidance for PPE use and disinfection practices for bat researchers and recreational cavers. Similarly, the emergence of SARS-CoV-2 and other recently emerged viruses will continue to alter the *status quo* of bat research, emphasizing the need to carefully weigh risks and benefits of wildlife research in the context of population-altering diseases.[132] For example, PPE including respiratory protection is a standard practice adopted by the bat virus research community but by few others studying and regularly handling bats [REFS]. Adopting a precautionary approach in the face of widespread COVID-19 transmission, U.S. and international wildlife organizations have advised limiting capturing and handling of bats in the field to minimize the risk of humans infecting wild bats with SARS-CoV-2 until further assessment can be made.[133,134] The urgent research priority of a rapid, quantitative risk assessment and analysis of various mitigation options is currently underway.[133] One key question is whether the proper use of optimal PPE, along with effective risk communication and adherence to other basic biosafety practices[131,135] during field work can significantly reduce the risk of transmission of SARS-CoV-2 from humans to bats. In the interim, until new guidelines are established for handling and near-proximity work with bats, important scientific inquiry can still be considered. For example, temporarily shifting to 'hands-off' bat research methods especially in temperate regions where *Sarbecoviruses* have not been found in bats seems prudent, wherever possible, and could facilitate ongoing work with reduced risk.

Examples of 'hands-off' research strategies

Multiple hands-off research strategies already exist for addressing critical gaps in understanding about CoV diversity, distribution, evolution, and potential health effects in temperate-zone bats. For example, a combination of host-cell receptor analyses and *in vitro* and *in vivo* experimental infections across a diversity of bat and other mammalian species have helped inform potential host range expansion for SARS-CoV-2. The receptors that many CoVs use to gain access to host cells, such as angiotensin-converting enzyme 2 (ACE2) and dipeptidyl peptidase-4 (DPP4/CD26), have undergone positive selection in bats, resulting in diverse and recombinant CoV strains that can likely bind to numerous variants of a host receptor protein and facilitate spillover into other animal species.[42,72] SARS-CoV-2 targets and strongly binds to mammalian ACE2 cell receptors.[72,136,137] Beta-CoVs of the subgenus *Merbecovirus* like those known to occur in the Americas are not known to target ACE2 cell receptors, instead using as a receptor DPP4/CD26 or possibly other receptors.[48,138] Current *in silico* predictions that bats will likely have low susceptibility to SARS-CoV-2 based on ACE2 structural analyses conflict with *in vitro*

evidence and do not take into account ACE2 amino acid sequence variation (including intraspecific variation) that occurs within bats.[19,72,136] Assessing SARS-CoV-2 host range will require additional virus-host receptor binding assays *in silico* and *in vitro*,[19,48,72,136,138] together with future experimental infection studies for confirmation of Koch's postulates. Together these investigations will help quantify the potential for North American bat infection and transmission among free-ranging populations.

Examples of hands-off methods applicable to both bat disease and conservation research include: virus discovery and characterization focused on existing specimens archived in scientific museums;[139,140] monitoring echolocation calls to determine the occurrence, distributions, and seasonal or nightly activity patterns of bats;[141,142] digital imaging methods for counting bats and studying physiology and behaviors in the context of disease;[105,143,144] and sampling guano from below bat roosts to determine bat species and individual identity, population dynamics, and daily or seasonal patterns of bat occupancy and pathogen shedding.[69,145-148] Promising areas for innovation include making technologies for bat research more accessible to a broader global user base, less expensive, easier to use, and scientifically reproducible through open-source hardware, software, and laboratory methods.[149-151] In addition to research, standardized field protocols and probabilistic sampling strategies are needed for monitoring bats and their viruses at continental scales (www.nabatmonitoring.org),[152,153] as are longitudinal studies across multiple sites to better understand the ecological drivers of CoV dynamics and spillover. Developing simple management tools and methods for rapidly assessing risks of virus spillover from humans to wildlife while maintaining scientific rigor could also help with future disease response. It might also be useful to prepare a suite of tools, protocols, and risk communication strategies for natural resource managers and public health officials to immediately deploy while risks are being assessed. Such prepared management resources could range from implementing precautionary approaches and public outreach about enhanced use of PPE for those in closest contact with potentially susceptible wildlife.

Conclusion

The current COVID-19 pandemic highlights the dramatic public health, economic, and societal consequences of virus spillover from a wildlife reservoir, and presents a new set of challenges when considering viral spill back from people to naïve animal populations. While CoVs and bats around the world are evolutionarily entwined, temperate-zone North American bats appear to be evolutionarily isolated from bat β-CoVs -- the group of viruses which have led to serious zoonotic disease outbreaks. Many questions remain about the risk of SARS-CoV-2 to naïve wildlife populations, the influences of human behavior on those risks, and the potential for forming new CoV reservoirs. Cross-species virus transmission events are relatively rare, requiring an infectious reservoir host to be in contact with a recipient host when conditions concurrently favor susceptibility and onward transmission.[12,110,111] The currently unknown but potentially high-consequence risk of SARS-CoV-2 transmission and establishment in North American bats (or other free-ranging mammals) warrants precaution. Strategically managing interactions between people and potentially susceptible recipient species can decrease the probability of cross-species virus spillover.[110] Humans that frequently handle and come into close contact with North American temperate-zone bats, such as bat researchers, rehabilitators, wildlife/pest control workers, and disease investigators, can help decrease any chances of spillover by carefully evaluating how their actions could put entire populations of bats at risk.

We are at a critical nexus of biosecurity and natural resource conservation that will require ingenuity and diligence to continue important research on bats whilst simultaneously evaluating the ecological future of SARS-CoV-2. Our actions during this current pandemic could profoundly influence and protect the health of both humans and bats.

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Table S1. Global patterns of β-CoV associations in bats. Bat species in which β-CoVs were detected, organized by viral subgenera, bat family, and bat suborder. Bats of the suborder Yinpterochiroptera highlighted in yellow and Yangochiroptera in blue.

β-CoV SUBGENER	BAT SPECIES	BAT FAMILY	GEOGRAPHIC REGION	REFERENCE	BAT SUBORDER
Sarbecoviruses	*Rhinolophus affinis*	Rhinolophidae	Asia	He et al. 2014	Yinpterochiroptera
Clade 3	*Rhinolophus ferrumequinum*	Rhinolophidae	Eurasia	Anthony et al. 2017	Yinpterochiroptera
	Rhinolophus hipposideros	Rhinolophidae	Eurasia	Rihtaric et al. 2010	Yinpterochiroptera
	Rhinolophus macrotis	Rhinolophidae	Asia	Tao and Tong 2019	Yinpterochiroptera
	Rhinolophus monoceros	Rhinolophidae	Asia	Chen et al. 2016	Yinpterochiroptera
	Rhinolophus pearsonii	Rhinolophidae	Asia	Tao and Tong 2019	Yinpterochiroptera
	Rhinolophus sinicus	Rhinolophidae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Aselliscus stoliczkanus	Hipposideridae	Asia	Tao and Tong 2019	Yinpterochiroptera
	Mops plicatus	Molossidae	Asia	Yang et al. 2013	Yangochiroptera
Clade 2	*Rhinolophus pusillus*	Rhinolophidae	Asia	Tao and Tong 2019	Yinpterochiroptera
	Rhinolophus rex	Rhinolophidae	Asia	Wong et al. 2019	Yinpterochiroptera
Clade 1	*Rhinolophus blasii*	Rhinolophidae	Africa	Drexler et al. 2010	Yinpterochiroptera
	Rhinolophus euryale	Rhinolophidae	Eurasia	Drexler et al. 2010; Kemenesi et al. 2014	Yinpterochiroptera
	Rhinolophus mehelyi	Rhinolophidae	Eurasia	Drexler et al. 2010	Yinpterochiroptera
	Rhinolophus sp. Kenya	Rhinolophidae	Africa	Tao and Tong 2019	Yinpterochiroptera
	Nyctalus leisleri	Vespertilionidae	Europe	Drexler et al. 2010	Yangochiroptera
	Plecotus auritus	Vespertilionidae	Europe	Lecis et al. 2019	Yangochiroptera
	Tadarida teniotis	Molossidae	Eurasia	Lecis et al. 2019	Yangochiroptera
Hibecoviruses	*Hipposideros armiger*	Hipposideridae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Hipposideros caffer	Hipposideridae	Africa	Anthony et al. 2017	Yinpterochiroptera
	Rhinolophus clivosus	Rhinolophidae	Africa	Anthony et al. 2017	Yinpterochiroptera
	Macronycteris commersoni	Hipposideridae	Africa	Tao and Tong 2019	Yinpterochiroptera
	Rhinolophus creaghi	Rhinolophidae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Hipposideros galeritus	Hipposideridae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Hipposideros larvatus	Hipposideridae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Hipposideros lekaguli	Hipposideridae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Hipposideros pratti	Hipposideridae	Asia	Tang et al. 2006	Yinpterochiroptera
	Hipposideros ruber	Hipposideridae	Africa	Anthony et al. 2017	Yinpterochiroptera
	Rhinonicteris aurantia	Rhinonycteridae	Australia	Smith et al. 2016	Yinpterochiroptera
Nobecoviruses	*Cynopterus brachyotis*	Pteropodidae	Asia	Watanabe et al. 2010; Anthony et al. 2017	Yinpterochiroptera
	Cynopterus horsfieldii	Pteropodidae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Cynopterus sphinx	Pteropodidae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Dobsonia moluccensis	Pteropodidae	Asia	Anindita et al. 2015	Yinpterochiroptera
	Dyacopterus spadiceus	Pteropodidae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Megaerops kusnotoi	Pteropodidae	Asia	Xu et al. 2016	Yinpterochiroptera
	Megaerops niphanae	Pteropodidae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Eidolon dupreanum	Pteropodidae	Africa	Razanajatovo et al. 2015	Yinpterochiroptera
	Eidolon helvum	Pteropodidae	Africa	Anthony et al. 2017	Yinpterochiroptera
	Ptenochirus jagori	Pteropodidae	Asia	Watanabe et al. 2010	Yinpterochiroptera
	Pteropus alecto	Pteropodidae	Asia	Smith et al. 2016; Anthony et al. 2017	Yinpterochiroptera
	Pteropus lylei	Pteropodidae	Asia	Wacharapluesadee et al. 2018	Yinpterochiroptera
	Pteropus medius	Pteropodidae	Asia	Kudagammana et al. 2017	Yinpterochiroptera
	Pteropus rufus	Pteropodidae	Africa	Razanajatovo et al. 2015	Yinpterochiroptera

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46			*Pteropus vampyrus*		Pteropodidae		Asia			Anthony et al. 2017	Yinpterochiroptera
47			*Epomophorus gambianus*		Pteropodidae		Africa			Anthony et al. 2017	Yinpterochiroptera
48			*Epomophorus labiatus*		Pteropodidae		Africa			Nziza et al. 2020	Yinpterochiroptera
49			*Epomops franqueti*		Pteropodidae		Africa			Anthony et al. 2017	Yinpterochiroptera
50			*Eonycteris spelaea*		Pteropodidae		Asia			Watanabe et al. 2010; Anthony et al. 2017	Yinpterochiroptera
51			*Macroglossus sp.*		Pteropodidae		Asia			Lacroix et al. 2016	Yinpterochiroptera
52			*Myonycteris angolensis*		Pteropodidae		Africa			Anthony et al. 2017	Yinpterochiroptera
53			*Megaloglossus woermanni*		Pteropodidae		Africa			Anthony et al. 2017	Yinpterochiroptera
54			*Micropteropus pusillus*		Pteropodidae		Africa			Anthony et al. 2017	Yinpterochiroptera
55			*Rousettus aegyptiacus*		Pteropodidae		Africa			Anthony et al. 2017	Yinpterochiroptera
56			*Rousettus amplexicaudatus*		Pteropodidae		Asia			Watanabe et al. 2010; Anthony et al. 2017	Yinpterochiroptera
57			*Rousettus leschenaulti*		Pteropodidae		Asia			Anthony et al. 2017	Yinpterochiroptera
58			*Hipposideros lekaguli*		Hipposideridae		Asia			Anthony et al. 2017	Yinpterochiroptera
59			*Triaenops persicus*		Hipposideridae		Africa			Anthony et al. 2017	Yinpterochiroptera
60			*Scotophilus dinganii*		Vespertilionidae		Africa			Anthony et al. 2017	Yangochiroptera
61			*Scotophilus heathii*		Vespertilionidae		Asia			Wacharapluesadee et al. 2015	Yangochiroptera
62			*Scotophilus kuhlii*		Vespertilionidae		Asia			Wacharapluesadee et al. 2015	Yangochiroptera
63			*Scotophilus leucogaster*		Vespertilionidae		Africa			Anthony et al. 2017	Yangochiroptera
64			*Mops condylurus*		Molossidae		Africa			Anthony et al. 2017	Yangochiroptera
65	***Merbecoviruses***		*Hipposideros armiger*		Hipposideridae		Asia			Anthony et al. 2017	Yinpterochiroptera
66			*Rhinopoma hardwickii*		Rhinopomatidae		Africa/Asia			Memish et al. 2013	Yinpterochiroptera
67			*Myotis daubentonii*		Vespertilionidae		Eurasia			Xu et al. 2016	Yangochiroptera
68			*Myotis pilosus*		Vespertilionidae		Asia			Anthony et al. 2017	Yangochiroptera
69			*Eptesicus isabellinus*		Vespertilionidae		Iberian Peninsula			Falcón et al. 2011	Yangochiroptera
70			*Eptesicus serotinus*		Vespertilionidae		Eurasia			Lee et al. 2018	Yangochiroptera
71			*Hypsugo savii*		Vespertilionidae		Iberian Peninsula			Falcón et al. 2011	Yangochiroptera
72			*Laephotis capensis*		Vespertilionidae		Africa			Ithete et al. 2013	Yangochiroptera
73			*Laephotis zuluensis*		Vespertilionidae		Africa			Ithete et al. 2013	Yangochiroptera
74			*Pipistrellus abramus*		Vespertilionidae		Asia			Lee et al. 2018	Yangochiroptera
75			*Pipistrellus coromandra*		Vespertilionidae		Asia			Anthony et al. 2017	Yangochiroptera
76			*Pipistrellus hesperidus*		Vespertilionidae		Africa			Anthony et al. 2017	Yangochiroptera
77			*Pipistrellus kuhlii*		Vespertilionidae		Eurasia			Moreno et al. 2017	Yangochiroptera
78			*Pipistrellus nathusii*		Vespertilionidae		Europe			Annan et al. 2013	Yangochiroptera
79			*Pipistrellus pipistrellus*		Vespertilionidae		Asia			Anthony et al. 2017	Yangochiroptera
80			*Pipistrellus pygmaeus*		Vespertilionidae		Europe			Annan et al. 2013	Yangochiroptera
81			*Plecotus auritus*		Vespertilionidae		Europe			Rizzo et al. 2017	Yangochiroptera
82			*Tylonycteris pachypus*		Vespertilionidae		Asia			Anthony et al. 2017	Yangochiroptera
83			*Vespertilio sinensis*		Vespertilionidae		Asia			Anthony et al. 2017	Yangochiroptera
84			*Ia io*		Vespertilionidae		Asia			Anthony et al. 2017	Yangochiroptera
85			*Vespertilio sinensis*		Vespertilionidae		Asia			Lee et al. 2018	Yangochiroptera
86			*Eumops glaucinus*		Molossidae		Latin America			Góes et al. 2016	Yangochiroptera
87			*Nyctinomops laticaudatus*		Molossidae		Latin America			Anthony et al. 2017	Yangochiroptera
88			*Taphozous perforatus*		Emballonuridae		Arabian Peninsula			Memish et al. 2013	Yangochiroptera
89			*Nycteris gambiensis*		Nycteridae		Africa			Annan et al. 2013	Yangochiroptera
90			*Pteronotus davyi*		Mormoopidae		Latin America			Goes et al. 2013	Yangochiroptera
91			*Pteronotus parnellii*		Mormoopidae		Latin America			Anthony et al. 2017	Yangochiroptera

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92			*Pteronotus personatus*		Mormoopidae		Latin America			Anthony et al. 2017	Yangochiroptera
93			*Artibeus lituratus*		Phyllostomidae		Latin America			Anthony et al. 2017	Yangochiroptera
94			*Artibeus obscurus*		Phyllostomidae		Latin America			Anthony et al. 2017	Yangochiroptera
95			*Artibeus phaeotis*		Phyllostomidae		Latin America			Anthony et al. 2017	Yangochiroptera
96			*Carollia perspicillata*		Phyllostomidae		Latin America			Corman et al. 2013	Yangochiroptera
97	***Embecovirus***		*Myotis emarginatus*		Vespertilionidae		Eurasia			Pauly et al. 2017	Yangochiroptera

From: Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)
Sent: Monday, April 27, 2020 11:51 AM EDT
To: Sleeman, Jonathan M ; Paul Cryan ; Runge, Michael C >; Grant, Evan H ; DeeAnn Reeder ; Kevin Olival ecohealthalliance.org>; Kading,Rebekah >; Amman, Brian R. (CDC/DDID/NCEZID/DHCPP)
CC: Harcourt, Brian H. (CDC/DDID/NCEZID/DHCPP)
Subject: FW: Dr. Yi presentation on Monday, 2pm April 27

Since the topic of PPE and using masks to limit source-based SARS2 spread was a central theme or the expert elicitation, I thought you might find this zoom talk relevant and hopefully informative. I didn't want to send it to the whole group since I just learned of the talk myself and I'm not really involved with this study, although other members of our branch are (Brian Harcourt, CC'd). Anyway, if you're interested, feel free to join.
Jon

From: Harcourt, Brian H. (CDC/DDID/NCEZID/DHCPP)
Sent: Monday, April 27, 2020 11:30 AM
To: Montgomery, Joel M. (CDC/DDID/NCEZID/DHCPP) Spiropoulou, Christina (CDC/DDID/NCEZID/DHCPP) ; Klena, John D. (CDC/DDID/NCEZID/DHCPP) ; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) ; Albarino, Cesar (CDC/DDID/NCEZID/DHCPP) < Taboy, Celine (CDC/DDID/NCEZID/DHCPP) ; Shoemaker, Trevor (CDC/DDID/NCEZID/DHCPP)
Subject: FW: Dr. Yi presentation on Monday, 2pm April 27

Hi all. One of our DeMaND study collaborators from Stanford, Yi Ciu, is giving a talk today for CDC. He has some interesting data about materials that can be used in community masks. Some of them out perform surgical masks. If he shows the EM/3D x-ray data of NaCl particles penetrating meltbond nonwoven material used in N95 masks, those images alone are worth the price of admission. Feel free to share with your teams, of course.

Thanks,
Brian

Brian H. Harcourt, PhD
Biosafety Officer
Viral Special Pathogens Branch

From: Chu, May
Sent: Friday, April 24, 2020 4:35 PM
To: Harcourt, Brian H. (CDC/DDID/NCEZID/DHCPP) ; Kilinc-Balci, F Selcen (CDC/NIOSH/NPPTL/RB) >; Florine Scholte >
Subject: Dr. Yi presentation on Monday, 2pm April 27

Please join us for a special presentation on **Face Masks during COVID-19: Disinfection, Reuse and Homemaking** by Dr. Yi Cui, Professor at Stanford University.

Access the meeting at: https://stanford.zoom.us/j/7350734078

May C. Chu, Ph.D.
Clinical Professor
Department of Epidemiology
Colorado School of Public Health
Anschutz Medical Center
Aurora, CO 80045 USA

From: William B. Karesh ecohealthalliance.org>
Sent: Friday, August 21, 2020 11:45 AM EDT
To: Kading,Rebekah >; Kevin Olival ecohealthalliance.org>; Tigga.Kingston Tigga.Kingston >; Rodrigo Medellin >; Kendra Phelps @ecohealthalliance. Isabella Mandl

CC: Dr. Melinda Rostal ecohealthalliance.org>; Catherine Machalaba ecohealthalliance.org>
Subject: guidelines for wildlife researchers in the time of COVID-19
Attachment(s): "WHSG and OIE COVID-19 Guidelines 20 Aug 2020.pdf","ATT00001.htm"

Dear all,

Thanks you for your input on the attached guidelines for wildlife researchers in the time of COVID-19. **And, special thanks to** Mindy Rostal, Tiggy Grillo and Marcy Uhart for taking the lead on drafting and integrating all of the valuable comments and suggestions.

This originated from requests for guidance to assist with field research decision making and permitting, but hopefully will be also be a useful more broadly for risk reduction and encouraging professionalism and best practices.

We arranged for this to be a joint guidance document from both the OIE and the IUCN SSC WHSG with the hopes of reaching wider audience.

Please feel free to share either the document attached below or this link: http://www.iucn-whsg.org/COVID-19GuidelinesForWildlifeResearchers

Thanks again for your help with the graphic!

All the Best,

Billy

William B. Karesh, D.V.M
Executive Vice President for Health and Policy

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www.ecohealthalliance.org

President, OIE Working Group on Wildlife

Co-chair, IUCN Species Survival Commission - Wildlife Health Specialist Group

EPT Partners Liaison, USAID Emerging Pandemic Threats - PREDICT-2 Program

Guidelines for Working with Free-Ranging Wild Mammals in the Era of the COVID-19 Pandemic

SUMMARY

The SARS-CoV-2 virus, the cause of COVID-19, emerged as a human pathogen in 2019. While it is thought to have a zoonotic source, the original wildlife reservoir and any potential intermediate hosts have not yet been identified. Phylogenetic analyses suggest the progenitor virus is related to beta-coronaviruses previously identified in bats. At this time, SARS-CoV-2 should be considered a human pathogen with people acting as reservoir and sustaining transmission. There is a possibility that SARS-CoV-2 will become endemic in the human population and thus, presents a risk of a potential reverse zoonosis to wildlife as with infectious diseases such as tuberculosis and influenza.

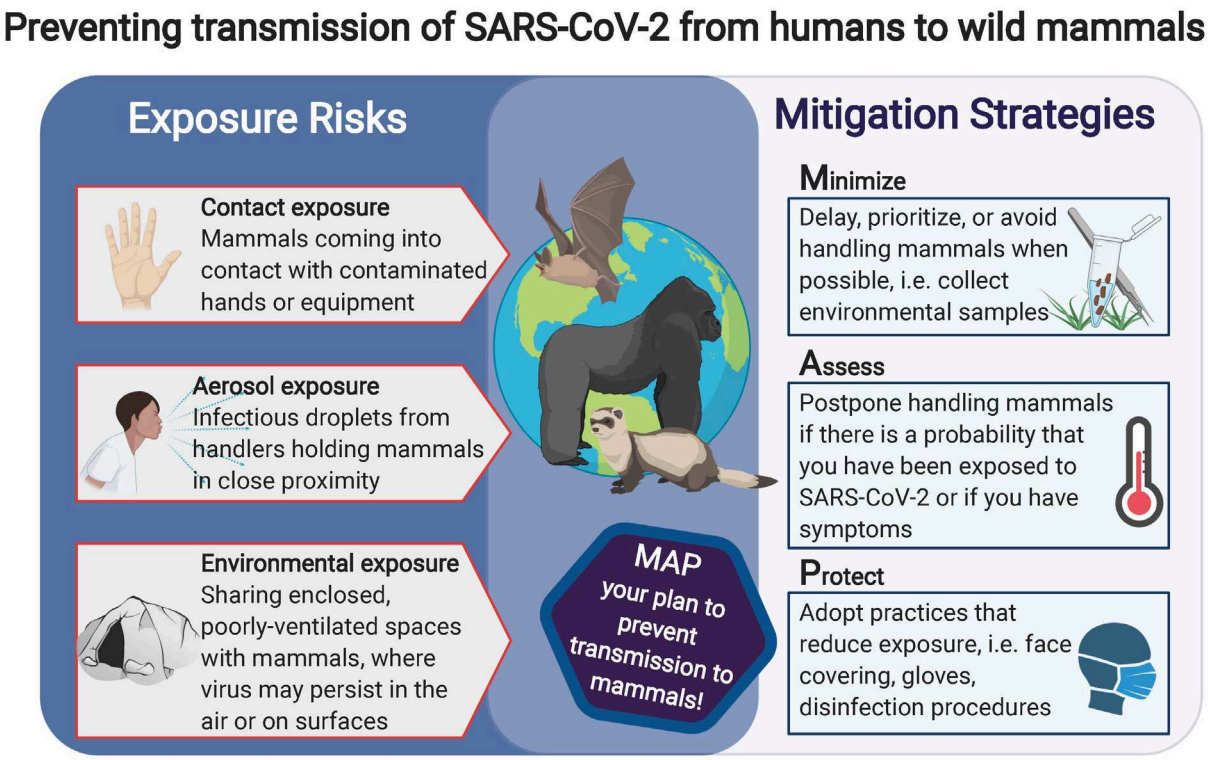
Currently the risk of human-to-animal transmission to non-captive wildlife species warrants concern. A number of cases have demonstrated natural human-to-animal transmission of SARS-CoV-2 in felids, canids and mustelids, the majority due to close and prolonged contact with infected households or people, and none has involved free-ranging wildlife. The identification of close phylogenetically-related viruses (e.g. in bats and pangolins), the presence of important cell receptor proteins (ACE2 receptors) and infection following natural exposure or experimental inoculation suggest that a wide range of mammalian species may be susceptible to SARS-CoV-2. Knowledge and experience with human-to-animal transmission with other human respiratory pathogens (e.g. metapneumovirus, measles, other human coronaviruses and tuberculosis) indicate that some species taxonomically closely related to humans (e.g. non-human primates) would likely be susceptible to infection and/or clinical disease caused by SARS-CoV-2.

There are valid concerns about the health of individuals or populations if infected with the virus and/or a wildlife population becoming a reservoir for SARS-CoV-2. Any wildlife species/taxa that becomes a reservoir for SARS-CoV-2 could pose a continued public health risk of zoonosis, a risk for the transmission of SARS-CoV-2 to other animal species, and risk negative perceptions resulting in human threats to that species or their populations.

Efforts that require working with free-living wildlife are vital to professional management and conservation as well as the health of wildlife, people and ecosystems. The recommendations below were developed to minimize the risk of SARS-CoV-2 transmission from people to free-ranging, wild mammals. Specifically, these recommendations are for people engaged in **wildlife work**[*] in the field, either in direct contact (e.g. handling) or indirect contact (e.g. within 2 meters

[*] These recommendations are provided for trained biologists, conservationists, researchers, veterinarians, etc who work with free-living wildlife in situ. They are not intended for people who interact with wild mammals under different circumstances, such as rehabilitators or ecotourists, etc.

or in a confined space) with free-ranging wild mammals, or working in situations in which free-ranging wild mammals may come in contact with surfaces or materials contaminated by infected personnel.



This figure was adapted in collaboration with the IUCN Bat Specialist group.

RECOMMENDATIONS

These recommendations are based on first principles of biosecurity and hygiene, current knowledge of human-to-animal SARS-CoV-2 transmission and the precautionary principle.

Minimize

In line with ethical considerations for working with wildlife, we recommend that the three "R's" be considered. If postponement is not possible, it is recommended to **"Replace"** work that involves animals with alternatives that do not require handling free-living wildlife (i.e. environmental sampling, remote monitoring); **"Reduce"** the number of animals required to conduct the work and **"Refine**" the methods used to minimize the impact of the handling on the individual animal and on that animal's population. The recommendations given below are focused on "Refine" however, "Replacing" and "Reducing" work with animals should also be considered at all times.

The primary aim of "Refining" work to be done with wild mammals is to reduce transmission of SARS-CoV-2 from a person to wild mammals. Like tuberculosis and measles, SARS-CoV2 may pose a serious threat of transmission from people to wild mammals. Thus, these additional refinements are recommended for those working indirectly with wild mammals within an enclosed space as well as those working directly with/handling free-living wild mammals.

Assess

The SARS-CoV-2 virus will likely be endemic in many human populations for the foreseeable future, making the potential for transmission of SARS-CoV-2 to wild mammals from people an on-going risk. It is recognised that as the local rate of transmission of SARS-CoV-2 in human populations in different localities fluctuates, the subsequent risk of transmission to wildlife will also vary, requiring continuous and adaptive risk assessment. As the level of community transmission (as defined by WHO) increases and decreases according to implemented control measures, so too will the level of risk. When community transmission rate increases, the potential that at least one person on the field team will be infected (even if they do not have symptoms) also increases. This is important as currently almost half of human infections are asymptomatic, which increases the risk of unknowingly transmitting the virus to wild mammals. These factors make it impossible to estimate the exact quantitative risk of human-to-animal SARS-CoV-2 transmission that working with wildlife represents. Thus, when assessing whether to proceed or postpone work it is recommended that one:

1) Postpone the work, unless it is urgent for the health and wellbeing of the animal, if there is known or suspected COVID-19 community transmission, as defined by the WHO, in the area around the site of the wild mammal work or in an area where the team members have been in the past two weeks. Wildlife work should be postponed at least until the transmission rate of COVID-19 has been limited to clusters of cases instead of community transmission (WHO).

2) Confirm that local authorities currently permit this type of work and always follow local public health guidelines regarding COVID-19 prevention; if the work is permitted,

3) Use one's best judgement as to when to work with wild mammals, erring on the side of the precautionary principle (i.e. uncertainty must be resolved in favor of prevention); if one decides to continue,

4) Assess the field team or individual:

    - If someone on the team tests positive for SARS-CoV-2 or has COVID-19 symptoms (WHO), they should follow public health advice on quarantining and avoid working with wild mammals for 2 weeks (WHO) after symptom onset and if symptoms persist, for at least three days after symptoms have resolved without the use of fever-reducing medications. In the case of an asymptomatic infection, avoid working with wild mammals for 2 weeks after the last positive test date.

    - If someone on the team has had contact with a confirmed or suspected person in the past 2 weeks, they should follow public health advice on quarantining and should not work with wildlife for 2 weeks since the potential/known exposure or until they are cleared by public health authorities.

        - This may mean the whole team needs to be quarantined if they were in contact with the team member that tested positive.

    - No one who is currently showing symptoms of SARS-CoV-2 (fever of 38°C [100.4 °F] or greater, cough etc.) should work with wild mammals.

        - Implement daily temperature checks on the days you will be in contact with wild mammals.

        - It is important to avoid taking fever-modifying medicine prior to the temperature check to prevent masking a fever.

    - If possible, each person on the field team should be tested for SARS-CoV-2 with negative confirmation at least 24-48 hours prior to fieldwork commencing, understanding that this may not be feasible in all circumstances/locations.

Protect

If, upon assessment of the local situation, it is determined that work with free-ranging wild mammals may proceed, it remains the team's duty to minimize the risk of asymptomatic transmission of SARS-CoV-2 to the wild mammals (and each other) by using the proper protective equipment and biosecurity measures. To do this, it is recommended that one:

- Follow local public health recommendations.
- Limit the number of personnel to the minimum necessary to safely complete the task and minimize the number of personnel who actually handle or come into close contact (within 2 meters [6 feet]) with wild mammals.
    - Maintain the same field team for the duration of the operation to minimize the number of different people contacting one another and animals.
    - To the extent possible, maintain physical distancing between personnel, particularly during transportation and activities in closed spaces.
- Minimize the amount of time people are in close or direct contact with wild mammals.
- Ensure the people on the team that will have direct contact with wild mammals have been properly trained in using personal protective equipment, infection control and animal handling.
- Wear clean, dedicated clothing (e.g. disposable (Tyvek coveralls) or clothing that will be removed and properly cleaned immediately after sampling, at the site).
- If working **indirectly** (e.g. >2m or in a confined space) with wild mammal species that are considered to be particularly susceptible[†] (e.g. bats, felids, mustelids, non-human primates and any species with the same ACE2 receptor):
    - Wear a face mask or covering, preferably a surgical mask or a more protective covering (e.g. fit-tested N95 without an air release valve).
        - Note a mask or other cloth face-covering is used to prevent the spread of respiratory droplets from your nose and mouth. If surgical masks or respirators are not available locally, it is recommended to use a fitted face covering to improve the ability of the mask to catch respiratory droplets.

[†] Note: as new information becomes available any other taxa / species in which SARS-CoV-2 transmission is demonstrated via natural or experimental inoculation should also be considered "potentially susceptible".

        - If working with a team, team members should wear face coverings regardless of the susceptibility of the animal species as recommended by local public health officials.

- If **directly** handling wild mammals:

    - Wear a face mask or covering, preferably a surgical mask or a more protective covering (e.g. fit-tested N95 without an air release valve) when handling/transporting wild mammals.

        - When handling potentially susceptible species[‡] (e.g. bats, felids, mustelids, non-human primates and any species with the same ACE2 receptor) wear an N95 respirator (**without an air release valve)** or other equivalent/increased respiratory protection (e.g. Powered Air Purifying Respirators).

    - Wash your hands with soap and water and/or apply hand sanitizer (>60% alcohol applied to clean hands) before and after handling wild mammals.

    - Wear disposable or clean reusable gloves, and change gloves between sampling events or handling individuals of solitary species.

    - Do not blow on mammals to see anatomical features or ectoparasites.

    - Keep captured animals separate from each other to greatest extent possible when capturing and handling.

    - Avoid touching your face or mask, and if contact occurs, change/disinfect your hands/gloves.

    - Clean and disinfect all reusable field gear and equipment that may come into contact with wild mammals prior to starting the work and after each field-work shift or between handling individuals of solitary species.

        - When selecting a disinfectant consider its efficacy against SARS-CoV-2 (EPA), its effectiveness against other pathogens (The Center for Food Security and Public Health) that the animal being sampled may carry, and its potential effect on the equipment that will be used and its environmental impact.

            - 70% isopropyl alcohol or a 10% solution of household bleach are recommended for disinfection against COVID-19 (WHO).

            - For both disinfectants, the surface must be cleaned before they are applied, and your working solution of bleach must be made fresh every day.

    - Properly dispose of used materials and biological and hazardous waste.

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‡ Note: as new information becomes available any other taxa / species in which SARS-CoV-2 transmission is demonstrated via natural or experimental inoculation should also be considered "potentially susceptible ".

- Follow more specific guidelines produced for each specific taxa group when available (see links below).

- In settings where peri-urban work is required, ensure that any onlookers from the public remain at least 10 meters away and are upwind from the work that is ongoing with the wild mammals.

These recommendations are deliberately broad to apply to multiple taxa of wild mammals. Some expert groups have developed their own recommendations (see below), which should be used in addition to these. The situation with the COVID-19 pandemic is continually evolving. As we learn more about the effects of SARS-CoV-2 in more species and transmission risks, these recommendations may change or be superseded by species or taxa-specific recommendations. As the SARS-CoV-2 will likely become endemic in human populations, it is our responsibility to prevent the same thing from occurring in the wild, free-ranging mammal species that are in contact with people.

ADDITIONAL RESOURCES

IUCN Great Apes Specialist Group Statement:
http://www.internationalprimatologicalsociety.org/docs/COVID-19_Advisory_for_conservation_field_teams.pdf

IUCN Bat Specialist Group Statement:
https://www.iucnbsg.org/uploads/6/5/0/9/6509077/map_recommendations_for_researchers_v._1.0_final.pdf

AZA Felid Statement: https://zahp.aza.org/felid-tag-statement-on-sars-cov-2/

AZA Small Carnivore Statement: https://zahp.aza.org/wp-content/uploads/2020/04/AZA-Small-Carnivore-TAG-SARS-CoV-Statement_8Apr2020.pdf

AFWA Statement: https://wildlifedisease.org/Portals/0/Covid-19%20Information/AFWA%20Statement%20on%20COVID-19%20and%20Mustelids%20Felids%20and%20Canids%20June%209%202020.pdf

European Association of Zoo and Wildlife Veterinarians – Transmissible Disease Handbook, Chapter 4.4 SARS-CoV2 and COVID-19. https://www.eazwv.org/page/inf_handbook

* The infographic was created using BioRender.com

From: Katie Leahy
Sent: Thursday, February 01, 2018 12:03 AM EST
To: Ian Mendenhall Joram Buza ; Vivek Kapur >; Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Kading,Rebekah ; Lela Urushadaze ; Tamar Kutateladze >; Supaporn Wacharapluesadee ; Abel Wade ; Catalino Demetria >; Tigga Kingston ; Paul Cryan >; DeeAnn Reeder ; Gavin Smith ; Nisreen Alhmoud ; Keti Sidamonidze >; Bounheuang, Kounnavong v>
CC: Stokes, Martha M CIV (US) >; mary.j.lancaster ; Newman, Carl I CIV DTRA J3-7 (US) ; christopher.r.lewis
Subject: IMPORTANT: Transportation to Ambassador's Reception

All,

There have been several inquiries. To be clear: CBEP **will not** be providing transportation to or from the Ambassador's reception this evening. You should have a hard copy of the invitation, please feel free to walk, cab, or uber to the residence address that is provided on your invitation. The reception runs from 1800-2000 and you are invited to arrive and leave at your discretion.

V/r,

Katie Leahy

Katie Leahy
Program Manager | Global Systems Engineering
6303 Little River Turnpike, Suite 208
Alexandria, VA 22305

http://globalsyseng.com

Attachment(s): "PMAC2018_Invitation_JICA.pdf"

"How Can Health Data and Technological Innovations Contribute to the Next-generation UHC to Ensure Global Human Security?"
Side meeting at the 2018 Prince Mahidol Award Conference

Tuesday, 30 January 2018

2:00pm-4:30pm
Lotus 10 Meeting Room, Convention Center, 22 Fl, Centara Grand Hotel at Central World

Dear Sir/Madam,

We are delighted to invite you to an event co-organized by Institute for Global Health Policy Research (iGHP), National Center for Global Health and Medicine (NCGM), Japan and "The Partnership Project for Global Health and Universal Health Coverage (GLO+UHC)" [Thailand Ministry of Public Health (MOPH)
National Health Security Office (NHSO) and Japan International Cooperation Agency (JICA)]

The event is a side meeting focusing on new approaches to making health systems person-centered, efficient, and sustainable with effective use of health data and ICT and to foster discussion among stakeholders from various sectors to promote partnerships at country and global levels.

The session outline is enclosed for your reference.

The session is open to all PMAC participants.

We would appreciate if you could kindly confirm your participation by 20 January 2018, using the online registration form here:https://goo.gl/forms/qXkf612X6nKbD7Y02

Sincerely,
Yohsuke TAKASAKI
Expert, Chief Advisor / Health Policy
The Partnership Project for Global Health and Universal Health Coverage

"How Can Health Data and Technological Innovations Contribute to the Next-generation UHC to Ensure Global Human Security?"
Prince Mahidol Award Conference (PMAC) 2018
14:00-16:30 on 30th January, 2018

1. Date and Venue

Date: 14:00-16:30 on 30th January, 2018
Venue: Lotus 10 Meeting Room, Convention Center, 22 Fl, Centara Grand Hotel at Central World

2. Backgrounds

When working towards effective and efficient Universal Health Coverage (UHC) implementation, the current trends surrounding health systems should be taken into consideration. These trends include human mobility at the global level, humanitarian crises, epidemiological and demographic transitions, emerging and re-emerging infectious diseases, and the ever-increasing needs for quality and equitable health-care services. Accordingly, health systems should be strengthened at multiple levels (community, national, regional and global), and person-centered quality health care needs to be delivered to everyone.

Novel approaches as well as mobilization of existing resources are necessary for planning effective and reliable health systems. Strategic utilization of health data and information and communication technology (ICT) is a significant measure in this era of sustainable development goals (SDGs). These technical innovations can potentially help design a next-generation UHC, to establish healthy and sustainable future societies. Stakeholders from different sectors should ideally be able to collaborate to deliver person-centered quality health care with effective use of health data. However, in reality, obstacles such as conflicts of interest among stakeholders need to be surmounted.

In this side meeting, speakers from diverse sectors will share their experiences and discuss new strategies to design health systems with effective use of health data that could ensure human security at individual levels irrespective of their locations; how to overcome challenges in collaborating with stakeholders; and global partnerships expected from the perspective of global human security.

3. Objectives

- To share knowledge of new approaches to making health systems person-centered, efficient, and sustainable with effective use of health data and ICT.
- To foster discussion among stakeholders from various sectors to promote partnerships at country and global levels.

4. Expected outcome

- The role of health data in making health systems person-centered, efficient, and sustainable are understood by audiences.
- Stakeholders from various sectors would be able to identify the key factors in promoting partnerships at national and global levels.

5. Meeting agenda

14:00-16:30 on 30th January, 2018

14:00-14:07	Welcome Remarks (Eiji Hinoshita, Director-General, Bureau of International Health Cooperation, NCGM)
14:07-14:22	Opening Remarks & Presentation (Manabu Sumi, Director, Global Health Policy Division, International Cooperation Bureau, MOFA, Japan)
14:22-14:29	Introduction of Thailand-Japan collaboration project (Yohsuke Takasaki, Chief Advisor, GLO+UHC)
14:30-14:45	Keynote Address 1 (Virasakdi Chongsuvivatwong, Professor, Prince of Songkla University, Thailand)
14:45-15:00	Keynote Address 2 (Hiroaki Miyata, Director, Department of Global Health Systems and Innovation, iGHP, NCGM)
15:00-15:10	Q&A Session
15:10-15:20	Coffee Break
15:20-16:20	Panel Discussion followed by a Q&A session Panelists include health data and public health specialists from various international organizations, academic institutions, and representatives from some of the ASEAN countries
16:20-16:30	Closing Remarks (Senior Official of Thailand)

6. Organizer and contact details

Institute for Global Health Policy Research (iGHP), National Center for Global Health and Medicine (NCGM), Japan

"The Partnership Project for Global Health and Universal Health Coverage (GLO+UHC)" Thailand Ministry of Public Health (MOPH)

National Health Security Office (NHSO)

Japan International Cooperation Agency (JICA)

From: Katie Leahy
Sent: Monday, January 29, 2018 10:30 PM EST
To: lance.r.brooks >; Newman, Carl I CIV DTRA J3-7 (US) >; Lancaster, Mary J CIV (US) christopher.r.lewis < >; Kading,Rebekah ; DeeAnn Reeder >; Cryan, Paul Vivek Kapur ; Gavin James Smith ; Tigga Kingston >; abelwade >; Ian Mendenhall tamar_kutateladze >; Keti Sidamonidze ; Lela Urushadze ; joram.buza c_demetria >; Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Jason Rao >; cryan.paul

CC: Stokes, Martha M CIV (US) >; Simmi Ghai >; S Wacharapluesadee >
Subject: NEW SLIDES
Attachment(s): "Working Groups.pptx"

Here are the working group slides that were live-edited for your use in break-out groups.

V/r,

Katie Leahy

From: Katie Leahy >
Date: Monday, January 29, 2018 at 9:01 PM
To: "lance.r.brooks , "Newman, Carl I CIV DTRA J3-7 (US)" >, "Lancaster, Mary J CIV (US)" , "christopher.r.lewis " , "Kading,Rebekah" DeeAnn Reeder , "Cryan, Paul" , Vivek Kapur >, Gavin James Smith , Tigga Kingston "abelwade " Ian Mendenhall "tamar_kutateladze , Keti Sidamonidze >, Lela Urushadze , "joram.buza " "c_ " < >, Kevin Olival ecohealthalliance.org>, Jon Epstein ecohealthalliance.org>, Jason Rao >, "cryan.paul " >
Cc: "Stokes, Martha M CIV (US)" >, Simmi Ghai , S Wacharapluesadee
Subject: Update to the BPERNet Slides

Hi, everyone! We made a couple changes to the slides for tomorrow. Nothing substantive, just our approach to conducting the brief-out discussions and the order of a couple of the initial slides.

A reminder again to please be in the lobby at 0745, the bus will depart for Chulalongkorn promptly at 0800.

V/r,

Katie Leahy

From: Katie Leahy >
Date: Monday, January 29, 2018 at 10:28 AM
To: "lance.r.brooks " "Newman, Carl I CIV DTRA J3-7 (US)" >, "Lancaster, Mary J CIV (US)" , "christopher.r.lewis " , "Kading,Rebekah" >, DeeAnn Reeder , "Cryan, Paul" >, Vivek Kapur , Gavin James Smith >, Tigga Kingston >, "abelwade , Ian Mendenhall "tamar_kutateladze " Keti Sidamonidze >, Lela Urushadze , "joram.buza "c_demetria " , Kevin Olival ecohealthalliance.org>, Jon Epstein ecohealthalliance.org>
Cc: "Stokes, Martha M CIV (US)" , Simmi Ghai >, S Wacharapluesadee >
Subject: BPERNet: Transportation Times and Other Useful Information (30 and 31 January 2017)

Hello, everyone! Welcome to Bangkok. On behalf of the Executive Committee (Dr. Martha Stokes and Dr. Mary Lancaster), we are so pleased that you are able to join us this week for our BPERNet planning meeting and other PMAC activities.

Please use this email as your resource for information regarding transportation, logistics, and other coordinating information for 30 January – 31 January.

30 January – BPERNet Meeting at Chulalongkorn Hospital

1. **The bus will depart from the Renaissance Hotel promptly at 0800** ; please be in the lobby for head count at 0745
2. We will provide coffee and light refreshment during the meeting; you will take lunch at one of the many canteen options at the hotel; please bring

about 200 - 300 thai baht (~10 USD) for lunch

31 January – PMAC / BPERNet Field Trip

1. **The bus will depart from the Renaissance Hotel promptly at 0630** ; please be in the lobby for head count at 0615; please make sure that you are on time, as we are caravanning with a delegation from the Centara Hotel and will receive a police escort to move us quickly through traffic
2. We will provide a box breakfast for the bus ride
3. Please make sure that you dress appropriately for this field trip; we strongly suggest covered shoes and loose, comfortable clothing; in addition to this mode of dress we also suggest that you bring accompaniments for spending a day outdoors amongst bat roosts; such as:
    a. Hat
    b. Sunscreen
    c. Sunglasses
    d. Bug spray
    e. Water bottle

We will provide information regarding the Ambassador's reception at the close of tomorrow's meeting.

Again, we are so excited to have you all here. Please do not hesitate to reach out to me or Megan Hudson (copied) if you have any questions.

V/r,

Katie Leahy

Katie Leahy
Program Manager | Global Systems Engineering
6303 Little River Turnpike, Suite 208
Alexandria, VA 22305

http://globalsyseng.com

Today's Agenda

0830 – 0840	Welcoming Remarks and Group Photo
0840 – 0900	Orientation and Meeting Context
0900 – 1000	Facilitated Focus Area Review and Discussion
1000 – 1015	Working Tea Break
1015 – 1115	Session 1: Focus Area Strategy Mapping
1115 – 1155	Session 1: Interactive Feedback (World Café Method)
1155 – 1215	Breakout Group Session 1 Brief-out (5-minutes / group)
1215 – 1330	Lunch
1330 – 1430	Session 1: Focus Area Strategy Mapping
1430 – 1510	Session 1: Interactive Feedback (World Café Method)
1510 – 1530	Breakout Group Session 2 Brief-out (5-minutes / group)
1530 – 1545	Working Tea Break
1545 – 1615	Close-out Discussion (next steps)

Revisit: Working Groups and Research Mentors

Working Group	Research Mentors
1. Host-pathogen biology and interactions	◦ Dr. Joram Buza ◦ Dr. Vivek Kapur ◦ Dr. DeeAnn Reeder ◦ Dr. Gavin Smith
2. Pathogen surveillance, diagnostic capacity, and epidemiology	◦ Dr. Catalino Demetria ◦ Dr. Jon Epstein ◦ Dr. Tamar Kutateladze ◦ Dr. Abel Wade ◦ Dr. Keti Sidamonidze
3. Ecology setting	◦ Dr. Paul Cryan ◦ Dr. Tigga Kingston ◦ Dr. Robert Kityo ◦ Dr. Rebekah Kading ◦ Dr. Eiichi Hondo
4. Human-bat interactions	◦ Dr. Kevin Olival ◦ Dr. Ian Mendenhall ◦ Dr. Supaporn Wacharapluesadee ◦ Dr. Lela Urushadze ◦ Dr. Nesreen Alhmoud

Cross-cutting Themes

Communication, outreach, and advocacy of group goals to decision-makers and policy-makers

List of recommendations for standardized language

Database management / IT

Modeling

Workforce development

Education and outreach with humans that live in close proximity to bat communities

NOTE: may want to consider other experts; e.g., working with statisticians (for modeling) and professional PR individuals (for communications); and expertise from social scientists

Note: these were edited by the SC during the PMAC side meeting (30 January 2018)

Working Group 1: Host / pathogen biology and interactions

Bat physiology (integration opportunity with Group 3 – Ecology)

Bat immunology

Bat pathology and pathophysiology

Bat pathogen community ecology (co-infections, co-morbidities)

Distribution of pathogens among species

Develop modeling approaches for host dynamics and epidemiology (individual to populations; and seasonality . . . integration opportunity with Group 2)

Group Challenges:

1. Very few reagents and cell lines
2. Lack of animal models

Note: these were edited by the SC during the PMAC side meeting (30 January 2018)

Working Group 2: Pathogen surveillance, diagnostic capacity, and epidemiology

Molecular epidemiology

Serological surveillance integrated with education and outreach

Distribution of pathogens geographically and phylogenetically

Detection, diagnosis, and reporting of bat-associated pathogens

Establish commonly used guidance on sampling

Challenges:

1. Workforce capacity
2. Sequencing the antigenic region or whole genomes
3. Integration with conservation communities and stakeholders

Note: these were edited by the SC during the PMAC side meeting (30 January 2018)

Working Group 3: Ecology setting (bat, domesticated animals, and wildlife interface)

Bat behavior (social ecology), distribution, and movement

Domesticated animals and wildlife behavior, distribution, and movement impact on interaction with bats.

The effect of anthropogenic disturbance and modification on pathogen dynamics and spillover risk

Bat population structures

Vector ecology

Acoustic surveys

Bat taxonomy

Effects of seasonality

Challenges:

1. Sampling protocol and common process for encountering new species
2. Identification and taxonomy issues

Note: these were edited by the SC during the PMAC side meeting (30 January 2018)

Working Group 4: Human-bat interactions

Human behavioral risk characterization
- Encroachment effects
- Climate change effects
- Opportunity for interaction with Group 3 on anthropogenic disturbance)

Hunting and commodity chain (e.g., bushmeat, guano, and pet trade)

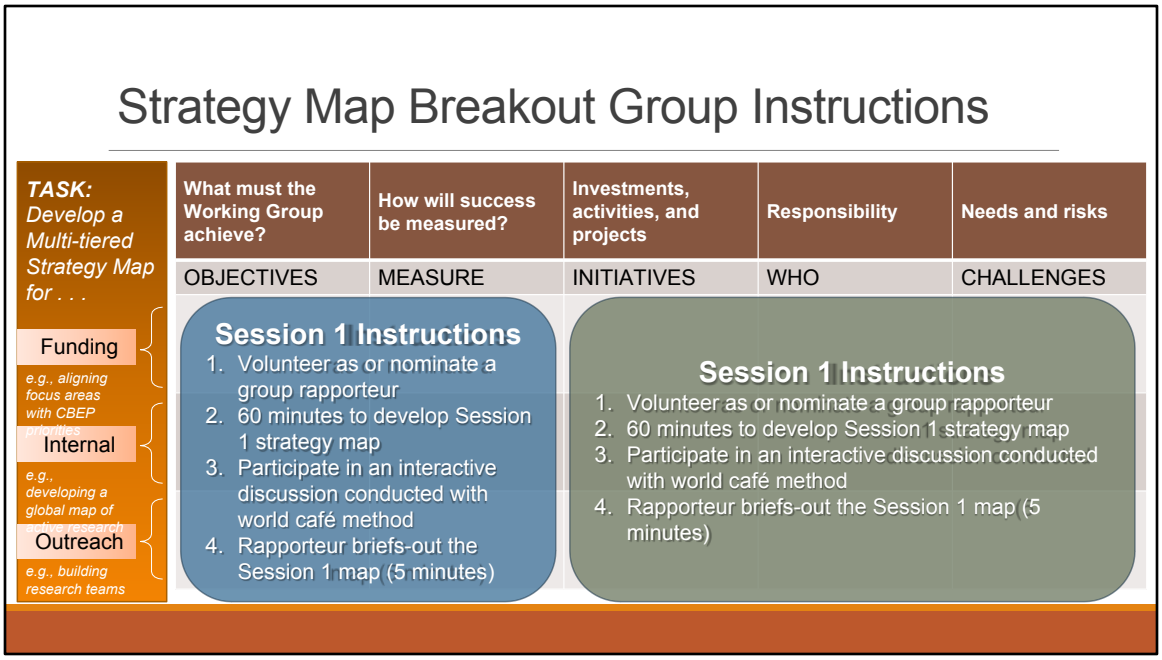
Ecotourism

Interactions in human dwellings

Influence of agricultural practices (consider all alspects; e.g., flora aspect and livestock practices, and use of guano in fertilization)

Note: these were edited by the SC during the PMAC side meeting (30 January 2018)

Strategy Map Breakout Group Instructions



Interactive Discussion Instructions (using world café method)

Will take place immediately following each 60 minute breakout group session

- Rapporteurs should stay in their focus areas to collect comments;
- At the buzzer, leave your group and rotate to a group of your choice and interact with the group rapporteur;
  - Ask questions
  - Provide feedback
  - Make additions to the established strategy
- At the next buzzer (after 10 minutes), leave your group and rotate to a new group and do the same;
- At the next buzzer, leave your group and rotate to a new group and do the same
- At the next (and final buzzer), leave your group and rotate back to your focus area for a quick discussion (10 minutes) to prepare your 5-minute outbrief

Session 1: Focus Area Strategy Mapping

60 MINUTES

Session 1: Strategy Map Scorecard

TASK: *Develop a Multi-tiered Strategy Map for . . .*

- **Funding**
  - *e.g., aligning focus areas with CBEP priorities*
- **Internal**
  - *e.g., developing a global map of active research*
- **Outreach**
  - *e.g., building research teams*

What must the Working Group achieve?	How will success be measured?
OBJECTIVES	MEASURE

Session 1: Interactive Feedback (World Café Method)

10 MINUTES / BREAKOUT GROUP ROTATION

40 MINUTES

Session 1: Outbrief

5 MINUTES / GROUP
BRIEFED BY GROUP RAPPORTEUR
20 MINUTES

Lunch

75 MINUTES

Session 2: Focus Area Strategy Mapping

60 MINUTES

Session 2: Strategy Map Scorecard

TASK: *Develop a Multi-tiered Strategy Map for . . .*

- **Funding**
  - *e.g., aligning focus areas with CBEP priorities*
- **Internal**
  - *e.g., developing a global map of active research*
- **Outreach**
  - *e.g., building research teams*

Investments, activities, and projects	Responsibility	Needs and risks
INITIATIVES	WHO	CHALLENGES

Session 2: Interactive Feedback (World Café Method)

10 MINUTES / BREAKOUT GROUP ROTATION

40 MINUTES

Session 2: Outbrief

5 MINUTES / GROUP
BRIEFED BY GROUP RAPPORTEUR
20 MINUTES

From: Kendra Phelps ecohealthalliance.org>
Sent: Friday, August 07, 2020 3:22 PM EDT
To: Kading,Rebekah
Subject: Out of office until Aug. 8th Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Thank you for your email. I am out of the office for fieldwork until August 8th and will have limited email access, but I will reply to your email as soon as possible.

Thank you for your patience!
Kendra

--
Kendra Phelps, PhD
Research Scientist

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200
New York, NY 10018

)
www.ecohealthalliance.org

From: Kendra Phelps ecohealthalliance.org>
Sent: Wednesday, September 16, 2020 12:25 PM EDT
To: Kading,Rebekah
Subject: Out of office until Sept 20 Re: Bat One Health Research Network directory

Thank you for your email. I am on vacation until Sept. 20th and will reply to your email as soon as possible.

Thank you for your patience!
Kendra

--

Kendra Phelps, PhD
Research Scientist
she/her

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200
New York, NY 10018

www.ecohealthalliance.org

From: Jon Epstein ecohealthalliance.org>
Sent: Monday, August 13, 2018 11:55 PM EDT
To: Kading,Rebekah
Subject: Out of the office until August 27th Re: Draft Executive Summary and Website Materials

Hello,
I will be on leave until August 27th and unable to receive email. I will respond to messages as soon as possible once I am back. For additional assistance, please contact Ms. Emma Lane: ecohealthalliance.org or call

Thank you,

Jon

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

web: ecohealthalliance.org

Twitter: @epsteinjon

-

From: Kevin Olival ecohealthalliance.org>
Sent: Wednesday, August 12, 2020 7:55 PM EDT
To: Cara Brook Hon S Ip Paul Cryan >; David Hayman >; epstein ecohealthalliance.org>; dreeder < ; Hume Field ecohealthalliance.org>; Charles H Calisher Brian R. Amman ; Wang Linfa ; Ralph S. Baric ; David S Blehert >; Kevin Castle Jeremy Coleman >; Peter Daszak cohealthalliance.org>; wfrick ; Amy Gilbert ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson >; Kading,Rebekah ; Tigga Kingston Lorch, Jeffrey M >; Ian MENDENHALL PhD >; alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; Jonathan D Reichard >; Jonathan M Sleeman >; Daniel Streicker >; Jonathan S. Towner
Subject: Paper Proof - please review. "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPA...
Attachment(s): "ppat.1008758_1.pdf"

Dear all,

The attached typeset proof of our paper just arrived, and I have two days to reply.*Acceptable corrections are limited to author name or affiliation errors, misleading scientific inaccuracies, and printer's errors.* Change requests beyond these items will not be accepted.

Please quickly double check your name and affiliation, and if you find any errors please let me know by COB tomorrow. If I don't hear back, I'll assume it is correct.

Our article currently has a provisional scheduled publication date of Sep 03, 2020. Please note that our paper will **remain under a strict press embargo** until 2 PM Eastern Time (US) on the date of publication, so please don't circulate or tweet! :)

Thanks!
Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

> On Aug 7, 2020, at 9:09 AM, Kevin Olival ecohealthalliance.org> wrote:
>
> Just wanted to send a quick update on our paper…. I'm honestly surprised at how long PLOS Pathogens is taking, but I guess the editorial process slowed down w COVID.
>
> We send in edits on pre-proofs a couple of times over the last few weeks, and have been waiting for over a week for the typeset proofs to come in. Once those come back and we have a publication date, I'll let you all know ASAP.
>
> Cheers,
> Kevin
>
> **Kevin J. Olival, PhD**
> *Vice President for Research*
>
> EcoHealth Alliance
> 520 Eighth Avenue, Suite 1201

New York, NY 10018

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

From: Kevin Olival ecohealthalliance.org>
Sent: Sunday, June 28, 2020 7:59:53 AM
To: David Hayman < ; Jon Epstein ecohealthalliance.org>; dreeder ; Hume Field ecohealthalliance.org>; Charles H Calisher ; Brian R. Amman Wang Linfa >; Ralph S. Baric ; Blehert, David S ; Cara Brook >; Kevin Castle >; Coleman, Jeremy T Peter Daszak < ecohealthalliance.org>; wfrick Gilbert, Amy T - APHIS ; Ip, Hon S >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson >; Kading,Rebekah >; Tigga Kingston >; Lorch, Jeffrey M : Ian MENDENHALL PhD >; alisonpeel ; Kendra Phelps >; Plowright, Raina >; Reichard, Jonathan D >; Sleeman, Jonathan M ; Daniel Streicker >; Jonathan S. Towner ; Cryan, Paul >
Subject: [EXTERNAL] Fwd: Editorial Acceptance of "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPATHOG...

Paper Accepted!! Thank you all for your patience, perseverance, and invaluable contributions. I haven't received the proofs yet, but will turn them around quickly when I do.

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

Begin forwarded message:

From: "PLOS Pathogens"
Subject: Editorial Acceptance of "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPATHOGENS-D-20-01177R1) - [EMID:902178ed8cb23641]
Date: June 26, 2020 at 4:39:55 PM EDT
To: "Kevin J. Olival" ecohealthalliance.org>
Reply-To: "PLOS Pathogens" >

CC: "Paul M. Cryan" "Brian R. Amman" "Ralph S. Baric" "David S. Blehert" , "Cara E. Brook" "Charles H. Calisher" "Kevin T. Castle" "Jeremy T. H. Coleman" "Peter Daszak" ecohealthalliance.org, "Jonathan H. Epstein" ecohealthalliance.org, "Hume Field" ecohealthalliance.org, "Winifred F. Frick" "Amy T. Gilbert" "David T.S. Hayman" , "Hon S. Ip" , "William B. Karesh" ecohealthalliance.org, "Christine Kreuder Johnson" "Rebekah C. Kading" "Tigga Kingston" "Jeffrey M. Lorch" "Ian H. Mendenhall" "Alison J. Peel" , "Kendra L. Phelps" "Raina K. Plowright" , "DeeAnn M. Reeder" "Jonathan D. Reichard" "Jonathan M. Sleeman" "Daniel G. Streicker" "Jonathan S. Towner" "Lin-Fa Wang"

Dear Dr. Olival,

We are pleased to inform you that your manuscript 'Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats

Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats' has been provisionally accepted for publication in PLOS Pathogens.

Before your manuscript can be formally accepted you will need to complete some formatting changes, which you will receive in a follow up email. A member of our team will be in touch with a set of requests.

Please note that your manuscript will not be scheduled for publication until you have made the required changes, so a swift response is appreciated.

IMPORTANT: The editorial review process is now complete. PLOS will only permit corrections to spelling, formatting or significant scientific errors from this point onwards. Requests for major changes, or any which affect the scientific understanding of your work, will cause delays to the publication date of your manuscript.

Should you, your institution's press office or the journal office choose to press release your paper, you will automatically be opted out of early publication. We ask that you notify us now if you or your institution is planning to press release the article. All press must be co-ordinated with PLOS.

Thank you again for supporting Open Access publishing; we are looking forward to publishing your work in PLOS Pathogens.

Best regards,

Seema Lakdawala, PhD
Reviews Editor
PLOS Pathogens

Aaron Mitchell
Section Editor
PLOS Pathogens

Kasturi Haldar
Editor-in-Chief
PLOS Pathogens
orcid.org/0000-0001-5065-158X

Michael Malim
Editor-in-Chief
PLOS Pathogens
orcid.org/0000-0002-7699-2064

****

Reviewer Comments (if any, and for reference):

PLOS PATHOGENS

REVIEW

Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: A case study of bats

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Abstract

The COVID-19 pandemic highlights the substantial public health, economic, and societal consequences of virus spillover from a wildlife reservoir. Widespread human transmission of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) also presents a new set of challenges when considering viral spillover from people to naïve wildlife and other animal populations. The establishment of new wildlife reservoirs for SARS-CoV-2 would further complicate public health control measures and could lead to wildlife health and conservation impacts. Given the likely bat origin of SARS-CoV-2 and related beta-coronaviruses (β-CoVs), free-ranging bats are a key group of concern for spillover from humans back to wildlife. Here, we review the diversity and natural host range of β-CoVs in bats and examine the risk of humans inadvertently infecting free-ranging bats with SARS-CoV-2. Our review of

the global distribution and host range of β-CoV evolutionary lineages suggests that 40+ species of temperate-zone North American bats could be immunologically naïve and susceptible to infection by SARS-CoV-2. We highlight an urgent need to proactively connect the wellbeing of human and wildlife health during the current pandemic and to implement new tools to continue wildlife research while avoiding potentially severe health and conservation impacts of SARS-CoV-2 "spilling back" into free-ranging bat populations.

Spillover of pandemic viruses

The threat of emerging infectious diseases (EIDs) to wildlife health and biodiversity conservation is recognized [1], but cross-species transmission of novel pathogens, or spillover, is typically viewed in the specific context of originating in a wildlife reservoir and transmitting to humans [2]. Research assessing EID risk has typically focused on identifying geographic regions [3, 4] and wildlife species [5–7] whereby spillover of zoonotic diseases into humans is most likely. Among recent pandemic zoonotic viruses, some have no evidence of transmission back to wildlife or domestic animal populations after establishment in people (e.g., human immunodeficiency virus, which causes acquired immunodeficiency syndrome), while others have repeatedly crossed species boundaries (e.g., pandemic H1N1 influenza A virus) [8, 9]. Evidence of "reverse zoonotic" transmission, sometime referred to as "spillback," from people to wildlife and domestic animals is widespread [9]; however, systematic surveys to determine the proportion of EIDs that spill back into novel wildlife hosts are lacking. Infection of bats by viruses of probable human origin has been recorded only twice [10, 11], and further transmission [12], or spread to a wider bat population, has not been recorded.

In December 2019, a novel coronavirus was detected from a cluster of 41 atypical pneumonia cases in Wuhan, China, and has since spread to cause a pandemic with significant global morbidity, mortality, and economic impact [13]. Phylogenetic evidence suggests that this virus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), and the clade of SARS-related coronaviruses (SARSr-CoVs) that it belongs in evolved in Old-World bats of the family Rhinolophidae [14–16]. There is no epidemiological evidence of direct or indirect transmission of SARS-CoV-2 from bats to people, but a full genome of its closest known relative (with 96.2% sequence similarity) was reported from an Intermediate Horseshoe Bat (*Rhinolophus affinis*) sampled from Yunnan province, China, in 2013 [17]. The timing of SARS-CoV-2 spillover from bats and any involvement of intermediate host species remain undetermined [18, 19]. The United States currently has the highest number of confirmed human cases of COVID-19, the disease caused by SARS-CoV-2. The consequences of this pandemic are many and include the possibility of SARS-CoV-2 transmission from humans to free-ranging wildlife populations. Given the likely bat origin of SARS-CoV-2, free-ranging bats are a key group of concern for spillover from humans. Humans frequently handle and come into close contact with North American temperate-zone bats during the course of ecological research, wildlife rehabilitation, wildlife/pest control, and disease investigations. Anticipating the need for similar risk assessments across many potentially vulnerable species of wildlife and domesticated mammals globally, we here examine the possibility of humans inadvertently infecting free-ranging North American bats with SARS-CoV-2. We further discuss the possible public health and wildlife conservation consequences of SARS-CoV-2 becoming endemic in bats outside its natural host range.

Threats of SARS-CoV-2 to North American bats

The pandemic spread of SARS-CoV-2 may directly or indirectly threaten North American bat populations in at least three different ways. First, SARS-CoV-2 might infect any of the diverse

and historically isolated 40+ endemic species of temperate-zone North American bats, with or without causing disease, morbidity, and mortality. Second, SARS-CoV-2 might infect and become established in one or more North American bat species, creating novel reservoirs capable of causing human infections (e.g., bat rabies lyssaviruses in the New World [20]). Third, if SARS-CoV-2 infection persists in North American bats of one or more species, it could potentially evolve or recombine with endemic viruses [19, 21] to become more pathogenic or infectious to humans or other animals. In addition to new public health challenges, the latter outcomes could quickly shift public perception of bats from mostly beneficial wildlife with associated disease risks that are manageable to bats posing unacceptable disease risks to human and animal health. Such a shift could increase the likelihood of negative human–bat interactions and conflicts, as well as undermine decades of concerted science, conservation, and education efforts aimed at conserving these valuable animals [22–24]. The potential threat of SARS-CoV-2 transmission from humans to other animals applies to many species of wildlife and domesticated mammals, but the likely bat origin of SARS-CoV-2 and the current threats to bat populations due to another disease in North America influenced us to focus this review on bats.

Lessons from an epizootic—Susceptibility of North American bats to an introduced pathogen

SARS-CoV-2 is not the first pathogen with the potential for inadvertent spread from people to North American bats. The COVID-19 pandemic follows the arrival of a fungal pathogen (*Pseudogymnoascus destructans*) that as early as 2006 began infecting hibernating bat populations in North America, spreading within and among species to alter the evolutionary trajectory of the continent's bats [25–28]. Genetic analyses indicate that *P. destructans* was introduced to North America [29], in our opinion likely by movement of humans or materials contaminated with fungal spores. White-nose syndrome (WNS), the disease caused by *P. destructans*, remains the only documented bat epizootic to cause multiyear, widespread mass mortality [30], although short-term bat die-offs have been also linked to Lloviu virus in Europe [31]. WNS has killed millions of North American bats, affected populations of at least 12 species of 3 genera, and has already spread across half of the US and Canada (whitenosesyndrome.org, accessed 11 May 2020). Effective methods to mitigate WNS spread and impacts remain elusive despite substantial research effort, and targeted mitigation actions have had limited success against its impacts [32]. It took years of concerted international scientific effort to identify the cold-growing fungus, determine that it likely originated somewhere in the temperate zones of Europe or Asia, understand its mechanisms of infection and pathogenicity, develop strategies to limit accidental translocation, and track its rapid spread through an immunologically naïve continental assemblage of hibernating bats [33–35].

The devastating impact of WNS on a diverse group of North American bats likely resulted from evolutionary isolation of the continent's bat fauna from other parts of the world for millions of years, despite other species of *Pseudogymnoascus* being present. Bats in both Europe and Asia can become infected by *P. destructans* but do not suffer mass mortality from WNS [36, 37]. The bat fauna spanning the higher latitudes of North America (in the US and Canada) is composed almost entirely of endemic species belonging to the family Vespertilionidae. Vespertilionid bats occur globally but likely originated and diversified in North America tens of millions of years ago before dispersing to other continents [38, 39]. No extant species of bat in the Americas also occurs outside of the Americas [40, 41], and no bats migrate across the Pacific or Atlantic Oceans [42, 43]. The WNS epizootic demonstrates that a large proportion of these historically isolated bats can be vulnerable to a pathogen introduced from another

continent during a single event. Additionally, bats already in a physiologically stressed condition due to WNS or other pressures may be more susceptible to viral infection, experience exacerbated disease outcomes, and/or experience increased viral shedding [44, 45]. The COVID-19 pandemic resembles WNS with respect to potential spread of a pathogen from another continent through interconnected, multispecies assemblages of North American bats that might be immunologically naïve and highlights deficits in our understanding of temperate-zone bat pathogens in North America.

Gaps in understanding global patterns of Bat–CoV diversity, evolution, and host range

Bats are among the world's most diverse mammals (comprising approximately 1,400 species [46]), and the global distribution and diversity of CoVs in bats proportionally reflects that of their hosts [47, 48]. Available evidence indicates that bats are natural reservoirs of CoVs, some of which have the potential to cause diseases in humans, domesticated animals, and wildlife [17, 47, 49–59]. Coronaviruses appear to have ancient and ancestral relationships with bats, diversifying globally through a process of within-host evolution and cross-taxonomic host-switching events [47, 59–61]. Bats are the likely mammalian progenitor hosts of all alpha (α-) and beta (β-) CoVs [58, 59, 62, 63] and potentially all coronaviruses [60]. Alpha-CoVs of likely bat origin include the causative agent of swine acute diarrhea syndrome (SADS), which caused mass mortality of over 25,000 piglets on farms in Guangdong province, China [57], and a variant strain of porcine epidemic diarrhea virus (PEDV) that spread rapidly from China in recent decades and caused mass piglet mortality in multiple US states [64]. Human CoVs NL63 and 229E also likely had their evolutionary origins in bats [59, 65]. Two recent human disease epidemics (severe acute respiratory syndrome [SARS] and Middle East respiratory syndrome [MERS]) and now the current COVID-19 pandemic are caused by viruses that probably originated from β-CoVs circulating in bat populations in regions where outbreaks occurred [17, 19, 50–54, 58, 66–68].

The emergence of diseases like SADS, PEDV, SARS, MERS, and now COVID-19 strongly indicates a close association between CoVs that become pathogenic in humans and the wildlife reservoirs from which they originate [17, 50–54, 67]. The evolutionary relationships of CoVs within bats are consistent with geographically structured transmission cycles, with occasional transmission among related bat species [47, 58, 69]. These phylogeographic factors are also universal determinants of viral sharing among all mammals [70]. However, bat–virus association patterns can be particularly difficult to discern because bats often roost together in multispecies aggregations that can facilitate viral sharing, with each species capable of harboring multiple CoV lineages [47, 58, 68, 71]. Host shifts from bats to more divergent taxa are more difficult to predict—firstly, because the potential host breadth for many CoVs is broad [55, 56, 60, 72], and secondly, because host susceptibility and onward transmission involve complex, multistage processes [2, 12]. Bat–CoV associations likely remain substantially undersampled and understudied in temperate-zone North America [47, 71, 73, 74].

Are viruses like SARS-CoV-2 already present in North American bats?

Our examination of CoV evolutionary lineages and global distribution patterns of the diversity of bat species they infect suggests that temperate-zone North American bats could be immunologically naïve to infection by viruses like SARS-CoV-2. Alpha and β-CoVs have been detected in bats on most continents, sometimes with both types occurring in bats of the same species [58, 68]. However, an exception to this pattern is the lack of published evidence that β-CoVs

infect bats of temperate-zone North America, despite several search efforts which used methods suitable to detect both α- and β-CoVs [59, 71, 74, 75]. Multiple novel α-CoVs have been detected and described in vespertilionid bats of the US and Canada, infecting species both living in close contact with humans and in remote wild areas [59, 71, 74–76]. However, SARSr-CoVs and β-CoVs of the viral subgenus *Sarbecovirus* have thus far been detected almost exclusively in species of the Old-World Chiropteran suborder Yinpterochiroptera (Fig 1A) [47, 58, 69]. The few exceptions to this pattern are the detection of novel Clade 3 and Clade 1 *Sarbecovirus* (*sensu* [53]) viruses in the wrinkle-lipped free-tailed bat (*Mops plicatus*, family Molossidae) in China [77] and the vespertilionid Leisler's noctule (*Nyctalus leisleri*) cohabiting a Bulgarian cave during autumn with several species of rhinolophids in which other SARSr β-CoVs were concurrently detected, suggesting cross-species infections (Fig 1A) [78]. Putative detections of a Clade 1 *Sarbecovirus* were also reported from guano samples of the vespertilionid brown long-eared bat (*Plecotus auritus*) and the molossid European free-tailed bat (*Tadarida teniotis*) on Sardinia, where the same novel β-CoV was described in the greater horseshoe bat (*R. ferrumequinum*) [79].

Viruses in the β-CoV subgenera *Hibecovirus* and *Nobecovirus* also have been reported mostly from Old-World bat families Rhinolophidae, Hipposideridae, Rhinonycteridae, and Pteropodidae, except for novel viruses of the latter subgenus detected in four species of the vespertilionid genus *Scotophilus* in Asia and Africa (Fig 1B and 1C) [47, 58, 69].

Bat β-CoVs of the subgenus *Merbecovirus* (MERS-related lineages) occur in a greater diversity of bat families and across more global regions than the other subgenera (Fig 1D) [47, 58, 69]. These widely distributed MERS-like viruses can cause disease in humans (e.g., MERS) and notably appear to be the only bat β-CoVs to diversify among several families of the globally distributed suborder Yangochiroptera (Fig 1*D*) [47, 58, 69].

Lack of evidence for β-CoVs in temperate-zone North American bats

The several hundred species of extant bats spanning the Americas all belong to the suborder Yangochiroptera, which likely diverged from the Old-World suborder Yinpterochiroptera more than 50 million years ago (Fig 2) [80]. The only β-CoVs detected in the Americas to date belong to the subgenus *Merbecovirus* and appear restricted to two exclusively Neotropical bat families (Phyllostomidae and Mormoopidae) and one that is globally distributed (Molossidae). Distinct CoV lineages in the subgenus *Merbecovirus* were described from three species of *Pteronotus* (family Mormoopidae), four species of *Artibeus*, and Seba's short-tailed bat (*Carollia perspicillata*; family Phyllostomidae) from tropical regions of Mexico [47, 81]. Novel β-CoVs of the subgenus *Merbecovirus* were detected in two neotropical bat species of the family Molossidae: Wagner's bonneted bat (*Eumops glaucinus*) in southern Brazil and the broad-eared free-tailed bat (*Nyctinomops laticaudatus*) in southern Mexico [81, 82]. In vitro infections have shown that primary kidney cells from the Jamaican fruit-eating bat (*Artibeus jamaicensis*) can be infected with MERS-CoV, and virus replication and shedding was reported in experimentally infected bats of this species but without obvious clinical signs of disease [83]. Similar to the evidence for natural invasion of bat rabies viruses among New World bats [84], available evidence suggests β-CoVs may have arrived through South America and have long been evolving in Neotropical bats. Although some bat hosts of *Merbecoviruses* overlap geographically with species of temperate-zone North American bats, none occur outside of the Neotropics. Sampling has been limited, but we are not aware of any published detections of *Merbecoviruses* or any other β-CoVs in temperate-zone North American vespertilionid bats.

Our inference of true patterns of CoV occurrence and distribution in bat populations is limited by uneven global sampling. Yet SARSr-CoVs (*Sarbecovirus* spp.), a focus of many

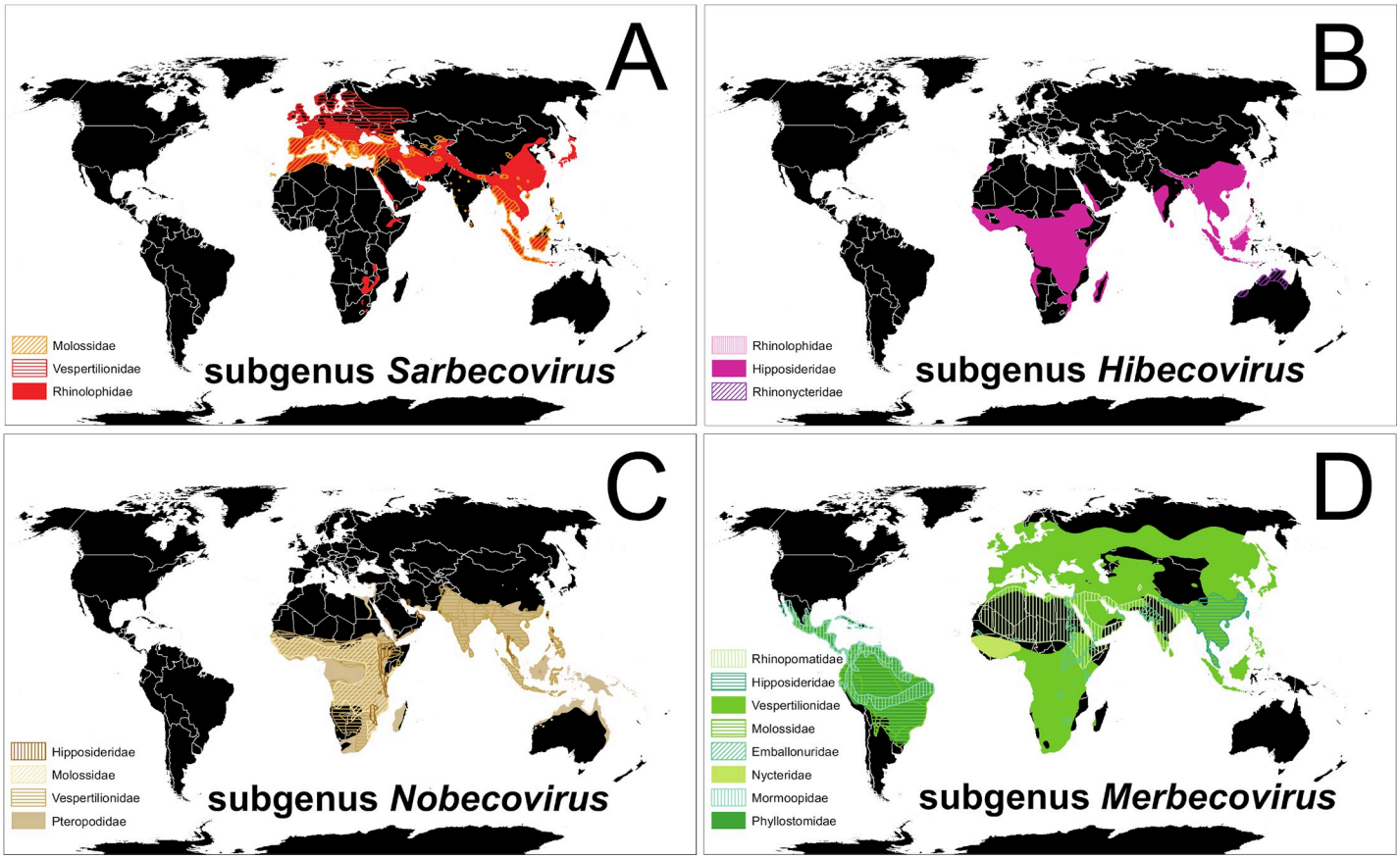

Fig 1. Global patterns of bats and associated β-CoVs. (A) Red-shaded distributions of bat species in which SARS-related β-CoVs of the subgenus *Sarbecovirus* have been detected; (B) pink-shaded distributions of bat species known to host β-CoVs of the subgenus *Hibecovirus*; (C) brown-shaded distributions of bats in which β-CoVs of the *Nobecovirus* lineage have been detected; and (D) green-shaded distributions of bats known to host MERS-related β-CoVs of the subgenus *Merbecovirus*. Different colors and shade styles within each panel represent different families of bats. A data table that includes all known bat species associations for each β-CoVs subgenus and peer-reviewed citations is available at US Geological Survey data release https://doi.org/10.5066/P9U461PJ. *Maps created using ArcMap (ESRI, Redlands, California, United States of America) and bat ranges derived from spatial data on terrestrial mammals from the International Union for the Conservation of Nature (IUCN 2020. The IUCN Red List of Threatened Species. January 2019 [version 6.2]. https://www.iucnredlist.org; Downloaded on 11 April 2020).* β-CoV, beta-coronavirus; MERS, Middle East respiratory syndrome; SARS, severe acute respiratory syndrome.

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surveillance efforts, have been almost exclusively documented in Old-World Yinpterochiroptera. SARSr-CoVs were only found in the ultra-diverse and globally distributed bat suborder Yangochiroptera under conditions with plausible transmission from co-roosting *Rhinolophus* sp. bats [53, 85]. This absence of evidence for SARS-like β-CoVs in yangochiropteran bats in general, and in temperate-zone vespertilionid bats of North America in particular, likely represents a unique biogeographic pattern driven by underlying factors of host susceptibility or life history. These observations also point to the susceptibility of vespertilionid bats under circumstances of SARSr-CoV environmental exposure and that they may not be naturally immune to these viruses.

Bats rank among the most ecologically important mammals and play varied roles in most of Earth's ecosystems; bats pollinate and disperse seeds of numerous plants in tropical regions, and all over the world, bats are primary nocturnal predators of flying insects [23, 24]. Across the Holarctic, chiropteran species diversity is greatest among hibernating vespertilionid bats. At least 25 of the ecologically diverse vespertilionid species of bats in the US and Canada hibernate [86], which might influence their susceptibility to or interactions with viruses, as has been

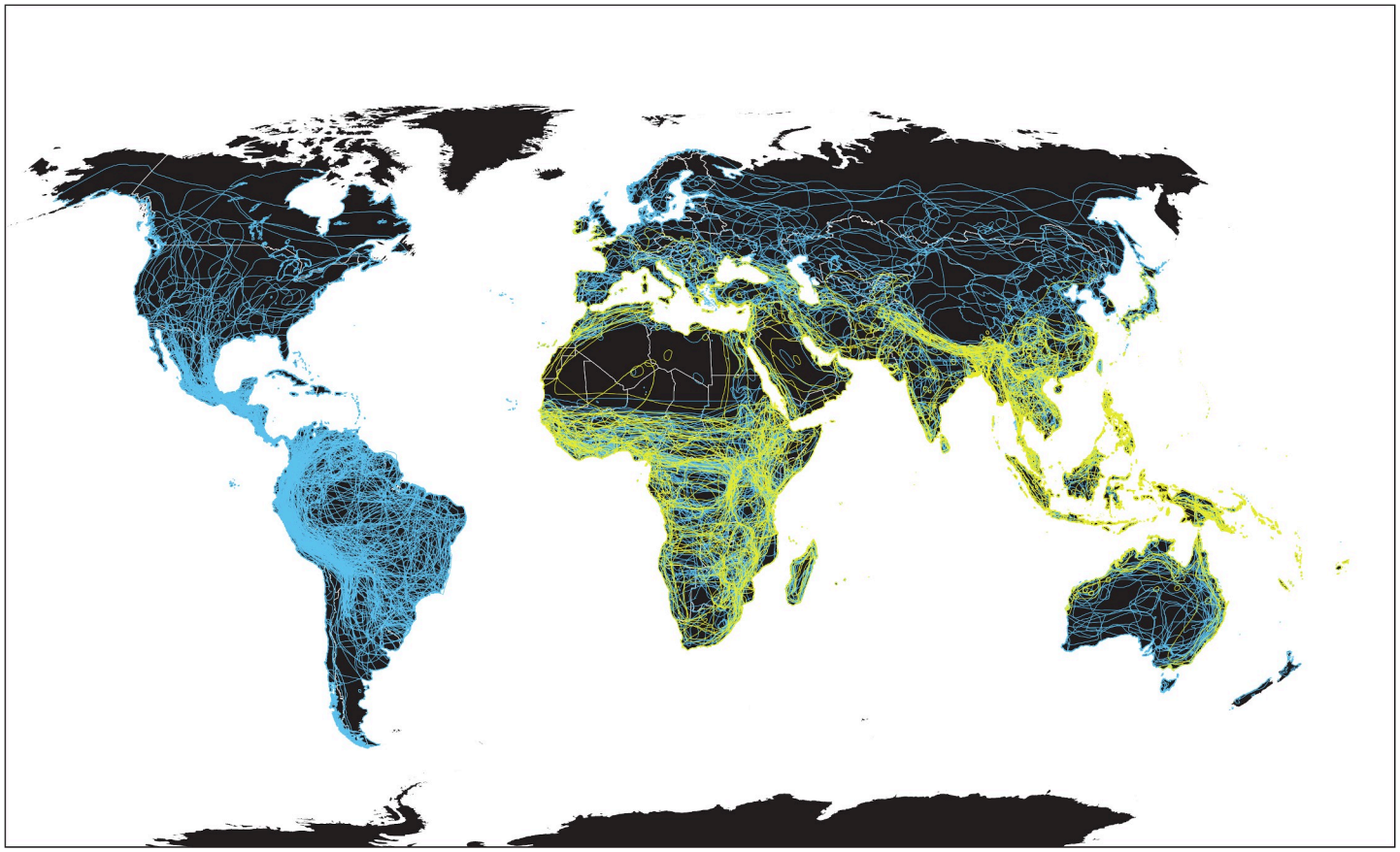

Fig 2. Old-World and New-World bats. Overlapping species distribution outlines of bats in the globally distributed suborder Yangochiroptera (blue) and Old-World Yinpterochiroptera (yellow). *Maps created using ArcMap (ESRI, Redlands, California, USA) and bat ranges derived from spatial data on terrestrial mammals from the International Union for the Conservation of Nature Red List of Threatened Species, January 2019 [version 6.2]. https://www.iucnredlist.org; Downloaded on 11 April 2020.*

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postulated for common vespertilionids infected with α-CoVs and rabies virus [44, 87–89]. Hibernation strategies vary among species of bats (e.g., degree of sociality, thermoregulatory behaviors, habitat selection) [90], but bat body temperatures during hibernation generally remain consistently below 10° C for periods lasting 7–9 months per year [91], providing a potential mechanism to limit viral replication and spread [92]. Experimental studies to assess the ability of SARS-CoV-2 or other β-CoVs to survive and replicate in bats (cell lines and individuals) at low temperatures [92, 93] would provide additional insight into risk of reverse zoonosis. However, appropriate tools for studying such possibilities are lacking, particularly immortalized cell lines from several hibernating, vespertilionid bats [59]. These tools would also enable interrogation of other physiological features of vespertilionids that may influence susceptibility, such as receptor-binding affinity and the expression of receptors across tissues. Scientists did not discover and isolate the obligately psychrophilic fungus that causes WNS until they collected samples in bat hibernation sites and moved culture dishes for incubation into laboratory refrigerators [25]. Similar innovative explorations outside the typical temperature conditions of laboratory experimentation could help assess the risk of SARS-CoV-2 infecting the more than two dozen species of bats in the US and Canada that hibernate to survive harsh temperate-zone winters.

Proactively connecting the wellbeing of human and bat populations

Scientists have long recognized the risk of pathogen spillover from humans to bats [94–96], but bat researchers in North America have not systematically addressed this risk prior to WNS. Outside of reservoir host studies, few bat researchers studied infectious diseases in bats before WNS emerged in 2007 [73] nor studied bat viruses (other than rabies) before bats were retrospectively connected to the SARS epidemic [15, 66, 97]. Fortunately, bat and wildlife disease researchers recently began addressing these knowledge gaps in more detail [7, 97, 98]. Possible explanations for why bats might host particularly pathogenic viruses include characteristics of their life history (e.g., long-lived, wide ranging, multispecies aggregations, daily and seasonal heterothermy) [97], unique physiology for repairing their damaged DNA [99], unique ability to suppress some of their innate immunity pathways [100–105], high species diversity [48], and unmatched metabolic range and high body temperatures during flight [106]. Bats also cryptically come into close contact with humans, increasingly in urban and periurban settings as a result of native habitat loss, often crossing human–wildlife interfaces [107–113].

Except for *Lyssavirus* infections, bats rarely show substantial signs of sickness from the same pathogens that cause virulent disease in humans. Bats cope with viral infections in ways that we do not yet fully comprehend, but learning how they do so may reveal important insights to develop therapeutics and ultimately to protect human health [103–105]. In vitro and laboratory studies demonstrate that bats can specifically regulate naïve immunity pathways to effectively cope with viral infection [114]. For example, dendritic cells generated from the bone marrow of the Egyptian rousette (*Rousettus aegyptiacus*) infected with Marburg virus down-regulate immune-stimulatory pathways and maturation of cells targeted by the virus while up-regulating pathogen-sensing pathways [115]. Unique bat immune regulation may occur with MERS-CoV infection, at least under experimental conditions [101]. Egyptian rousette bats experimentally challenged with SARS-CoV-2 by intranasal inoculation became transiently infected, shed virus, and one cohoused bat became infected but showed no clinical signs of disease other than rhinitis [116]. Our potential lack of understanding of clinical signs of illness in bats and the cryptic habits of many species also generally inhibit our ability to easily detect spillover of pathogens from human to bat populations. This may add to uncertainty about cross-species transmission and dispersal of CoVs among human and animal communities. Laboratory findings suggest human viruses that likely originated in bats, such as HCoV-NL63, are capable of infecting bat cells, at least in vitro [59]. SARS-CoV-2 and other CoVs have some of the longest genomes among all RNA viruses, and despite having specialized RNA proofreading machinery [117, 118], they are still prone to recombination and copy errors in hosts, sometimes resulting in functional adaptations (e.g., altered receptor binding capacity or temperature adaptation of enzymes) [119]. CoVs can even recombine with functional fragments of other virus families, such as when a bat-derived CoV gained a functional gene from a reovirus [21]. Spillover of SARS-CoV-2 from infected humans to North American bats they handle or come in close contact with could lead to the virus becoming either less or more pathogenic to bats or other wildlife, domesticated animals, or humans through genetic mixing in one or more novel hosts. The public health and conservation consequences of a more virulent virus could be severe, whereas genetic mixing in a bat host that resulted in a less-virulent virus might go unnoticed.

Need for an interdisciplinary response

Effectively managing risks of human disease caused by emerging zoonotic pathogens and ensuring the health and conservation of wildlife species that are potential reservoirs of those

disease agents can be synergistic goals under a One Health framework. Spillover risk (from or to wildlife) is often greatest in disturbed ecosystems where there is an elevated frequency of human–wildlife interactions or disruption of ecological patterns [3, 120–124]. Thus, effective bat conservation and management requires understanding both pathogens that cause disease in bats, as well as human activities and ecological contexts that increase direct and indirect interactions with bats that could present health risks [2]. Furthermore, fear-based reactions to disease risk from wildlife, such as culling infected bat populations or indiscriminate killing, often have negative unintended consequences for the interconnected health of both humans and bats (e.g., culling of bats in a Uganda mine led to a more than doubling of Marburg virus prevalence in the bats living there) [30, 125–127]. Temperate-zone vespertilionid bats inhabiting human dwellings in the US and Canada represent a particularly relevant human–wildlife interface, in which conservation and management actions to proactively address the potential consequences for pathogen spillover are worth careful consideration [73].

Conservation-compatible surveillance of bat viruses has demonstrated the potential for mutually beneficial collaboration between public health scientists and conservation stakeholders [94, 113, 125, 128, 129]. Disease-focused studies that integrate ecological principles into a rigorous study design provide the most informative context to interpret bat–virus associations and patterns of richness globally [130–132]. Assessing the risks of SARS-CoV-2 spillover into North American bats presents a timely opportunity to form multidisciplinary scientific teams that include experts on emerging infectious diseases and ecologists with expertise on North American bats [128]. Scientists researching emerging infectious diseases can benefit from sampling opportunities and methods that bat researchers have developed for observing, counting, and noninvasively sampling bats [73, 133]. Bat researchers can learn about human and animal health monitoring and supporting laboratory methods, including biosafety, secure handling/transport of CoV-positive samples, and training in the proper use of personal protective equipment (PPE) from professionals with expertise in veterinary and medical sciences [113, 131, 134, 135]. A shared goal of all stakeholders is to identify and implement simple, widely available diagnostic tests for detecting SARS-CoV-2 infection that are species-independent, practical for field and laboratory use, highly specific and sensitive, and that do not require strict biosafety containment [136]. All investigators can also work together to develop mutually beneficial goals, such as joint risk communications to the public with effective and balanced messaging about bat populations and higher risk activities for human–bat contact.

Adopting a precautionary approach in the face of global COVID-19 transmission among human populations, national and international wildlife organizations have advised limiting capturing and handling of bats in the field to minimize the risk of humans infecting wild bats with SARS-CoV-2 until further assessment can be made [137, 138]. The emergence of WNS in 2007 prompted a similar surge in interdisciplinary collaboration that enabled the rapid advances already mentioned and introduced changes to guidance for PPE use and disinfection practices for bat researchers and recreational cavers. Similarly, the emergence of SARS-CoV-2 and other viruses will likely alter the status quo of bat research, emphasizing the need to carefully weigh risks and benefits of wildlife research in the context of population-altering diseases. For example, PPE, including respiratory protection, is a standard practice adopted by many bat virus researchers but by few others studying and regularly handling bats [134, 139]. The urgent research priority of a rapid, quantitative risk assessment and analysis of various mitigation options is currently underway [137, 140]. One key question is whether the proper use of optimal PPE, including bidirectional N95 or equivalent masks, along with effective risk communication and adherence to other basic biosafety practices [134, 141, 142] during field work, can significantly reduce the transmission risk of SARS-CoV-2 from humans to bats. In the interim, until new guidelines are established for handling and for close-proximity work with

bats, we have outlined gaps in our understanding of SARS-CoV-2 spillover risks at the interface between humans, domesticated animals, and free-ranging wildlife. Temporarily shifting to "hands-off" bat research methods also seems prudent, wherever possible, and could facilitate ongoing work with reduced risk.

Examples of "hands-off" research strategies

Multiple research strategies that do not involve close contact with free-ranging bats already exist for addressing critical gaps in understanding CoV diversity, distribution, evolution, and potential health effects in temperate-zone bats. For example, a combination of host-cell receptor analyses and in vitro and in vivo experimental infections across a diversity of bat and other mammalian species have helped inform potential host range expansion for SARS-CoV-2. The receptors that many CoVs use to gain access to host cells, such as angiotensin-converting enzyme 2 (ACE2) and dipeptidyl peptidase-4 (DPP4/CD26), have undergone positive selection in bats, resulting in diverse and recombinant CoV strains [72, 143]. These strains can likely bind to numerous variants of a host receptor protein and facilitate spillover into other animal species [72, 144]. SARS-CoV-2 targets and strongly binds to mammalian ACE2 cell receptors [72, 145, 146]. Beta-CoVs of the subgenus *Merbecovirus* (like those known to occur in the Americas) are not known to target ACE2 cell receptors, instead using as a receptor DPP4/CD26 or possibly other receptors [53, 144]. Current in silico predictions that bats will likely have low susceptibility to SARS-CoV-2 based on ACE2 structural analyses conflict with in vitro evidence and do not comprehensively account for ACE2 amino acid sequence variation (including intraspecific variation) that occurs within bats [17, 72, 145]. Assessing SARS-CoV-2 host range will require additional virus-host receptor binding assays in silico and in vitro [17, 53, 72, 144, 145], together with future experimental infection studies for confirmation of Koch's postulates. In addition, in vitro studies could evaluate species variability in innate immune responses. These investigations will help quantify the potential for North American bat infection and transmission among free-ranging populations.

Examples of other "hands-off" methods applicable to both bat disease and conservation research include the following: virus discovery and characterization focused on existing specimens archived in scientific museums or through partnerships and collaboration with established national bat disease monitoring or surveillance programs [147, 148]; monitoring echolocation calls to determine the occurrence, distributions, and seasonal or nightly activity patterns of bats [133, 149]; digital imaging methods for counting bats and studying physiology and behaviors in the context of disease [90, 108]; sampling guano from below bat roosts to determine bat species and individual identity, population dynamics, and daily or seasonal patterns of bat occupancy and pathogen shedding [71, 150–152]; and mathematical modeling to predict susceptible host species, virus sharing among hosts, spread patterns, or to estimate mortality in affected populations [5, 70, 122, 135]. Promising areas for innovation include making technologies for bat research more accessible to a broader global user base, less expensive, easier to use, and scientifically reproducible through open-source hardware, software, and laboratory methods [153, 154]. In addition to research, standardized field protocols and probabilistic sampling strategies are needed for monitoring bats and their viruses at continental scales (www.nabatmonitoring.org) [155, 156], as are longitudinal studies across multiple sites to better understand the ecological drivers of CoV dynamics and spillover [157]. Developing simple management tools and methods for rapidly assessing risks of virus spillover from humans to wildlife, while maintaining scientific rigor, could also help with future disease response. It might also be useful to prepare a suite of tools, protocols, and risk communication strategies for natural resource managers and public health officials to immediately deploy

while risks are being assessed. Such prepared management resources could include public outreach material and guidelines for enhanced use of PPE for those in closest contact with potentially susceptible wildlife.

Conclusion

Many questions remain about the risk of SARS-CoV-2 to naïve wildlife populations, the influences of human behavior on those risks, and the potential for establishment of new CoV reservoirs. Cross-species virus transmission events are relatively rare, requiring an infectious reservoir host to be in contact with a recipient host when conditions concurrently favor susceptibility and onward transmission [12, 113, 114]. The currently unknown, but possible and potentially high-consequence, risk of SARS-CoV-2 transmission and establishment in North American bats (or other free-ranging mammals) warrants precaution [116, 140]. Strategically managing interactions between people and potentially susceptible or at risk species can decrease the probability of cross-species virus spillover [113]. Humans that frequently handle and come into close contact with North American temperate-zone bats, such as bat researchers, wildlife rehabilitators, wildlife/pest control workers, and disease investigators, can help decrease any chances of spillover by adopting basic PPE and biosafety practices and carefully evaluating how their actions might adversely affect bat populations. We are at a critical nexus of biosecurity and natural resource conservation that will require ingenuity and diligence to continue important research on bats whilst simultaneously evaluating the ecological future of SARS-CoV-2. Our actions during this current pandemic could profoundly influence and protect the health of both humans and wildlife in North America.

Supporting information

S1 Table. Global patterns of betacoronavirus (β-CoV) associations in bats. The table lists bat species in which betacoronaviruses (β-CoVs) were detected, organized by viral subgenera and clade (for Sarbecorviruses), bat family, bat suborder, and general global region where the species of bat occurs. Reference to the published literature sources of information for each row are listed in the last column. Provided in comma-separated value (.csv) format at https://doi.org/10.5066/P9U461PJ.
(XLSX)

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From: Katie Leahy
Sent: Tuesday, January 16, 2018 5:30 PM EST
To: lance.r.brooks >; Newman, Carl I CIV DTRA J3-7 (US) ; christopher.r.lewis1 BounheuangK >; cryanp ; Kading,Rebekah ; vkapur <v >; ecohealthalliance.org ecohealthalliance.org >; ian.mendenhall >; l.urushadze >; gavin.smith ; abelwade ; c demetria >; spwa >; kityrob >; tamar_kutateladze >; nisreen.hmoud < joram.buza >; Tigga Kingston ; DeeAnn Reeder >; Keti Sidamonidze >; jason >
CC: martha.m.stokes. >; mary.j.lancaster >; Megan Hudson >
Subject: Pre-event Information for BPERNet / PMAC Meetings
Attachment(s): "2018 Prince Mahidol Awards Reception_invitation_cdc.pdf","BPERNet PMAC Meeting_Revision 2[1].docx","BPERNet Meeting Prep.docx","TORFTA_BPERNet_Final.pdf","BPERN Executive Summary_rev2.docx"

All,

Good afternoon! In advance of the upcoming trip to Bangkok for our BPERNet Meeting and the PMAC conference, this email should serve as a resource of information for the meeting and the conference.

Please note that our meeting is on 30 January at 0830 at the King Chulalongkorn Memorial Hospital. The PMAC planning committee has graciously arranged for a van to pick up our group to take us to the hospital from the Rennaissance Ratchaprasong; the van will leave our hotel at 0800.

On the 31st, the PMAC planning committee has also arranged for our group to attend the EID preparedness Linking Community-Based Approach and Research to National System Field Trip (outline included in the attached agenda). The times for pick-up will be provided at our meeting on the 30th.

Regarding the Embassy reception on the 1st. By now, you should have all received an invitation from the protocol office. Please respond with your acceptance of this invitation to Protocol-Bangkok I have also attached a copy of the invitation, which you will need to print out and bring with you to the Embassy function. The embassy is within walking distance from our hotel, so we will likely coordinate as a group and walk. More information to follow.

In preparation for our meeting BPERNet Meeting, I am attaching several documents that should help everyone prepare for the discussions: 1) a copy of the read-out from our June meeting as a refresher; (2) the final TORFTA, and (3) a preparation questionnaire, which should get you thinking about the objectives-driven strategic mapping sessions that we intend to conduct.

Please let me know if you have any questions.

V/r,

Katie Leahy

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The Ambassador of the United States of America
Glyn T. Davies and Jacqueline M. Davies
request the honor of your company

at a reception
in honor of the 2017 Prince Mahidol Award laureates
from the Human Genome Project and
the Hib vaccine development team

on Thursday, February 1, 2018
at 6:00-8:00 p.m.

R.S.V.P. by Thursday, January 25, 2018 *The Ambassador's Residence*
Email: Protocol-Bangkok
02-205-4934; 02-205-4107
Attire: Business

(Please present this invitation upon arrival)

MEETING OVERVIEW

BACKGROUND

In 2013, the Defense Threat Reduction Agency (DTRA) Cooperative Biological Engagement Program (CBEP) began leveraging, enhancing, and convening research networks to accelerate its programmatic and research driven targets and end states. CBEP uses this approach as a way to connect its active funded research projects with other projects to help influence effective change for global health security; translating data into policy. Further, by using relationship-based research networks around the globe, made up of interdisciplinary relationships, it will allow for novel and transformative scientific solutions for the world's largest infectious disease threats.

The Bat-associated Pathogen and Research Network (BPERN) is a CBEP research network that connects multidisciplinary and One Health expertise to address challenges and threats posed by bat-associated pathogens of security concern. The BPERN maintains the standards of all research networks that are supported by CBEP, in which members convene as a body of experts and researchers to: (1) share information, data, samples, and protocols; (2) coordinate research activities; (3) build training events and awareness-building workshops at all levels of decision-making authority; (4) develop community standards and best research practices; (5) create mentorship-based opportunities for students, trainees, and early-career researchers to convene, present, and share ideas; (6) establish a community of international research leaders and champions; and (7) reduce outbreak / transmission risk.

Some of the world's most deadly emerging zoonotic diseases are found in bats, including Nipah, Hendra, and Marburg viruses. There are a number of factors which make bats unique disease reservoirs, including their social behavior, distinct physiology and metabolism, ability to travel long distances, nocturnal activity, species diversity, and long life span (10-20 years, compared with a rat's average life of two years).[1] These special bat characteristics, coupled with the impact of human mediated interactions and environmental changes, create research challenges to understanding the bat's role in the global zoonotic disease ecology, which is further complicated by being difficult animals to control within a typical laboratory setting. The BPERN creates opportunities for policy makers, researchers, conservationists, funders, and students to identify community challenges, develop priority research lists and associated action plans that target needs and gaps, and work at all levels to build awareness of bat-associated disease burden and transmission risks to improve the prevention, detection, diagnosis, and reporting of pathogens of security concern.[2]

EXECUTIVE SUMMARY

On June 29, 2017, CBEP convened a group of multidisciplinary and One Health-focused research scientists, conservationists, and medical / veterinary practitioners for a one-day meeting in Fort Collins, Colorado to discuss organization and objectives for a bat-related research-based network (the complete

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[1] Hayman, David T.S., "As the bat flies," *Science* 02 Dec 2016: Vol. 354, Issue 6316, pp. 1099-1100 http://science.sciencemag.org/content/354/6316/1099

[2] Schountz, Tony, "Immunology of Bats and Their Viruses; Challenges and Opportunities," *Viruses,* 2014 Dec; 6(12): 4880-4901. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4276934/

agenda for the meeting may be found in Annex B). The representatives and experts in attendance work in CBEP regions (a full list of participants may be found in Annex A). The meeting was held at the University Center for the Arts, at Colorado State University, in concurrence with the 2nd International Symposium on Infectious Diseases of Bats.

The meeting began with an introduction to CBEP's mission and its use of networks as a way to foster coordination across regions and build sustainable connections through research. The two CBEP science leads, Drs. Mary Lancaster and Marty Stokes, outlined their vision to enhance regional and global research capacity, which starts with a complete understanding of the existing research landscape. CBEP believes this approach mitigates duplication of effort, by working with and building off of existing relationships; this could include an amalgamation of individuals, institutions, or other communities of practice. The CBEP representatives emphasized that their broad objective is to fuse actively funded expertise and projects to better inform and drive global, regional, and national health security policies.

Following an introduction, the CBEP leads facilitated a conversation to build consensus on ways to organize and administrate the network through a Terms of Reference for Trusted Agents (TORFTA). A draft of the TORFTA was emailed to participants in advance of the meeting so the discussions were analytical and substantive. The meeting ended with notes for a new draft that participants agreed could be virtually edited via SharePoint.

The discussions regarding the TORFTA led to other discussions about the objectives for the network, which were revised in-real-time. The group agreed on the following objectives for the BPERN:

- Facilitate interdisciplinary relationships and collaboration to identify research goals and needs for bat-associated disease research and disease threat reduction;
- Unify CBEP regions to create a common action plan that yields collaborative and sustainable projects that achieve the following end states: (1) better informed policy-makers; (2) better informed scientific community regarding funding targets and gaps in areas of research and development; (3) better defined threat to global health security from bat-associated pathogens; and (4) improved national, regional, and global capacity to detect and respond to pathogens of security concern; and
- Enable better communication, coordination, and outreach at the research and conservation interface.

The meeting ended with a thorough discussion about the research focus areas for the group. The meeting participants self-nominated into Working Groups to serve as research mentors (note: a list of working groups and mentors is outlined under the Research Focus Areas section of this document). The group agreed that discussions about priorities within the Working Groups should occur at the next steering committee meeting.

The first meeting of the BPERN was a success. Participants readily took part in discussions and shared ideas from their respective multidisciplinary backgrounds. Many had experience forming similar research-based networks, and they appeared energized to solve global challenges related to spillover opportunity of bat-borne pathogens of security concern. While there were many unresolved topics of conversation (e.g., a new name for the network), the group agreed that they would communicate virtually on these subjects through email and SharePoint interaction, initiated by CBEP. They agreed to nominate and vote for individuals to serve as co-chairs of the Steering Committee as well as identifying an opportunity to

meet again within the calendar year (note: a full list of outlying issues and recommendations for action may be found in the Action Items section of this document).

RESEARCH FOCUS AREAS

WORKING GROUP 1: HOST / PATHOGEN BIOLOGY AND INTERACTIONS

- Bat physiology and immunology
- Bat pathogen community biology (co-infections, co-morbidities)
- Distribution of pathogens among species

WORKING GROUP 1 RESEARCH MENTORS

- Dr. Joram Buza, Nelson Mandela African Institute of Science and Technology, Tanzania
- Dr. Vivek Kapur, Penn State University, U.S.
- Dr. DeeAnn Reeder, Bucknell University, U.S.

WORKING GROUP 2: PATHOGEN SURVEILLANCE, DIAGNOSTIC CAPACITY, AND EPIDEMIOLOGY

- Molecular epidemiology
- Distribution of pathogens geographically and phylogenetically
- Detection, diagnosis, and reporting of bat-associated pathogens

WORKING GROUP 2 RESEARCH MENTORS

- Dr. Catalino Demetria, Research Institute for Tropical Medicine, Philippines
- Dr. Jon Epstein, EcoHealth Alliance, U.S.
- Dr. Tamar Kutateladze, National Center for Disease Control and Public Health, Georgia
- Dr. Lela Urushadze, National Center for Disease Control and Public Health, Georgia
- Dr. Supaporn Wacharapluesadee, WHO CC for Research and Training in Viral Zoonoses, King Chulalongkorn Memorial Hospital, Thailand
- Dr. Abel Wade, National Veterinary Laboratory, Cameroon

WORKING GROUP 3: ECOLOGY SETTING (BAT, DOMESTICATED ANIMALS, AND WILDLIFE INTERFACE)

- Bat behavior, distribution, and movement

- Domesticated animals and wildlife behavior, distribution, and movement impact on interaction with bats.
- The effect of anthropogenic disturbance and modification

WORKING GROUP 3 RESEARCH MENTORS

- Dr. Paul Cryan, United States Geological Survey (USGS) Fort Collins Science Center, U.S.
- Dr. Tigga Kingston, Texas Tech University, U.S.
- Dr. Robert Kityo, Makerere University, Uganda
- Dr. Rebekah Kading, Colorado State University, U.S.

WORKING GROUP 4: HUMAN-BAT INTERACTIONS, RISK CHARACTERIZATION

- Hunting and commodity chain (e.g., bushmeat, guano, and pet trade)
- Ecotourism
- Interactions in human dwellings

WORKING GROUP 4 RESEARCH MENTORS

- Dr. Kevin Olival, EcoHealth Alliance, U.S.
- Dr. Ian Mendenhall, Duke/NUS, Singapore

ACTION ITEMS

The following Action Items were recorded and compiled by the organizational and administrative support staff of CBEP / Executive Committee for the BPERN.

ACTION	APPROACH FOR COMPLETION WITH DATES	RESPONSIBLE AGENTS
Generate and send out options for new network name	(1) Send email to steering committee members soliciting options (with one week deadline) – 18 July (2) Preview options with Executive Committee – 25 July (3) Send all name options to group via polling application – 26 July	(1) Leahy (GSE) (2) Leahy (3) Leahy
Generate and send out solicitation for co-chair nominations	(4) Send request to steering committee members soliciting nominations (with one week deadline) in combination with the email from Task (1) (5) Preview options with EC – 25 July (6) Send all nominations to group for voting via polling application – 26 July	(4) Leahy (5) Leahy (6) Leahy
Generate and send out solicitation for next meeting conference opportunities and dates	(1) Send request to steering committee members soliciting nominations (with one week deadline) in combination with the email from Task (1) (2) Preview options with EC – 25 July (3) Send all nominations to group for voting via polling application – 26 July	(7) Leahy (8) Leahy (9) Leahy
Update TORFTA with recommendations from meeting	(4) Send invitation to steering committee members with editing options via APAN SharePoint – 19 July (5) Send Editing Form with above email – 19 July (6) Open editing period for one week – 19- 26 July (7) Collect comments and negotiate updates with EC 26-31 July	(10) Sander (CTR A&AS) (11) Sander (12) Sander (13) Sander / Leahy
Create CV Format for new members	(8) Create a CV Format (9) Upload to APAN	(14) Leahy (15) Sander
Finalize fact sheet	(10) Finalize fact sheet with updates from discussions (11) Send to PAO for review	(16) Leahy (17) Sander

ANNEX A – PARTICIPANTS

The following participants attended or were invited to attend the BPERN Kickoff Meeting in Fort Collins, Colorado on 29 June 2017.

STEERING COMMITTEE MEETING INVITEES, DID ATTEND		
Kityo	Robert	Makerere University, Uganda
Mendenhall	Ian	Duke-NUS, Singapore
Buza	Joram	Nelson Mandela African Institute of Science and Technology (NM-AIST) (attended virtually)
Kapur	Vivek	Penn State University (attended virtually)
Olival	Kevin	EcoHealth Alliance
Epstein	Jonathan	EcoHealth Alliance
Kading	Rebekah	Colorado State University
Urushadze	Lela	National Center for Disease Control and Public Health (NCDC) Georgia
Kutateladze	Tamar	National Center for Disease Control and Public Health (NCDC) Georgia
Wacharapluesadee	Supaporn	WHO CC for Research and Training in Viral Zoonoses, King Chulalongkorn Momorial Hospital, Thailand
Wade	Abel	National Veterinary Laboratory of Cameroon (LANAVET)
Demetria	Catalino	RITM, Philippines
Kingston	Tigga	Texas Tech University
Cryan	Paul	USGS Fort Colliins Science Center
Reeder	DeeAnn	Bucknell University
INVITEES, DID NOT ATTEND		
Smith	Gavin	Duke-NUS, Singapore
Alhmoud	Nesreen	Royal Scientific Society
CBEP AND CBEP CONTRACTOR INVITEES, DID ATTEND		
Lancaster	Mary	DTRA CBEP
Stokes	Marty	DTRA CBEP
Gamboa	Omar	DTRA CBEP
Sander	Will	CTR A&AS Booz Allen
Leahy	Katie	GSE
Devaney	Caitlin	GSE

ANNEX B – MEETING AGENDA

The following agenda was set for the meeting. The majority of discussions focused on administration, organization, and focus of the network. The group did not get to the topics to prioritize research gaps and set action plans with short and long-term milestones and deliverables. Event facilitators organized questions and prompts for those sessions, which they will use for the next BPERN meeting.

Time	Agenda Topic and Facilitator or Speaker	Expected Outcomes
0930 – 1000	**Welcome and Introductions**	
1000 – 1015	**Global Bat Alliance Overview** *Dr. Mary Lancaster (Africa Science Lead)* *Dr. Marty Stokes (SEA Science Lead, CBEP)*	• Review discussions leading up to this meeting • Discuss how this meeting is an opportunity to formalize the central / steering committee node for the distributed network • Emphasize that the steering committee shall focus on mentorship and connecting individuals and institutions across the globe
1015 – 1045	**Review Charter and Move to Agreement** *TBD*	• Vote to accept organizational document for steering committee • Unanimous (??) acceptance • We will advertise intent ahead of meeting • We will convene a meeting on 7 June to review and discuss the draft TORFTA
1045 – 1115	**Identify and discuss research focus areas** *TBD*	• Group will identify and discuss overarching focus areas and sub focus areas • Steering committee and invitees shall self nominate to groups and agree to serve as research mentors for the groups
1115 – 1230	**Breakout: Prioritize research needs and gaps** *TBD*	• Group will breakout into their research focus areas and begin identifying needs and gaps • Groups will then work to prioritize their lists
1230 – 1330	**Working Lunch** *TBD*	• Buffett • Convene back as a group, hold discussions about the overarching objectives of the alliance

		• Discuss One Health and Vector-based International meetings as an opportunity to re-convene semi-annually
1330 – 1400	**Breakout: Draft timelines and workplans** *TBD*	• Begin drafting short and long-term timelines and workplans for each focus area • Short-term milestones could include identifying key researchers and networks • Long-term milestones could include training events and focus area meetings
1400 – 1430	**Closing / review of actions** *TBD*	• Close-out meeting / 5min brief out for each group (2 slides) • Review action items and next steps

Bat-associated Pathogen and Ecology Research Network (BPERNet) Meeting
Pre-meeting Questionnaire

This BPERNet side meeting will bring together a multidisciplinary and One Health-focused group of scientists, policy makers, research scientists, and medical/veterinary practitioners with interests in bat-related research involving pathogens of security concern. The BPERNet identifies and shares information on research funding opportunities offered by multiple institutions. Most importantly, this network fosters international relationships among collaborators, agencies, and organizations, that can produce long-term, sustainable partnerships that withstand changes in government and organization budgets, priorities, postures, and policies.

We are working to define working group focus areas, identify resource needs and creating outreach plans. Ultimately, BPERNet will unify CBEP regions to create a common action plan that yields collaborative and sustainable projects. In order to accomplish our objectives, the following should be considered before our meeting on January 30th:

- **What are the "big" questions within your scope of research?**
- **How will you answer these "big" questions?**
- **What resources do you need to answer these questions?**
- **What are the end goals for your working group?**
- **What would be an indicator of success for your group?**
- **How would you measure your success?**
- **What are the limiting factors for achieving these goals?**
- **What risk or challenges do you foresee that would hinder your working group's success?**
- **Are there any common misunderstandings in your research community?**

ITTEE MEETING AGENDA

gen and Ecology Research Network (BPERNet)
0 January – 3 February 2018

Date: Tuesday, 30 January 2018

BPERNet

Time	Session	Notes
0830 - 0845	Introduction and Meeting Objectives	Marty Stokes and Mary Lancaster will welcome all participants and provide a brief overview of the meeting objectives for the week
0845 - 0900	Þ Review interim accomplishments since 27 June Þ Q&A on TORFTA changes Þ Call for votes to accept TORFTA	Executive Committee members will provide an overview of the TORFTA and mission areas; all participants will receive final version ahead of meeting
0900 - 1000	Working Group Focus Areas	Review WG focus areas that were outlined during the 27 June meeting Þ Review breakout group objectives and end goals Þ Review strategy map
1000 - 1015	Tea Break	
1015 - 1115	Breakout Group Session I	Breakout Group Session 1 Objectives: Þ Define WG research areas (sub-focus area definitions) Þ List and prioritize research questions and potential projects for each area Þ Identify internal and external research dependencies for each Working Group **Working Group 1: researching host / pathogen biology and interactions** (Dr. Deeann Reeder, Dr. Vivek Kapur, Dr. Joram Buza) **Working Group 2: researching pathogen surveillance, diagnostic capacity, and epidemiology** (Dr. Abel Wade, Dr. Jon Epstein, Dr. Catalino Demetria, Dr. Lela Urushadze, Dr. Supaporn Wacharapluesadee, Dr. Tamar Kutateladze)

		Working Group 3: researching ecology (bat, domesticated animal, and wildlife interface) (Dr. Paul Cryan, Dr. Tigga Kingston, Dr. Robert Kityo) **Working Group 4: researching human – bat interactions and risk characterization** (Dr. Kevin Olival, Dr. Ian Mendenhall)
1115 - 1200	Breakout Group Session I Brief-out	Each group briefs out their discussions according to the objectives; brief-out 10 minutes / WG; Q&A 5 minutes / WG
1200 – 1330	Working lunch / Open discussion	Open discussion objectives Þ Discuss group marketing campaign Þ Members should be prepared to introduce other network affiliations, conferences, and meeting opportunities to market the network, globally Þ Discuss long-term process to collect and collate applications to the network
1330 – 1430	Breakout Group Session II	Breakout Group Session 2 Objectives: Þ List out WG research coverage (who is researching what and where) Þ Identify research gaps and needs Þ Identify WG resource and coverage needs (e.g., target environmentalists in Europe); identify critical POCs for membership Þ Begin drafting short and long timelines and work plans
1430 – 1445	Tea Break	
1445 – 1545	Breakout Group Session II Brief-out	Each group briefs out their discussions according to the objectives; brief-out 10 minutes / WG; Q&A 5 minutes / WG
1545 – 1630	End of session	End of Session Objectives: Þ Review Strategy Map Þ Review Action Items Þ Discuss date, level of participation, and location for next meeting (all participants should come prepared to briefly discuss their ideas for this topic)

ITTEE MEETING AGENDA

gen and Ecology Research Network (BPERNet)

0 January – 3 February 2018

ITTEE MEETING AGENDA

gen and Ecology Research Network (BPERNet)
0 January – 3 February 2018

Date: Wednesday, 31 January 2018

Site 4 Field Trip EID preparedness Linking Community-Based Approach and Research to National System

<table>
<tr><th>Time</th><th>Session</th><th>Notes</th></tr>
<tr><td>0630 - 0700</td><td>Check-In Meeting point, ground floor Centara</td><td>Grand Hotel at Central World and get a group T-Shirt. *Please be advised that you have breakfast from the hotel of your stay before checking in for this trip.</td></tr>
<tr><td>0700</td><td>Depart</td><td>Depart from the Centara Grand Hotel to Wat-Luang Health Promoting Hospital</td></tr>
<tr><td>0700 - 0830</td><td>Activities on the Bus</td><td>Þ Introductions and getting to know the group
Þ Introducing the field trip agenda
Þ Overview of the field trip program and Department of Disease Control (VCD)</td></tr>
<tr><td>0830 - 0840</td><td>Arrive at Wat-Luang Health Promoting Hospital</td><td>Welcome performance by Village Health Volunteers</td></tr>
<tr><td>0840 - 0850</td><td>Welcome</td><td>Welcome speech by Chonburi Governor</td></tr>
<tr><td>0850 - 0900</td><td>Introduction</td><td>Roles of Village Health Volunteers and community in disease prevention and control</td></tr>
<tr><td>0900 - 1000</td><td>Breakouts</td><td>Divide participants into three groups (20 minutes/group)
<table>
<tr><th>Group</th><th>0900-0920</th><th>0920-0940</th><th>0940-1000</th></tr>
<tr><td>A</td><td>Emerging Infectious Disease prevention and control system of Wat-Luang Health Promoting Hospital</td><td>Exhibition of bat lifestyle at Wat-Luang Promawas School</td><td>Roles of Village Health Volunteers in Emerging Infectious Disease prevention and control</td></tr>
<tr><td>B</td><td>Exhibition of bat lifestyle at Wat-Luang Promawas School</td><td>Roles of Village Health Volunteers in Emerging Infectious</td><td>Emerging Infectious Disease prevention and control</td></tr>
</table></td></tr>
</table>

				Disease prevention and control	system of Wat-Luang Health Promoting Hospital
		C	Roles of Village Health Volunteers in Emerging Infectious Disease prevention and control	Emerging Infectious Disease prevention and control system of Wat-Luang Health Promoting Hospital	Exhibition of bat lifestyle at Wat-Luang Promawas School
1000 - 1030	EIDs and bts	Observe bat lifestyle at Wat-Luang Phromawas Temple by Kevin Olival			
1030	Depart	Depart to Phanat Nikhom Hospital			
1045 - 1100	Refreshments	Refreshments at Phanat Nikhom Hospital			
1100 - 1200	Overview of Emerging Infectious Disease Prevention and Control Systems	▷ Roles of Government Agencies ▷ Roles of Community ▷ Revisit Emerging Infectious Disease research			
1200 - 1300	Lunch	Lunch at Phanat Nikhom Hospital			
1300 - 1400	Break out groups	Divide Participants into two groups (30 minutes/group)			
		Group	1300-1330	1330-1400	
		A	Emerging Infectious Disease prevention and control systems of Phanat Nikhom Hospital	Infectious Unit and Thai Traditional Medicine	
		B	Infectious Unit and Thai Traditional Medicine	Emerging Infectious Disease prevention and control systems of Phanat Nikhom Hospital	

1400 - 1500	Conclusion	Open discussion and conclusion
1500 - 1515	Refreshments	
1515	Depart	Leave for Centara Grand Hotel
1700	Arrive	Arrive at the Centara Grand Hotel

Date: Thursday, 1 February 2018

Main Conference Program

Time	Session	Notes
0900 - 1030	Opening Session and Keynote Address	Opening Session by **Her Royal Highness Princess Maha Chakri Sirindhorn** Keynote Address Þ Prince Mahidol Award Laureate 2017 Þ Prince Mahidol Award Laureate 2017 Þ **TBC**
1030 - 1100	Break	
1100 - 1230	Plenary 0	Vision 2100: Re-Imagining the End Game for the End of the Pandemic Era
1230 - 1330	Lunch	
1330 - 1430	Plenary 1	Leadership Needed for Managing Emerging Infectious Diseases of the 21st Century
1430 - 1630	PMAC Sessions	PS1.1: Lessons Learned in Managing Emerging Infectious Diseases (EID) PS1.2: Strategic Information and the Evolution of Emerging Infectious Diseases: Lessons from the Past and New Opportunities PS1.3: Safeguarding Medicines in the Era of AMR: What Do We Know? What Works? PS1.4: Financing Pandemic Preparedness: Where is the Money?

		PS1.5: One Health on the Move: Nomadic Communities
1630 - 1700	Break	
1700 - 1800	Plenary 2	Futures of Partnerships for a Safer World

ITTEE MEETING AGENDA

gen and Ecology Research Network (BPERNet)
0 January – 3 February 2018

Date: Friday, 2 February 2018

Main Conference Program

Time	Session	Notes
0830 - 0930	Plenary 3	Managing Emerging Infectious Disease and AMR Risk across the Livestock Revolution
0930 - 1000	Break	
1000 - 1200	PMAC Sessions	PS2.1: Beyond MERS and Zika: Are we Prepared for the Next Big Epidemic? PS2.2: AMR: Addressing Excessive and Inappropriate Use of Antibiotics PS2.3: Dealing with an Inter-Connected World: Partnerships for Preparedness, Detection and Response during Mass Gatherings PS2.4: Changing Dynamics: Emerging Infectious Diseases and Antimicrobial Resistance in an Era of Expanding Global Human Population Growth and Movement PS2.5: Reducing the Gap: Addressing Neglected Disease; Neglected Populations
1200 - 1300	Lunch	
1300 - 1500	PMAC Sessions	PS3.1: PS3.2: Lessons Learned from a One Health Approach to AMRPS3.3: Climate Change and Emerging Diseases: The Importance of Resilient Societies PS3.4: PS3.5: Policy Coherence: Effective Partnerships for Global Health
1500 - 1530	Break	

1530 - 1730	PMAC Sessions	PS4.1: Moving Forward and Outward: Progress in Implementation of Global Frameworks and Initiatives PS4.2: Multi-sectoral Partnerships for Action on AMR PS4.3: Community Systems: The Bedrock of Responses to EID and AMR PS4.4: Finding the Win-Win Solutions for Better Health from Better Food Systems PS4.5: Bringing Solutions into Focus: Harnessing the Power of an Economic Lens
1800 - 2030	Welcome Dinner	Welcome Speech by Þ Minister, Ministry of Public Health, Thailand Þ President, Mahidol University, Thailand Þ Dinner Speech by Bill Gates, Bill and Melinda Gates Foundation, USA (TBC)

Date: Saturday, 3 February 2018

Main Conference Program

Time	Session	Notes
0900 - 0930	Closing Session	**Speech** by **Margaret Chan**, Former Director General, World Health Organization, Switzerland (TBC)
0930 - 1030	Synthesis	Summary, Conclusion, and Recommendations
1030 - 1100	Statement	
1100 - 1200	Closing Performance	
1200 - 1330	Lunch	
1400 - 1630	International Organizing Committee (IOC) Meeting	IOC Meeting for PMAC 2018/2019

Terms of Reference for Trusted Agents

BPERNET

BAT-ASSOCIATED PATHOGEN AND ECOLOGY RESEARCH NETWORK

Version 1
September 2017

TERMS OF REFERENCE FOR TRUSTED AGENTS OF THE BAT-ASSOCIATED PATHOGEN AND ECOLOGY RESEARCH NETWORK (BPERNET)

1. BACKGROUND

In 2013, the Defense Threat Reduction Agency (DTRA) Cooperative Biological Engagement Program (CBEP) began leveraging, enhancing, and convening research networks to accelerate its programmatic and research driven targets and end states. CBEP uses this approach to connect its active funded research projects with other projects to help influence effective change for global health security; translating data into policy. Further, by using relationship-based research networks around the globe, made up of interdisciplinary relationships, This approach allows for novel and transformative scientific solutions for the world's largest infectious disease threats.

The Bat-associated Pathogen and Ecology Research Network (BPERNet) is a CBEP research network that connects multidisciplinary and One Health expertise to address challenges and threats posed by bat-associated pathogens of security concern. The BPERNet maintains the standards of all research networks that are supported by CBEP, in which members convene as a body of experts and researchers to: (1) share information, data, samples, and protocols; (2) coordinate research activities; (3) build training events and awareness-building workshops at all levels of decision-making authority; (4) develop community standards and best research practices; (5) create mentorship-based opportunities for students, trainees, and early-career researchers to convene, present, and share ideas; (6) establish a community of international research leaders and champions; (7) support and conduct responsible research, including communication to the public, which prioritizes bat conservation and welfare; and (8) reduce outbreak / transmission risk.

Some of the world's most deadly emerging zoonotic diseases are found in bats, including Nipah, Hendra, and Marburg viruses. There are a number of factors that make bats unique disease reservoirs, including their social behavior, distinct physiology and metabolism, ability to travel long distances, nocturnal activity, species diversity, and long life span (10-20 years, compared with a rat's average life of two years).[1] This combination of traits, coupled with the impact of human-mediated interactions and environmental changes, challenge researchers to understand the role of bats in global zoonotic disease ecology. This, a challenge is further complicated by the difficulty of bat husbandry in laboratory settings. The BPERNet creates opportunities for policy makers, researchers, conservationists, funders, and students to identify community challenges, develop priority research lists and associated action plans that target needs and gaps, and work at all levels to build awareness of bat-associated disease burden and transmission risks to improve the prevention, detection, diagnosis, and reporting of pathogens of security concern.[2]

2. BPERNET MISSION AND VISION

The BPERNet brings together a multidisciplinary and One Health-focused group of scientists, policy makers, research scientists, and medical/veterinary practitioners with interests in bat-related research involving pathogens of security concern. The network builds on community standards and best

[1] Hayman, David T.S., "As the bat flies," *Science* 02 Dec 2016: Vol. 354, Issue 6316, pp. 1099-1100 http://science.sciencemag.org/content/354/6316/1099

[2] Schountz, Tony, "Immunology of Bats and Their Viruses; Challenges and Opportunities," *Viruses,* 2014 Dec; 6(12): 4880-4901. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4276934/

practices for research. The BPERNet identifies and shares information on research funding opportunities offered by multiple institutions. Most importantly, this network fosters international relationships among collaborators, agencies, and organizations, which can produce long-term, sustainable partnerships that withstand changes in government and organization budgets, priorities, postures, and policies.

All members, or "Trusted Agents" of the Alliance play a role in operationalizing the objectives of the BPERNet, strengthening linkages and reducing overlap in global research on high-priority pathogens of bats (especially zoonoses) to maximize the efficient use of expertise and resources and accelerate the coordinated development of better disease surveillance and control methods.

3. OBJECTIVES

CBEP created a standard framework of objectives that it uses for its research networks, which is outlined in the Background Section of this document. The specific, research-focused objectives of the BPERNet are as follows:

- Facilitate interdisciplinary relationships and collaboration to identify research goals and needs for bat-associated disease research and disease threat reduction; and
- Unify CBEP regions to create a common action plan that yields collaborative and sustainable projects that achieve the following end states: (1) better informed policy-makers; (2) better informed scientific community regarding funding targets and gaps in areas of research and development; (3) better defined threat to global health security from bat-associated pathogens; and (4) improved national, regional, and global capacity to detect and respond to pathogens of security concern
- Enable better communication, coordination, and outreach at the research and conservation interface

4. APPROACH

The Terms of Reference for Trusted Agents (TORFTA) establishes ground rules and responsibilities for all members – known heretofore as "Trusted Agents" (TAs) of the BPERNet. The leadership structure of the BPERNet is made up of subject matter experts who serve as mentors and function as independent, trusted advisors and honest brokers for research within the BPERNet.

All TAs function within an organizational structure that consists of an Executive Committee (EC), a Steering Committee (SC), and four subject matter-focused Working Group (WG) subcommittees. The BPERNet employs a bottom-up design. This is an organizational approach that encourages ideas, solutions, and projects to start with TAs within the WGs. The ideas, solutions, and projects will filter through the WG mentors, who then link people, ideas, solutions, and projects together at the SC level; ultimately, this approach will (1) foster lasting relationships at an individual or institutional level, and (2) yield more data outcomes and/or fields of study. A visual representation of the responsibilities and organizational flow of the BPERNet is found in Figure 1.

Roles and responsibilities of the TAs within Committees and Working Groups are as follows:

4.1 Working Groups (WGs)

The WGs serve as subdivisions of the BPERNet designed to foster multinational and multidisciplinary participation and meet the wide spanning research challenges associated with bat-borne diseases. TAs from the SC serve as research mentors and subject matter experts within each WG, providing guidance on projects.

There are limited barriers to entry for becoming a TA in the BPERNet and joining a WG. Non-steering committee members should work or reside in CBEP engaged countries, which can be found in Annex B, and may be students, entry to mid-level career professionals, or anyone interested in contributing to the bat research community. Entry for individuals who do not work or reside in CBEP engaged countries will be considered by the EC on a case-by-case basis. Non-steering committee TAs do not have term limits, but are encouraged to collaborate, contribute, and participate evenly across the WGs. TAs receive invitation or nomination to participate in a WG by members of the EC or SC.

The WGs focus on the following research areas *(**note:** these focus areas were agreed upon at the BPERNet kickoff in Fort Collins, CO 29 June 2017*):

Working Group 1: Host / pathogen biology and interactions; specifically:

1. Bat physiology and immunology
2. Bat pathogen community ecology (co-infections, co-morbidities)
3. Distribution of pathogens among species

Working Group 2: Pathogen surveillance, diagnostic capacity, and epidemiology; specifically:

1. Molecular epidemiology
2. Distribution of pathogens geographically and phylogenetically
3. Detection, diagnosis, and reporting of bat-associated pathogens

Working Group 3: Ecology setting (bat, domesticated animals, and wildlife interface); specifically:

1. Bat behavior, distribution, and movement
2. Domesticated animals and wildlife behavior, distribution, and movement impact on interaction with bats.
3. The effect of anthropogenic disturbance and modification on pathogen dynamics and spillover risk

Working Group 4: Human-bat interactions; specifically:

1. Human behavioral risk characterization
2. Hunting and commodity chain (e.g., bushmeat, guano, and pet trade)
3. Ecotourism
4. Interactions in human dwellings

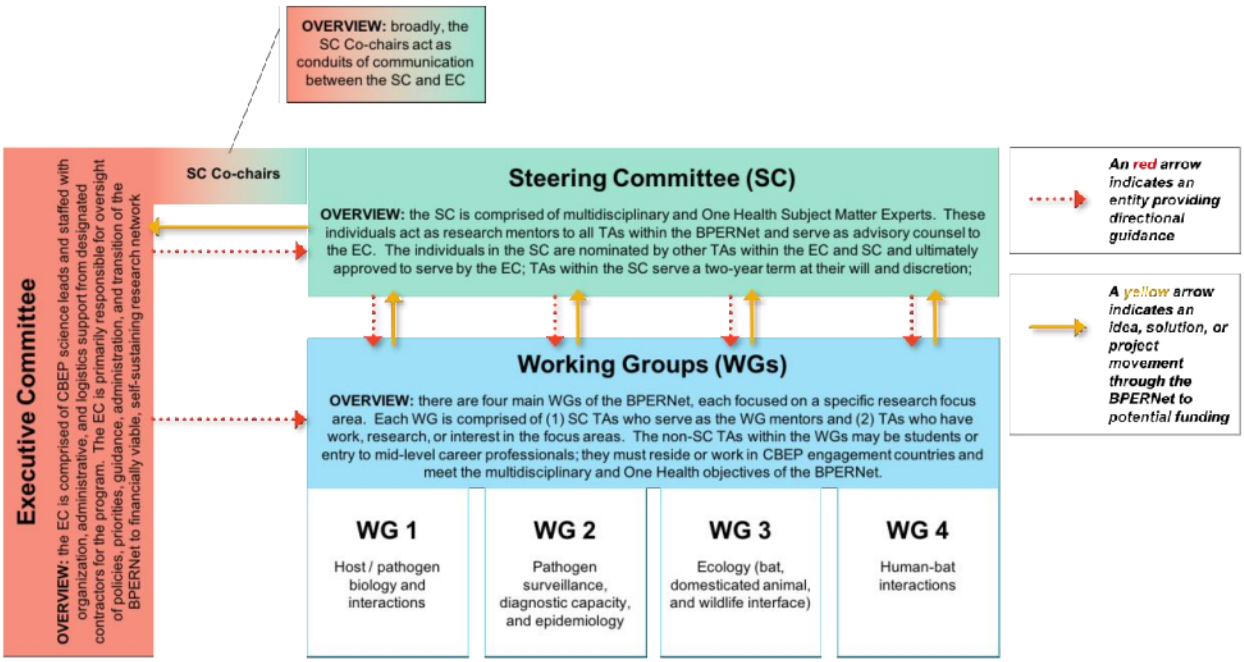
4.2 Steering Committee (SC)

The SC includes multidisciplinary subject matter experts. They fill two important roles to operationalize the objectives of the BPERNet, (1) acting as advisory counsel to the EC for global bat research (providing analysis of research gaps and needs and priority targets for future funds) and (2) serving as scientific mentors within WGs.

TAs within the SC advise on the scientific merit of proposals to the EC and assist with implementation per TORFTA guidance and EC direction. The selection process for SC membership gathers a multidisciplinary body of global representation, both geographically and across the bat research spectrum. Two SC Co-chairs are elected to serve as communication

between the SC and EC. Their roles and responsibilities are outlined in more detail later in this section.

TAs are nominated to join the SC by active members of the SC and EC. The inaugural SC was gathered together by the EC on 29 June 2017 in Fort Collins, Colorado. There is a two-year term limit for a TA in the SC, however, they have the option to leave and nominate a replacement at any time and with sufficient notification to the SC Co-chairs.



NOTE: *CBEP considers all contributors and participants of the BPERNet as "members" of the network; designating the term "Trusted Agents" (TAs) to all individuals regardless of role, affiliation, seniority, or responsibilities*

FIGURE 1 ORGANIZATIONAL STRUCTURE AND RESPONSIBILITIES OF THE BPERNET

The SC is responsible for the following items (at a minimum):

- Act as a scientific coordinating body for the BPERNet
- Consider and provide analysis on the scientific merit of proposals at the direction of the EC
- Serve as subject matter experts and research mentors for implementation of accepted BPERNet-endorsed projects
- Work within WGs to gather information on challenges, and propose research priorities to EC
- Identify possible conflicts of interest and make recommendations to SC Co-chairs and EC (e.g., one solution might be a temporary hiatus from the BPERNet or from service on the SC for a period of time)
- Annually review and make recommendations on policy and guidance of the BPERNet, which could include revision of the objectives, terms of reference, terms for membership, or structure of the BPERNet
- Work with the EC to determine challenges for transition to a self-sustaining network, which could include sources and means of political and financial support
- Define objectives, schedules, milestones, and deliverables of the WGs, as well as identifying need for proposing establishment of new or closing-out existing WGs

- Support WGs in organizing gap analyses and research prioritization
- Promote interactions between WGs
- Assess and report progress of the WGs to other members of the SC and EC
- Develop and encourage exchange of protocols and best practices, and agree on standard operating procedures, good research practice, and roadmap to reach BPERNet goals (short and long-term)
- Establish compliance rules for ethical practice, create training SOP

SC Co-chairs: Two members of the SC are chosen by majority voting during annual meeting of the EC and SC. All other TAs on the SC have two-year term limits; however, the Co-chairs hold one-year term limits, with the possibility of a one-year additional term upon re-nomination and approval from of the EC. These two individuals serve as the communication node between the EC and SC. They engage with the WG mentors that serve on the SC from the bottom-up, to identify candidates and projects. Other responsibilities include:

- Coordinate and communicate with EC organization and administration staff to arrange meeting schedule for EC/SC (virtual and in-person)
- Identify opportunities to broaden the network, e.g., conference attendance, paper presentations, etc.
- Communicate EC requirements to SC and set standards for good management practices within WGs
  - Reports
  - Schedules
  - Membership distribution
  - Information flow
- At the direction of the EC, act as a spokesperson for the network and interact with complimentary fields of study outside the network
- Work with the EC to determine and seek other funding opportunities
- Communicate regularly with EC on potential risks to self-sustainability of the network
- Advise the EC on potential conflicts of interest and recommended courses of action

4.3 Executive Committee (EC)

The EC ultimately sets policy and guidance for the BPERNet. It is chaired by the CBEP Science Leads from Africa and Southeast Asia and staffed with organization, administrative, and logistics support from designated contractors assigned to the program. The EC is primarily responsible for oversight of BPERNet governance policies and guidelines, which includes funding decisions, research priorities, adjudication of potential conflicts of interest, and BPERNet membership at all levels of participation. As such, the EC is the sole decision-making body of the research network for funding.

The EC is comprised of members from the CBEP Research Program, therefore, the details regarding program requirements and processes for funding can be found in Annex A of this document and should be used as a resource for all BPERNet Trusted Agents who wish to submit projects to CBEP. Any TAs considering application for projects will be governed by the terms for Conflict of Interest (in 5.2 under Governance and Membership) and are required to work with the EC, who will in-turn work with the TA to avoid any real or perceived individual or institutional conflicts of interest.

The EC and their team are broadly responsible for the following tasks (at a minimum):

- Review and approve objectives and goals for the BPERNet
- Review and approve Steering Committee and Working Group schedules and deliverables
- Provide organizational, administrative, and logistics support for meetings, conferences, and training events (virtual and in-person) of the BPERNet SC and WGs
- Work with Chairman and Deputy Chairman of the SC on marketing, communication, and outreach with other experts, fields of study, policy makers, international organizations, non-governmental organizations, and other networks
- Disseminate network information to all TAs, which could include newsletters, website links, press releases, and dates for upcoming meetings and conferences (inside and outside the network)
- Build connections with other funding agencies and organizations
- Convene a bi-annual research review for four focus areas of the network
- Measure network performance goals
- Score indicators of network transition to self-sustainability readiness

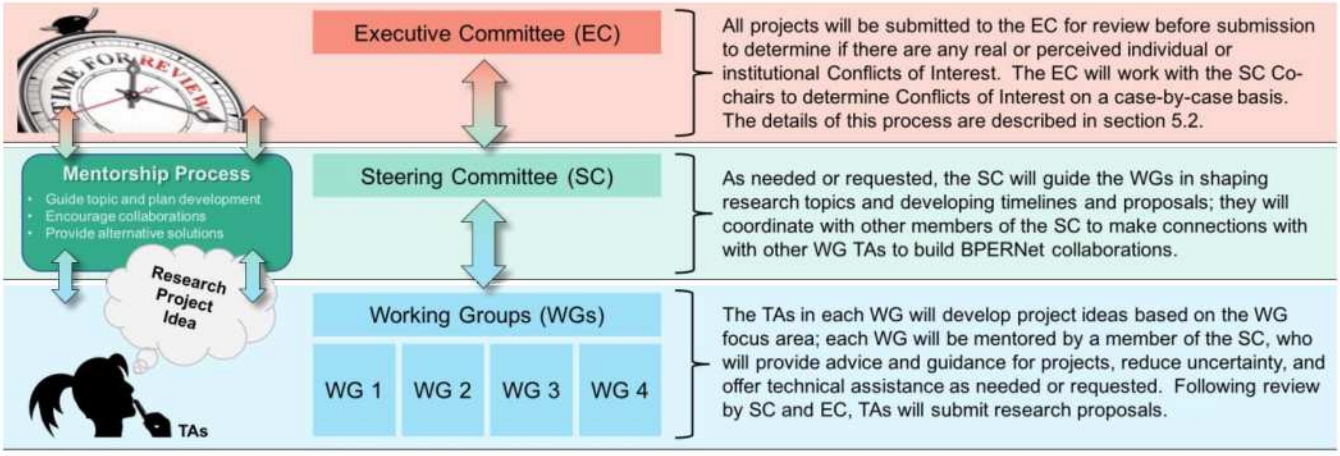


FIGURE 2 PROCESS FOR PROJECT DEVELOPMENT AND REVIEW

5. GOVERNANCE AND MEMBERSHIP

5.1 Accountability

The overarching duty of the BPERNet is to develop multi-disciplinary and multi-national, hypothesis driven, research projects and training opportunities that meet the prioritized challenges defined by the EC under advice from the SC with the goal of outlining community standards of practice. All TAs are accountable for the following:

- TAs must be familiar with the TORFTA and the mandate of the committees or WGs on which they serve
- TAs must promote a culture of responsible practice for scientific research
- TAs must work towards the short and long-term goals for the benefit of the BPERNet with a particular emphasis on the foci that fall within their WG
- TAs on the SC are selected for their breadth of experience, insight and knowledge, integrity and character, and sound and independent judgment; therefore, they are expected to bring

these personal qualities to their role on the SC and apply impartial judgment to help the EC make informed and independent decisions

5.2 Conflicts of Interest

The TORFTA document chooses the National Academy of Sciences (NAS) definition of Conflict of Interest: "a conflict of interest in research exists when the individual has interests in the outcome of the research that may lead to a personal advantage and that might therefore, in actuality or appearance compromise the integrity of the research."

No member of the Steering Committee may participate in a discussion where such participation would give rise to a potential conflict of interest. As defined in section 4.1, the EC shall review all situations and decisions insofar as a financial obligation is at stake. SC members may leave their term of service on the SC if they wish to participate in a funding opportunity that would otherwise be perceived as a conflict of interest. SC TAs must recuse themselves if any personal advantage, not just those of financial benefit, is perceived. Any member of the SC may discuss possible conflicts of interest with the EC before recusing themselves or stepping down from their term of service.

The EC arbitrates final decisions regarding potential conflicts of interest. With advice from the SC Co-chairs, they will determine if a recusal, resignation, or termination is required. The EC will determine the terms of recusal on a case-by-case basis, which could include being directed to abstain from any or all of the following: (1) meetings; (2) votes; (3) exchange of information; or (4) other correspondence. Ultimately, the EC advocates for complete transparency within the BPERNet, with an emphasis on early and frequent communication about any matter that could be perceived as a conflict of interest; this approach will mitigate ethics concerns and should eliminate the need for termination of service.

5.3 Selecting **TAs**

As stated in previous sections, all members of the BPERNet are referred to as "Trusted Agents" (TAs) of the network. TAs must reflect the One Health, multi-disciplinary, and multi-national nature of the BPERNet. There are no term limits for non-committee associated TAs, who are allowed to participate at will in accordance with terms of the TORFTA, additional selection rules are as follows:

5.3.1 ***Terms of service –*** *none*

5.3.2 ***Eligibility*** *– representation from each CBEP region must be maintained*

5.3.3 ***Nomination process –*** *nominated or invited to participate by the EC or SC at conferences, meetings, or electronically*

5.3.4 ***Selection process –*** *reviewed by members of the EC under advisement of the SC*

5.4 Selecting SC TAs

The SC includes TAs that are regarded as subject matter experts in their fields of research. TAs of the SC agree to the following rules for selection:

5.3.5 ***Terms of service –*** *2 years, no term limit*

5.3.6 ***Eligibility*** *– representation from each CBEP region must be maintained*

5.3.7 ***Nomination process –*** *nominated biennially by members of the SC (or more frequently as needed or requested by EC and SC Co-chairs); nomination process takes place in-person or virtually, selection is achieved through majority vote*

5.3.8 ***Selection process –*** *upon nomination by an SC member, potential applicant will submit an application consisting of a CV, letter of interest, and area(s) of interest related to the WG focus areas to the nominating SC member. The nominated applicant will be presented to the SC and EC by the nominating SC member. The applicant may be accepted as a SC TA upon majority vote by the SC and EC.*

5.5 Consensus

A quorum within the BPERNet is constituted by 2/3 approval within the SC, and rounded up when the number is uneven. The SC may decide by consensus or majority vote to ask other TAs to join a meeting to exchange information, material, or knowledge. The SC may establish sub-committees consisting of three or more of its members to conduct training or outreach (or any effort not explicitly within the stated focus areas of the SC and WGs). However, the Co-chairs should be informed of these efforts to communicate the need and seek approval from the EC

ANNEX A: APPLYING FOR FUNDING VIA EXECUTIVE COMMITTEE / CBEP

A.1 CBEP Research Scope

In order for CBEP to remain relevant, agile, and sustainable, research projects must be aimed at threat reduction objectives and demonstrate a clear nexus with the biosurveillance mission. The scope of CBEP research priorities include (but are not limited to):

- Understanding the ecology and epidemiology of pathogens of security concern, including HHS and USDA Biological Select Agents and Toxins and pathogens of pandemic potential, emerging, and re-emerging infectious diseases (e.g., avian influenza [low and highly pathogenic], African swine fever, Middle East Respiratory Syndrome (MERS), Ebola)
- Differentiating infectious diseases presenting clinical signs and symptoms similar to those of pathogens of security concern (e.g., influenza-like illness, acute febrile illness, fever of unknown origin)

CBEP will not support research projects that have no clear link to its threat reduction mission, are not sustainable for the partner country, or propose activities constituting Dual Use Research of Concern. These and other requirements and constraints are outlined in the figure below.

CBEP Fundamental Research Scope	
In Scope	Out of Scope

Projects that demonstrate:
• Clear relationships to pathogens of security concern
  ○ U.S. Biological Select Agents *
  ○ Pathogens of pandemic potential
  ○ Pathogens with potential to be weaponized
  ○ Emerging or re-emerging infectious diseases
  ○ Differentiating pathogens of security concern from agents with similar clinical signs and symptoms
• Links to threat reduction mission
• Support of BS&S and biosurveillance capabilities that reduce the threat of pathogens of security concern
  ○ Rapid, accurate, and safe detection, diagnoses, and reporting
• Alignment with both CBEP and partner country infectious disease priorities
• Use of sustainable techniques, procedures, and approaches in appropriate facilities
	Projects that focus on:
	• Dual-Use Research of Concern (DURC)
	• Diagnostic assay / novel technology
	• Development **
	• Medical countermeasures, including vaccine development
	• Non-infectious diseases
	
	Projects that contain:
	• Establishment of new pathogen repositories
	• No link to pathogens of security concern
	• No clear alignment to threat reduction mission
	• Use of unsustainable techniques, procedures, or inappropriate facilities
	  ○ Requires use of supplies or resources not available in country
	• No clear research question or hypothesis
	• No potential to generate knowledge that may result in scientific publications

* Pathogens on the HHS and USDA Biological Select Agent and Toxins List

** Field or country-specific validation of new diagnostic assays, novel technologies or equipment may be in scope if meeting other in-scope criteria

A.2 Applying for DTRA CBEP Research Funding

CBEP Research Objectives and Scope

DTRA CBEP is continuously seeking new collaborators, partners and international partners to conduct cooperative biological research to inform and enhance disease surveillance and global health security. Projects that are hypothesis-driven and contain substantive engagement with and contribution by partner country governments, institutions and scientists are appropriate for CBEP research funding. Research projects that support CBEP objectives in partner countries include those that promote One Health, improve disease surveillance, enhance understanding of endemic pathogens, explore the microbial ecology of endemic organisms, and enhance host country capabilities in support of World Health Organization International Health Regulations and World Organization for Animal Health reporting standards. Pathogens of interest include Biological Select Agents and Toxins, pathogens of pandemic potential, pathogens with the potential to be weaponized, emerging and re-emerging infectious diseases, and pathogens that are co-syndromic with associated select agent etiologies such as Influenza-Like Illness or Acute Febrile Illness. CBEP does not support research topics that involve Dual- Use Research of Concern or focus on disease agents that are sexually transmitted, non-infectious, or do not pose a threat to global health security.

Research projects supported by CBEP must align with CBEP's overarching goals to reduce the threat to U.S. and global health security and are expected to produce results suitable for scientific publication.

Applying to the Broad Agency Announcement (BAA) and Government Call

CBEP welcomes research funding applications from domestic and foreign academic, private, and government institutions, and has multiple solicitations available for proposals.

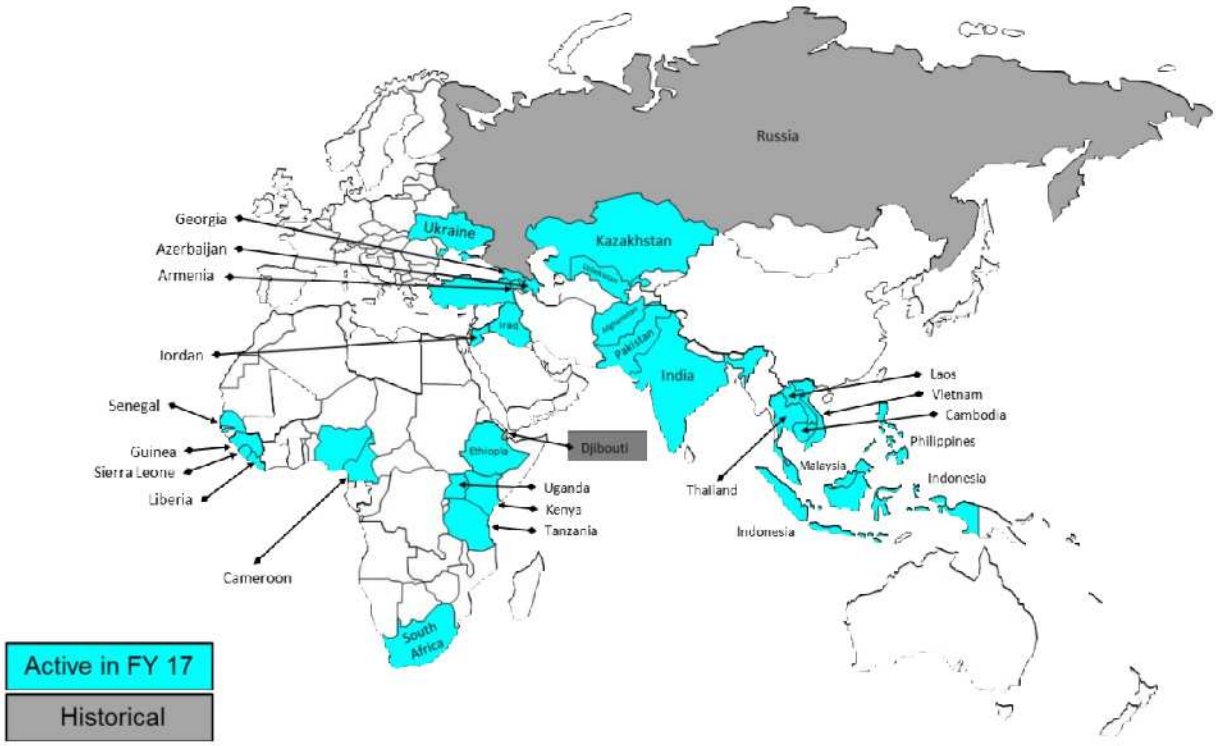
- Academic institutions, non-governmental organizations, industry, foreign laboratory equivalents, and members of the private sector must apply through Thrust Area 6: Cooperative Counter Weapons of Mass Destruction (CWMD) Research with Global Partners of the Fundamental Research to Counter Weapons of Mass Destruction (FRCWMD) – BAA (HDTRA1-14-24- FRCWMD-BAA).
- U.S. Government partners and Federally Funded Research and Development Centers (FFRDCs) must apply through Thrust Area 6 of the FRCWMD Government Call (HDTRA1-12-17- FRCWMD-Call).

All research ideas MUST be pre-coordinated through submission of an abstract to HDTRA1-FRCWMD-TA6@mail.mil prior to submitting a white paper. White papers (aka Phase I proposal) must be submitted and a full proposal (aka Phase 2 Proposal) invited prior to submission of a full proposal. Phase 1 and Phase 2 proposals to the FRCWMD-BAA must be submitted through www.grants.gov. Phase 1 and Phase 2 proposals to the FRCWMD-Call must be submitted through www.dtrasubmission.net. White papers and proposals will be peer reviewed in accordance with the evaluation criteria published in the BAA and Call and in coordination with appropriate CBEP Regional

and Country Managers. To be successful, a white paper and/or proposal must align with both the DTRA/SCC-WMD CBEP mission and regional priorities.

Detailed instructions for the FRCWMD-BAA and the FRCWMD-Call can be found through the solicitation links at www.dtrasubmission.net. Please ensure that you are downloading and reviewing the latest amended full announcement for the most accurate information and instructions. Offerors may submit questions of an administrative nature for BAA to HDTRA1-FRCWMD-A@mail.mil or for Service Call to HDTRA1-FRCWMD-C@mail.mil.

ANNEX B: CBEP ENGAGEMENT COUNTRIES



From: Megan Hudson >
Sent: Thursday, October 18, 2018 11:19 AM EDT
To: nisreen.hmoud ; joram.buza ; tigga.kingston ; kityrob ; spwa abelwade ; raina.plowright >; wanda.markotter ; allisonpeel >; jkerbis ; pilotdovih >; abubasha >; mervem.lemrani ; c demetria ; paalviola >; ryanahih ; ecohealthalliance.org ; ecohealthalliance.org >; Kading,Rebekah ; wava ; sara.b >; sarabumrungsri ; julianas ; wiantoro ; benjamin lee ; lisamarep >; pipat ; vudinhthong ; iroro.tanshi ; benneth.obitte >; jjlutwama ; jil >; astghik.ghazaryan ioseb.natradze <ioseb.natradze >; docshusmitadutta >; shahanajshano ecohealthalliance.org ; ksidamonidze >; l.urushadze ; mariano.sanchez-lockhart. ; farlowscience ; payscue stsang ; bhbird >; bbrooks ; ahandel ; tgoldstein >
CC: Stokes, Martha M CIV (US) ; Becker, Stephen M CTR DTRA J3-7 (US) >; Katie Leahy < >
Subject: Quad Chart Request: BOHRN Vienna Workshop
Attachment(s): "BOHRN_QUADCHART[2].docx"

Dear BOHRN participants,

For our upcoming workshop in Vienna, we ask that you please fill in the attached quad chart. Each participant will be asked to present the attached quad chart during the workshop day 1 event (about five minutes per chart). The information presented will be used to aid breakout group and large group discussions. Directions on how to fill in the quad chart are outlined in the attached document on page 1 and a blank template is located on page 2.

If you and other participants are collaborating on the same research, you can submit one quad chart for the entire team. If you oversee funding applicable to this workshop, please let us know and we will send you additional information for this quad chart.

Along with the quad chart, we are requesting that you send a picture of yourself. The quad charts and pictures will be printed to display around the room during the two day workshop. If you are not able to attend the day 1 meeting, please still submit a quad chart.

Please send the attached quad chart and picture by Friday 26 October.

Kind Regards,

Megan

Megan Hudson
Task Lead | Global Systems Engineering
6303 Little River Turnpike #208
Alexandria, VA 22312

http://globalsyseng.com

Quad Chart Instructions: Please fill out all four portions of the quad chart. The chart is read in a clockwise direction starting with the technical description. This activity is intended to provide a big picture overview and not an in-depth report of your research. Please limit the text to provide only the most important aspects of each quad. You will be given 5 minutes to present the information within this chart. Refer to the questions in each box for more guided assistance.

TECHNICAL DESCRIPTION AND OBJECTIVES

Briefly describe the research you are currently conducting and why. What questions are you trying to answer and what is the importance of this research to your field and the region? What are the specific aims of your research? What is currently known about your research? Consider the following:

1. **Objectives of research**
2. **Current state of understanding**
3. **Location of research (city/country and or coordinates)**

KEY PARTNERS AND REGIONS OF STUDY

Briefly describe the key partners and funders in your research. List the region(s) your research is being conducted in and any networks you are working with formally or informally. Consider the following:

1. **Who are the key partners involved in your research?**
2. **Who are the key funders involved in your research?**
3. **What region(s) is your research being conducted in?**
4. **Are you working with any networks (formally or informally)?**

MILESTONES, STATUS, AND CHALLENGES

Briefly explain the timeline of your research. When do you anticipate your research to be completed? Are there deliverables or steps along the way that will show substantial progress? Identify the challenges you will face. Consider the following:

1. **Provide timeline for delivery**
2. **Overview on project status**
3. **List challenges or needs in your research**

REGIONAL IMPACT

Describe the potential regional impact of your research. What will the impact be for the regional area? Will this lead to the need for future studies? Consider the following:

1. **Define the quantitative impact of project.**
2. **Define the regional impact.**

TECHNICAL DESCRIPTION AND OBJECTIVES

KEY PARTNERS AND REGIONS OF STUDY

MILESTONES, STATUS, AND CHALLENGES

REGIONAL IMPACT

From: Katie Leahy >
Sent: Tuesday, August 25, 2020 1:54 PM EDT
To: Kingston, Tigga ; martha.m.stokes.
CC: jamechia.d.hoyle ; Guzal Masharipova ;
Kading,Rebekah epstein ecohealthalliance.org>
Subject: Re: [External Sender] RE: BOHRN Status, publication

Hi, Tigga. Guzal (copied) should be able to help. I can make sure she has all the passwords; give us a day to make sure all the links are active. I talked with her today about it and she is ready to support in any way.

V/r,

Katie Leahy

KATIE LEAHY | ***Director, Science Engagement***
Global Systems Engineering, LLC
A Certified HUBZone Company
www.globalsyseng.com

From: "Kingston, Tigga" >
Date: Tuesday, August 25, 2020 at 1:51 PM
To: "martha.m.stokes.civ" >
Cc: Katie Leahy , "jamechia.d.hoyle Guzal
Masharipova "Kading,Rebekah" , Jon Epstein
@ecohealthalliance.org>
Subject: [External Sender] RE: BOHRN Status, publication

Dear Marty
Thanks for the speedy response and support! Great to hear of the documentation efforts and continued commitment.

The lynchpin to everything that we'd like to do is the BOHRN website – is there a webmaster, or can one be allocated, so that we can host content, build membership, post some of the materials that have been developed.

Best
Tigga

From: Stokes, Martha M CIV (USA)
Sent: Tuesday, August 25, 2020 8:45 AM
To: Kingston, Tigga >
Cc: Katie Leahy >; Hoyle, Jamechia D CTR (USA) Guzal
Masharipova >; Kading,Rebekah ; Jon Epstein
ecohealthalliance.org>
Subject: RE: BOHRN Status, publication

Hi Tigga,

Congratulations on having your piece accepted (with revisions, as always)! I would really appreciate you adding detail about BOHRN and highlighting the network's efforts. All of the positive outcomes you mention are well noted and align with our goals and objectives, which remain steadfast.

The current situation has certainly created unexpected challenges for all our work, but we're adapting, and want to ensure that we continue moving forward and position the network to pick up where it left off last summer, once things return to a more normal environment. In the meantime, we'll do what we are able virtually.

Let us know what you need to support this. Katie and I, along with our teams, recently updated a huge amount of documentation, reports, participant lists, etc. for BOHRN and other our TRNs for the incoming BTRP Director, in order to deposit it on our internal database, so it should be very easy to provide whatever you need. Just let us know how we can help.

Thanks so much!

Best,
Marty

Martha M Stokes, PhD
Southeast Asia Regional Science Manager
Biological Threat Reduction Program (BTRP)

From: "Kingston, Tigga" >
Date: Monday, August 24, 2020 at 5:09 PM
To: "martha.m.stokes >
Cc: Katie Leahy >, "jamechia.d.hoyle , Guzal Masharipova , "Kading,Rebekah" >, Jon Epstein cohealthalliance.org>
Subject: [External Sender] BOHRN Status, publication

Dear Marty,

Rebekah Kading and I wrote a perspectives piece that is in revision for PLOS Biology. It calls for greater integration of ecologists/virologists (hmm, sounds familiar) and builds on analysis of a publication coauthor network. We conceptualized this at BORHN meetings and consider it a true BOHRN output, supporting BOHRN's message.

One of the reviewers specified some simple, but concrete actions that they would like to see in the revision. These actions closely ally with things we've begun at BOHRN (e.g., mission statement, contact lists of researchers). We would really like to be able to respond using BOHRN's infrastructure as it would be a good fit and would draw substantial attention to BOHRN and help boost the distributed membership and get us more on the map. The reviewer called for a mission statement, a list of who is doing what, and other simple things that could easily be integrated into the BOHRN website.

Currently, we refer to BOHRN in the acknowledgements, but have been reluctant to feature the network too centrally because we are unsure of its status and stability. It would be great to move forward with BOHRN featured more prominently, but we could do with some clarity of where things are heading. At minimum we need support of the website as that is where we will be directing people. Currently people can't join, or reset passwords etc, and we would need to work with someone on updates supporting these simple collations of information.

We have a bit less than a month to turn this around and get our revision in, so it would be great to hear your thoughts. I hope we can talk soon. I am now free fairly consistently between 10 am-Noon Mo-Thursday. I have other windows here and there as well.

All the best

Tigga

From: Kevin Olival ecohealthalliance.org>
Sent: Friday, August 07, 2020 3:09 PM EDT
To: Cara Brook >; Hon S Ip >; Paul Cryan ; David Hayman >; epstein ecohealthalliance.org>; dreeder >; Hume Field @ecohealthalliance.org>; Charles H Calisher ; Brian R. Amman Wang Linfa >; Ralph S. Baric ; David S Blehert ; Kevin Castle ; Jeremy Coleman ; Peter Daszak @ecohealthalliance.org>; wfrick < >; Amy Gilbert ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson >; Kading,Rebekah >; Tigga Kingston >; Lorch, Jeffrey M >; Ian MENDENHALL PhD < >; alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina >; Jonathan D Reichard >; Jonathan M Sleeman ; Daniel Streicker < >; Jonathan S. Towner
Subject: Re: [EXTERNAL] Editorial Acceptance of "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPA...

Just wanted to send a quick update on our paper…. I'm honestly surprised at how long PLOS Pathogens is taking, but I guess the editorial process slowed down w COVID.

We send in edits on pre-proofs a couple of times over the last few weeks, and have been waiting for over a week for the typeset proofs to come in. Once those come back and we have a publication date, I'll let you all know ASAP.

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

From: Kevin Olival ecohealthalliance.org>
Sent: Sunday, June 28, 2020 7:59:53 AM
To: David Hayman ; Jon Epstein ecohealthalliance.org>; dreeder >; Hume Field ecohealthalliance.org>; Charles H Calisher >; Brian R. Amman ; Wang Linfa >; Ralph S. Baric >; Blehert, David S >; Cara Brook >; Kevin Castle >; Coleman, Jeremy T >; Peter Daszak ecohealthalliance.org>; wfrick >; Gilbert, Amy T - APHIS < ; Ip, Hon S >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson >; Kading,Rebekah >; Tigga Kingston >; Lorch, Jeffrey M >; Ian MENDENHALL PhD >; alisonpeel >; Kendra Phelps ecohealthalliance.org>; Plowright, Raina >; Reichard, Jonathan D >; Sleeman, Jonathan M ; Daniel Streicker < ; Jonathan S. Towner >; Cryan, Paul >
Subject: [EXTERNAL] Fwd: Editorial Acceptance of "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPATHOG...

Paper Accepted!! Thank you all for your patience, perseverance, and invaluable contributions. I haven't received the proofs yet, but will turn them around quickly when I do.

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

Begin forwarded message:

From: "PLOS Pathogens" >
Subject: Editorial Acceptance of "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPATHOGENS-D-20-01177R1) - [EMID:902178ed8cb23641]
Date: June 26, 2020 at 4:39:55 PM EDT
To: "Kevin J. Olival" ecohealthalliance.org>
Reply-To: "PLOS Pathogens"

CC: "Paul M. Cryan" "Brian R. Amman" , "Ralph S. Baric" "David S. Blehert" "Cara E. Brook" "Charles H. Calisher" "Kevin T. Castle" "Jeremy T. H. Coleman" "Peter Daszak" ecohealthalliance.org, "Jonathan H. Epstein" ecohealthalliance.org, "Hume Field" ecohealthalliance.org, "Winifred F. Frick" "Amy T. Gilbert" "David T.S. Hayman" , "Hon S. Ip" "William B. Karesh" ecohealthalliance.org, "Christine Kreuder Johnson" , "Rebekah C. Kading" "Tigga Kingston" , "Jeffrey M. Lorch" "Ian H. Mendenhall" "Alison J. Peel" "Kendra L. Phelps" "Raina K. Plowright" "DeeAnn M. Reeder" , "Jonathan D. Reichard" , "Jonathan M. Sleeman" "Daniel G. Streicker" "Jonathan S. Towner" "Lin-Fa Wang"

Dear Dr. Olival,

We are pleased to inform you that your manuscript 'Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats

Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats' has been provisionally accepted for publication in PLOS Pathogens.

Before your manuscript can be formally accepted you will need to complete some formatting changes, which you will receive in a follow up email. A member of our team will be in touch with a set of requests.

Please note that your manuscript will not be scheduled for publication until you have made the required changes, so a swift response is appreciated.

IMPORTANT: The editorial review process is now complete. PLOS will only permit corrections to spelling, formatting or significant scientific errors from this point onwards. Requests for major changes, or any which affect the scientific understanding of your work, will cause delays to the publication date of your manuscript.

Should you, your institution's press office or the journal office choose to press release your paper, you will automatically be opted out of early publication. We ask that you

notify us now if you or your institution is planning to press release the article. All press must be co-ordinated with PLOS.

Thank you again for supporting Open Access publishing; we are looking forward to publishing your work in PLOS Pathogens.

Best regards,

Seema Lakdawala, PhD
Reviews Editor
PLOS Pathogens

Aaron Mitchell
Section Editor
PLOS Pathogens

Kasturi Haldar
Editor-in-Chief
PLOS Pathogens
orcid.org/0000-0001-5065-158X

Michael Malim
Editor-in-Chief
PLOS Pathogens
orcid.org/0000-0002-7699-2064

****

Reviewer Comments (if any, and for reference):

From: calisher
Sent: Friday, August 07, 2020 3:11 PM EDT
To: Kevin Olival ecohealthalliance.org>; Cara Brook >; Hon S Ip Paul Cryan >; David Hayman ; epstein ecohealthalliance.org>; dreeder Hume Field ecohealthalliance.org>; Brian R. Amman Wang Linfa ; Ralph S. Baric David S Blehert >; Kevin Castle ; Jeremy Coleman ; Peter Daszak ecohealthalliance.org>; wfrick ; Amy Gilbert William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah >; Tigga Kingston >; Lorch, Jeffrey M ; Ian MENDENHALL PhD >; alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina <r >; Jonathan D Reichard Jonathan M Sleeman Daniel Streicker ; Jonathan S. Towner
Subject: RE: [EXTERNAL] Editorial Acceptance of "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPA...

Thanks. I already have requests for reprints, from Tony Fauci's office.

Charlie

From: Kevin Olival ecohealthalliance.org>
Sent: Friday, August 7, 2020 1:09 PM
To: Cara Brook ; Hon S Ip >; Paul Cryan ; David Hayman ; Jon Epstein ecohealthalliance.org>; dreeder Hume Field ecohealthalliance.org>; Charles H Calisher Brian R. Amman Wang Linfa ; Ralph S. Baric < David S Blehert < ; Kevin Castle ; Jeremy Coleman < ; Peter Daszak ecohealthalliance.org>; wfrick ; Amy Gilbert < William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah ; Tigga Kingston Lorch, Jeffrey M ; Ian MENDENHALL PhD ; alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; Jonathan D Reichard Jonathan M Sleeman ; Daniel Streicker ; Jonathan S. Towner
Subject: Re: [EXTERNAL] Editorial Acceptance of "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPA...

Just wanted to send a quick update on our paper…. I'm honestly surprised at how long PLOS Pathogens is taking, but I guess the editorial process slowed down w COVID.

We send in edits on pre-proofs a couple of times over the last few weeks, and have been waiting for over a week for the typeset proofs to come in. Once those come back and we have a publication date, I'll let you all know ASAP.

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org
EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

From: Kevin Olival ecohealthalliance.org>
Sent: Sunday, June 28, 2020 7:59:53 AM
To: David Hayman >; Jon Epstein ecohealthalliance.org>; dreeder >; Hume Field ecohealthalliance.org>; Charles H Calisher < >; Brian R. Amman ; Wang Linfa ; Ralph S. Baric >; Blehert, David S ; Cara Brook ; Kevin Castle ; Coleman, Jeremy T >; Peter Daszak @ecohealthalliance.org>; wfrick <wfrick Gilbert, Amy T - APHIS >; Ip, Hon S

William Karesh ecohealthalliance.org>; Christine Kreuder Johnson Kading,Rebekah Tigga Kingston ; Lorch, Jeffrey M <jlorch >; Ian MENDENHALL PhD alisonpeel < ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina >; Reichard, Jonathan D ; Sleeman, Jonathan M ; Daniel Streicker Jonathan S. Towner >; Cryan, Paul >

Subject: [EXTERNAL] Fwd: Editorial Acceptance of "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPATHOG...

Paper Accepted!! Thank you all for your patience, perseverance, and invaluable contributions. I haven't received the proofs yet, but will turn them around quickly when I do.

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

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520 Eighth Avenue, Suite 1201
New York, NY 10018

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Begin forwarded message:

From: "PLOS Pathogens" >
Subject: Editorial Acceptance of "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPATHOGENS-D-20-01177R1) - [EMID:902178ed8cb23641]
Date: June 26, 2020 at 4:39:55 PM EDT
To: "Kevin J. Olival" ecohealthalliance.org>
Reply-To: "PLOS Pathogens"

CC: "Paul M. Cryan" "Brian R. Amman" "Ralph S. Baric" "David S. Blehert" , "Cara E. Brook" "Charles H. Calisher" "Kevin T. Castle" , "Jeremy T. H. Coleman" , "Peter Daszak" ecohealthalliance.org, "Jonathan H. Epstein" ecohealthalliance.org, "Hume Field" ecohealthalliance.org, "Winifred F. Frick" , "Amy T. Gilbert" "David T.S. Hayman" "Hon S. Ip" "William B. Karesh" ecohealthalliance.org, "Christine Kreuder Johnson" "Rebekah C. Kading" "Tigga Kingston" "Jeffrey M. Lorch" "Ian H. Mendenhall" "Alison J. Peel" "Kendra L. Phelps" "Raina K. Plowright" DeeAnn M. Reeder" "Jonathan D. Reichard" , "Jonathan M. Sleeman" "Daniel G. Streicker" , "Jonathan S. Towner" "Lin-Fa Wang"

Dear Dr. Olival,
We are pleased to inform you that your manuscript 'Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats

Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats' has been provisionally accepted for publication in PLOS Pathogens.
Before your manuscript can be formally accepted you will need to complete some formatting changes, which you will receive in a follow up email. A member of our team will be in touch with a set of requests.
Please note that your manuscript will not be scheduled for publication until you have made the required changes, so a swift response is appreciated.

IMPORTANT: The editorial review process is now complete. PLOS will only permit corrections to spelling, formatting or significant scientific errors from this point onwards. Requests for major changes, or any which affect the scientific understanding of your work, will cause delays to the publication date of your manuscript.
Should you, your institution's press office or the journal office choose to press release your paper, you will automatically be opted out of early publication. We ask that you notify us now if you or your institution is planning to press release the article. All press must be co-ordinated with PLOS.
Thank you again for supporting Open Access publishing; we are looking forward to publishing your work in PLOS Pathogens.
Best regards,

Seema Lakdawala, PhD
Reviews Editor
PLOS Pathogens

Aaron Mitchell
Section Editor
PLOS Pathogens

Kasturi Haldar
Editor-in-Chief
PLOS Pathogens
orcid.org/0000-0001-5065-158X

Michael Malim
Editor-in-Chief
PLOS Pathogens
orcid.org/0000-0002-7699-2064

****

Reviewer Comments (if any, and for reference):

From: Cara Brook
Sent: Sunday, June 28, 2020 10:37 AM EDT
To: Kevin Olival ecohealthalliance.org>
CC: Hon S Ip ; Paul Cryan >; David Hayman ; epstein ecohealthalliance.org>; dreeder ; Hume Field ecohealthalliance.org>; Charles H Calisher >; Brian R. Amman ; Wang Linfa >; Ralph S. Baric ; David S Blehert >; Kevin Castle ; Jeremy Coleman ; Peter Daszak ecohealthalliance.org>; wfrick ; Gilbert, Amy T - APHIS ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah ; Tigga Kingston ; Lorch, Jeffrey M ; Ian MENDENHALL PhD >; alisonpeel >; Kendra Phelps ecohealthalliance.org>; Plowright, Raina Jonathan D Reichard >; Jonathan M Sleeman ; Daniel Streicker ; Jonathan S. Towner
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Congrats! Thanks, Paul and Kevin, for all the hard work.

Best,
Cara

On Sun, Jun 28, 2020 at 6:16 AM Kevin Olival ecohealthalliance.org> wrote:

> Thanks Hon… and especially PAUL who did a ton of heavy lifting!
>
> **Kevin J. Olival, PhD**
> *Vice President for Research*
>
> EcoHealth Alliance
> 520 Eighth Avenue, Suite 1201
> New York, NY 10018
>
> www.ecohealthalliance.org
>
> *EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.*
>
> On Jun 28, 2020, at 9:14 AM, Ip, Hon S > wrote:
>
> Yay! Congratulations everyone but especially Kevin.
>
> Sent from iOS Outlook.
>
> ---
>
> **From:** Kevin Olival ecohealthalliance.org>
> **Sent:** Sunday, June 28, 2020 7:59:53 AM
> **To:** David Hayman ; Jon Epstein @ecohealthalliance.org>; dreeder ; Hume Field ecohealthalliance.org>; Charles H Calisher Brian R. Amman ; Wang Linfa ; Ralph S. Baric ; Blehert, David S Cara Brook ; Kevin Castle >; Coleman, Jeremy T ; Peter Daszak ecohealthalliance.org>; wfrick < Gilbert, Amy T - APHIS >; Ip, Hon S ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson Kading,Rebekah >; Tigga Kingston Lorch, Jeffrey M >; Ian MENDENHALL PhD alisonpeel >; Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; Reichard, Jonathan D Sleeman, Jonathan M Daniel Streicker ; Jonathan S. Towner >; Cryan, Paul >
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Reply-To: "PLOS Pathogens"

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Thank you again for supporting Open Access publishing; we are looking forward to publishing your work in PLOS Pathogens.

Best regards,

Seema Lakdawala, PhD
Reviews Editor
PLOS Pathogens

Aaron Mitchell
Section Editor
PLOS Pathogens

Kasturi Haldar
Editor-in-Chief
PLOS Pathogens
orcid.org/0000-0001-5065-158X

Michael Malim
Editor-in-Chief
PLOS Pathogens
orcid.org/0000-0002-7699-2064

****

Reviewer Comments (if any, and for reference):

From: Cryan, Paul
Sent: Friday, March 23, 2018 5:43 PM EDT
To: Tamar Kutateladze
CC: nisreen.hmoud c demetria ; ecohealthalliance.org Kading,Rebekah vkapur >; kityrob ; ian.mendenhall ecohealthalliance.org >; dreeder >; ksidamonidze ; gavin.smith ; l.urushadze ; spwa ; abelwade Megan Hudson m>; Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) ; Gano Cohen, Kelsey A CTR DTRA J3-7 (US) >; Katie Leahy >; Stokes, Martha M CIV (US) ; Becker, Stephen M CTR DTRA J3-7 (US)
Subject: Re: [EXTERNAL] Re: BOHRN Steering Committee/One Health Congress Meeting

Dear Megan and others,

Unfortunately the BOHRN meeting dates coincide with a field demonstration and contract signing for a new research project I'm starting here in Colorado. Despite my best efforts to reschedule, I don't think I'm going to be able to make it. Regardless, please keep me in the loop and I'll do my best to participate remotely if there are options to do so.

All the best,
Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info
ORCID

On Fri, Mar 23, 2018 at 3:05 AM, Tamar Kutateladze< wrote:

> Dear Megan,
>
> Thanks for information.
>
> I confirm my attendance to the meeting and one health congress.
>
> Yours Sincerely,
> Tamar
>
> *Tamar Kutateladze,*
>
> *MD, PhD,Department of Virology, MolecularBiology and Genome Research,*
> *R. Lugar Center for Public Health Research*
> *National Center for Disease Control & Public Health*
>
> On Thursday, March 22, 2018, 9:46:06 PM GMT+4, Megan Hudson > wrote:
>
> All,
>
> You are receiving this email, as part of a save the date to attend our BOHRN Steering Committee meeting and the 5th International One Health Congress (OHC) in Saskatoon, Canada.
>
> Our meeting will take place on 20-21 June (location TBD, though likely at the Hilton Garden Inn). The agenda and travel information for this two day event will follow shortly. The OHC will take place 22-25 June.
>
> On behalf of Dr. Marty Stoke and Dr. Mary Lancaster, CBEP will provide funding your travel and registration to the OHC and BOHRN Planning Meeting. While the OHC is not required it would be a good opportunity for networking on behalf of BOHRN. CBEP will be paying for OHC attendance next week. **Therefore, we need you to confirm your attendance to the OHC NLT tomorrow 23 March.** However, please note if regulations for DoD travel are not met by the specified due date, funding for the conference and travel will not be provided.

Please respond with your availability to attend the meeting NLT 23 March.

v/r,

Megan

	**Megan Hudson** *Task Lead* | Global Systems Engineering 6303 Little River Turnpike #208 Alexandria, VA 22312 http://globalsyseng.com

From: DeeAnn Reeder >
Sent: Saturday, March 24, 2018 4:22 PM EDT
To: Cryan, Paul >
CC: Tamar Kutateladze ; nisreen.hmoud ;
c demetria >; ecohealthalliance.org
; Kading,Rebekah vkapur
; kityrob >; ian.mendenhall
ecohealthalliance.org ; ksidamonidze
; gavin.smith < ; l.urushadze
>; spwa ; abelwade ;
Megan Hudson >; Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US)
>; Gano Cohen, Kelsey A CTR DTRA J3-7 (US) >; Katie
Leahy ; Stokes, Martha M CIV (US) < ; Becker, Stephen M
CTR DTRA J3-7 (US) >
Subject: Re: [EXTERNAL] Re: BOHRN Steering Committee/One Health Congress Meeting

Dear Megan et al.,

Sorry for the delay - I was in the field with absolutely no email access. I will attend the BOHRN and the one health congress meetings!

Thanks - DeeAnn

On Sat, Mar 24, 2018 at 12:43 AM, Cryan, Pau wrote:

> Dear Megan and others,
>
> Unfortunately the BOHRN meeting dates coincide with a field demonstration and contract signing for a new research project I'm starting here in Colorado. Despite my best efforts to reschedule, I don't think I'm going to be able to make it. Regardless, please keep me in the loop and I'll do my best to participate remotely if there are options to do so.
>
> All the best,
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>
> Paul Cryan
> Research Biologist
> USGS Fort Collins Science Center
>
> Web Page and Contact Info
> ORCID
>
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>> *National Center for Disease Control & Public Health*
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Please respond with your availability to attend the meeting NLT 23 March.

v/r,

Megan

Megan Hudson

Task Lead | Global Systems Engineering

6303 Little River Turnpike #208

Alexandria, VA 22312

http://globalsyseng.com

--
DeeAnn M. Reeder, PhD
Presidential Professor
Department of Biology
Bucknell University
Lewisburg, PA 17837

http://deeannreeder.scholar.bucknell.edu

From: Cryan, Paul
Sent: Thursday, April 30, 2020 5:20 PM EDT
To: Kading,Rebekah >; ecohealthalliance.org
Subject: Re: [EXTERNAL] Re: Final version of North American bat/SARS2 ms - PLEASE REVIEW

That is hilarious! Ah the humanity of it all!

Thanks, I needed that.

Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Kading,Rebekah >
Sent: Thursday, April 30, 2020 11:35 AM
To: Cryan, Paul ; ecohealthalliance.org
Subject: Re: [EXTERNAL] Re: Final version of North American bat/SARS2 ms - PLEASE REVIEW

Yeah, exactly! Might be Thursday, but it might also be Saturday. :-) This made me laugh yesterday so I thought I'd pass it along.
Take care -
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University
Office:

From: Cryan, Paul >
Sent: Thursday, April 30, 2020 10:17 AM
To: Kading,Rebekah ecohealthalliance.org <
Subject: Re: [EXTERNAL] Re: Final version of North American bat/SARS2 ms - PLEASE REVIEW

What, there's a difference between weeks and weekends?!?!?

Thanks Rebekah!

P

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Kading,Rebekah >
Sent: Wednesday, April 29, 2020 5:07 PM
To: ecohealthalliance.org >; Cryan, Paul <
Subject: [EXTERNAL] Re: Final version of North American bat/SARS2 ms - PLEASE REVIEW

p.s. Kevin AND Paul, I mean to say in my previous email. Sorry, it's been a long week already! Thanks to both of you!!
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University
Office:

From: Kading,Rebekah >
Sent: Wednesday, April 29, 2020 5:05 PM
To: Kevin Olival cohealthalliance.org>; 'Paul Cryan' >
Subject: Re: Final version of North American bat/SARS2 ms - PLEASE REVIEW

Hi Kevin,

Very nice job on this! Only spotted a couple small things.
1) "highlights" is misspelled on line 128.
2) looks like a ref is still needed in line 342 regarding PPE usage in the field. This ref might fit...it's more broadly on wildlife professionals though (PMID: 31993824)
3) don't forget to delete the [...] on line 421

Yes, I would be delighted to be a co-author.

My ORCID is 0000-0002-4996-915X.

Thanks so much!
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University
Office:

From: Kevin Olival ecohealthalliance.org>
Sent: Sunday, April 26, 2020 10:11 PM
To: Paul Cryan ; Brian R. Amman ; Ralph S. Baric < David S Blehert ; Cara Brook < ; Charles H Calisher >; Kevin Castle ; Jeremy Coleman >; Peter Daszak ecohealthalliance.org>; epstein ecohealthalliance.org>; Hume Field ecohealthalliance.org>; Winifred F Frick, Ph.D. ; Gilbert, Amy T - APHIS >; David Hayman ; Hon S Ip ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson >; Kading,Rebekah Tigga Kingston ; Lorch, Jeffrey M ; Ian Mendenhall ; alisonpee Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; DeeAnn Reeder ; Jonathan D Reichard >; Jonathan M Sleeman < ; Daniel Streicker ; Jonathan S. Towner >
Subject: Final version of North American bat/SARS2 ms - PLEASE REVIEW

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Please review the attached penultimate draft of our manuscript (now entitled: **"Possible risks of SARS-CoV-2 spillover to free-ranging wildlife: a case study of bats")**, together with the supplementary table and refs. Our plan is to submit to *Lancet Infectious Diseases* as a review article (correct length and they allow 150 refs) in the next week - references are currently formatted for that journal. We would also like to post it on bioRxiv as a pre-print once we get it submitted to *Lancet ID*. Please let me know if you have any concerns with that plan.

Thank you all for your excellent comments and edits on the previous draft. Paul and I have gone back and forth on several rounds of revisions since then (and multiple late night texts), aiming to take each and every suggestion into account, and we believe it's a much better manuscript now! Very excited about this one, and looking forward to getting it published!

By Thursday April 30th (or ASAP), could you each please:

1. Confirm that you agree to be a co-author.
2. Double check your name and affiliation, and send me your ORCID number if you have one.
3. Read through the ms and send any important, last minute changes or edits you feel are necessary. Please use track changes. If you're okay with the ms as is, please just confirm so.
4. For my Federal US Gov't friends (USFWS, USGS, CDC, USDA) - please let us know what we need to do for approval on your end. I know Paul is working with USGS now to hopefully get rapid clearance.

No need to cc all if you don't want, but please include both me and Paul on your response.

Looking forward to hearing from you all soon!

Cheers,

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
460 West 34th Street, Suite 1701
New York, NY 10001

www.ecohealthalliance.org
EcoHealth Alliance develops science-based solutions to prevent pandemics *and* promote conservation

From: Cryan, Paul
Sent: Thursday, April 30, 2020 12:17 PM EDT
To: Kading,Rebekah ecohealthalliance.org < >
Subject: Re: [EXTERNAL] Re: Final version of North American bat/SARS2 ms - PLEASE REVIEW

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New York, NY 10001

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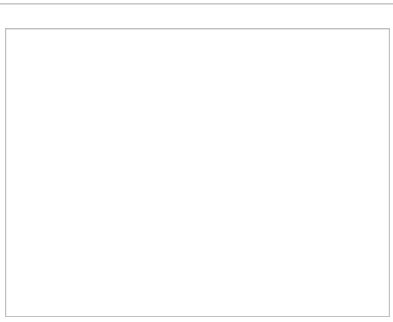
EcoHealth Alliance develops science-based solutions to prevent pandemics *and* promote conservation

From: Cryan, Paul
Sent: Wednesday, April 15, 2020 9:11 PM EDT
To: Kading,Rebekah >; Kingston, Tigga
CC: ecohealthalliance.org
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Great to know we're on the same path! I'm finding that coordinating and obsessively researching/writing/getting-up-to-speed on a issue are difficult to pull off at the same time!

https://www.youtube.com/watch?v=onoaKEEyNEI



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Sent: Wednesday, April 15, 2020 8:43 AM
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Cc: ecohealthalliance.org
Subject: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

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CC: ecohealthalliance.org
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Hi Rebekah and Tigga,

Thanks for the awesome and quick improvements to the manuscript. I'm assuming you're okay with being co-authors, cause you are now. ☺

I'm working through the comments from everyone now and will get back to you with thoughts about the more strategic and substantive ideas after I've had some time to think about them and catch up with myself.

In the meantime, one easy answer is that I see I created some confusion by citing Tao and Tong for Nyctalus leisleri and Hipposideros pratti in the supplemental table, which were actually reported by Drexler et al. 2010 (attached)...oops, good catch! I'll add country of origin to that table and flesh out the cross-referencing a little better for the next iteration.

And Tigga, thanks for those taxonomy updates! I didn't know about those changes, so thanks for that. DeeAnn is also looking at this and said she'd send a new table of the African pteropodid names, so I'm learning a lot.

Stay tuned and thanks again,
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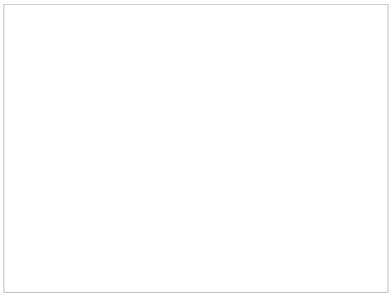

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From: Kading,Rebekah >
Sent: Wednesday, April 15, 2020 8:27 PM
To: Cryan, Paul ; Kingston, Tigga
Cc: ecohealthalliance.org
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Oh my goodness Paul! LOL!
Hang in there - you're doing great.

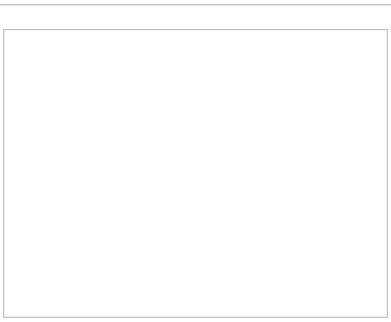
Rebekah
😂

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University
Office:

From: Cryan, Paul
Sent: Wednesday, April 15, 2020 7:11 PM
To: Kading,Rebekah ; Kingston, Tigga
Cc: ecohealthalliance.org
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Great to know we're on the same path! I'm finding that coordinating and obsessively researching/writing/getting-up-to-speed on a issue are difficult to pull off at the same time!

https://www.youtube.com/watch?v=onoaKEEyNEI



Lead, Follow, or Get Out of the Way

From the woefully underrated Mike Judge film "Idiocracy." Joe isn't what you'd call a highly-motivated individual.

www.youtube.com

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Kading,Rebekah >
Sent: Wednesday, April 15, 2020 8:43 AM
To: Kingston, Tigga ; Cryan, Paul >
Cc: cohealthalliance.org
Subject: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Hi Paul, Kevin, Tigga,

I'll just reply to this thread. Yes, I'd be happy to take a look at the paper as well -- thank you very much for spearheading that effort! As Tigga mentioned we're working on something as well that we'll reach out to you guys separately about. Seems like BOHRN is mobilizing on multiple fronts, which is great to see.

Take care and talk to you soon -
Rebekah

Rebekah C. Kading, PhD
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Department of Microbiology Immunology and Pathology
Colorado State University
Office:

From: Kingston, Tigga >
Sent: Wednesday, April 15, 2020 7:52 AM
To: Cryan, Paul ; Kading,Rebekah
Cc: ecohealthalliance.org
Subject: RE: SARS-CoV-2 spillback risk to North American bats

Hi Paul
Very interested to see the MS. Rebekah and I have been working on something that arose out of BOHRN that would be very complementary and might be worth trying to coordinate dissemination in some way. We are meeting today and will take stock of where we are at.

I just started an email to you and Kevin about the state of affairs as we Rodrigo and I are getting quite a bit of push-back on the IUCN BSG recommendation to suspend field studies while further data are gathered (primarily from western scientists with access to PPE). It would be good to hear what those committees are finding sooner rather than later.

Best wishes
Tigga

From: Cryan, Paul
Sent: Tuesday, April 14, 2020 2:16 PM
To: Kingston, Tigga >
Cc: ecohealthalliance.org
Subject: SARS-CoV-2 spillback risk to North American bats

Hi Tigga,

Sorry for the silence since my call for help about the risks of humans potentially infecting bats in North America with the SARS-CoV-2 virus. Thanks for your patience and willingness to get involved in what we're hoping can be another disease response where scientists coming at disparate aspects of bats and pathogens can help each other. Those of us in the bat research world that focused most of our past efforts in the U.S. on conservation and management of bat populations can certainly use your expertise and help adjusting to the new situation.

A lot happened during my silence. Another group in USGS has been working at the behest of decision makers across federal and state natural resource management agencies to pull off a formal risk assessment by querying a subset of the experts we've reached out to. You lucked out and were not chosen for that exercise (yet), but we will keep you posted on the outcomes of that rapid assessment.

The other thing keeping me silent over the past couple of weeks is a short manuscript (currently 5 pages single spaced) that Kevin Olival and I drafted to articulate the potential risks of humans infecting North American temperate-zone bats with SARS-CoV-2, potentially relevant patterns we observed in bat-CoV distributions at a global scale, and the likely benefits of disease and bat researchers working together to draw on the strengths of our various disciplines. We hope to have a draft to circulate by tomorrow and would appreciate input and feedback from any of you willing to read it and help us stress test the concepts and assertions therein. Please let me know if you are interested.

Thanks again for your help and patience.

All the best,
Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

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Is there a risk of SARS-CoV-2 infection and transmission in North American bats?

Kevin J. Olival, Paul M. Cryan*, Kevin T. Castle, and multiple invited co-authors…*

*These authors contributed equally

Spillover and "spillback" of pandemic viruses

The threat of emerging infectious diseases (EIDs) to wildlife populations and biodiversity conservation is recognized (*1*), but cross-species transmission of novel pathogens, or spillover, is typically viewed in the narrow context of originating *from* a wildlife reservoir and transmitting *to* humans. Research assessing EID risk has focused on identifying geographic regions (*2, 3*) and wildlife species (*4-6*) where spillover of zoonotic diseases into human populations is most likely. Among recent pandemic viruses of zoonotic origin, some have no evidence of "spillback" to wildlife or domestic animal populations after they were established in people (e.g., HIV, which causes AIDS), and others cross species boundaries with fluidity (e.g. pandemic H1N1 Influenza A virus (*7, 8*)). Evidence of spillback, or reverse zoonosis, into wildlife and domestic animals is widespread (*9*), but viral spillback to wild bats has not been recorded. In December 2019, a novel coronavirus (now SARS-CoV-2) infected a cluster of humans in Wuhan, China and has since spread to become a global pandemic. The virus has reached over 185 countries, infected >2.1 M people, and killed >147,000. Phylogenetic evidence suggests that SARS-CoV-2, along with the entire clade of SARS-related coronaviruses (SARSr-CoVs), are zoonotic and evolved in Old-World bats from the family *Rhinolophidae* (*10-13*). The closest known virus to SARS-CoV-2 was discovered in *Rhinolophus affinis* from Yunnan province in China with 96% sequence similarity across the virus' genome (*14*), yet which proximate species led to human spillover remains unclear (*15*). The United States (US) is currently the epicenter of the largest recognized outbreak of COVID-19, with community transmission in all 50 states. The unintended consequences of this pandemic are many and include the possibility of SARS-CoV-2 spillback to free-ranging wildlife populations. Here we assess the possibility of SARS-CoV-2 spillback from humans to North American (NA) bats and discuss possible consequences of the virus becoming endemic in bats outside its natural host range.

The triple threat of SARS-CoV-2 to North American bats

The pandemic human spread of SARS-CoV-2 may threaten NA bat populations in three different ways. First, SARS-CoV-2 might infect and cause disease among the diverse and historically isolated 40+ species of temperate-zone NA bats. Second, SARS-CoV-2 might be able to infect and become established in one or more of these NA species, creating a diverse new suite of temperate-zone wildlife disease reservoirs. Third, if SARS-CoV-2 can persistently infect one or more species of NA bats, it could potentially evolve, or recombine with other endemic viruses, to become more pathogenic to humans and other mammals. The latter outcomes would undoubtedly shift public perception of bats from mostly beneficial wildlife with manageable associated disease risks, to bats as harmful nuisance animals posing unacceptable disease risks to human health. In addition to new public health challenges, such shifts could undermine decades of concerted science, conservation, and education efforts aimed at these important animals.

Lessons from an epizootic -- susceptibility of North American bats to introduced pathogens

SARS-CoV-2 is not the first pathogen that humans could inadvertently spread to NA bats. The COVID-19 pandemic follows the arrival of a fungal pathogen (*Pseudogymnoascus destructans*) that in 2007 began infecting NA populations, crossing species barriers, spreading among, and altering the evolutionary trajectory of the continent's bats (*16-19*). The disease of hibernating bats caused by that fungus, White-Nose Syndrome (WNS), remains the first and only documented bat epizootic (*20, 21*). WNS has killed millions of NA bats, affected populations of at least 12 species of 3 genera, and has already spread across half of the United States (US) and Canada. Methods of mitigating WNS spread and impacts remain elusive. It took years of concerted international scientific effort to first identify the novel cold-growing fungus, determine that it probably originated somewhere in the temperate zones of Europe or Asia, understand its mechanisms of infection and pathogenicity, and to track its rapid spread through an immunologically naïve continental assemblage of hibernating bats that lacked many defenses against it (*22*). The devastating impact of WNS on a diverse group of NA bats likely resulted from evolutionary isolation of the continent's bat fauna from large parts of the world for millions of years. Bats in both Europe and Asia can become infected by *P. destructans*, but do not suffer mass mortality from WNS (*23, 24*). No extant species of bat that occurs in the Americas also occurs outside of the Americas (*25, 26*), and no bat species regularly migrates or likely survives flights across the Pacific or Atlantic oceans (*27, 28*). The bat fauna spanning the higher latitudes of NA (e.g., US and Canada) is composed almost entirely of species belonging to the world's largest bat family -- Vespertilionidae. Vespertilionid bats occur all over the world, but likely originated and diversified in NA tens of millions of years ago -- they are the only bat family to increase in diversity northward out of the tropics and consistently reach high latitudes (50ºN;(*29, 30*). The WNS epizootic taught us that a large proportion of this historically isolated bat fauna can be vulnerable to pathogens introduced from other continents. The COVID-19 pandemic invokes the specter of WNS and highlights deficits in our understanding of pathogens in NA bats.

Gaps in understanding global patterns of bat-CoV diversity and evolution

Bats are among the most diverse mammals (approximately 1,400 species), and global distributions and diversity of CoVs in bats proportionally reflects that of their hosts (*31, 32*). Bats also rank among the most ecologically important but underappreciated mammals that play varied roles in most of Earth's ecosystems (*33, 34*). Coronaviruses appear to have ancient and ancestral relationships with bats, diversifying globally through a process of within-host evolution and cross-taxonomic host-switching events (*31, 35, 36*). Available evidence indicates that bats are natural reservoirs of CoVs with pre-emergent potential to cause diseases in humans, livestock, and other types of domestic animals and wildlife (*14, 31, 37-50*). Indeed, bats are the likely progenitor hosts of all alpha (α-) and beta (β-) CoVs (*51*) and potentially all *Coronaviridae* (*52-57*). Two recent human disease epidemics (Severe Acute Respiratory Syndrome [SARS], Middle East Respiratory Syndrome [MERS]) and now the COVID-19 pandemic were caused by viruses that probably originated from CoVs circulating in populations of wild bats near the outbreak origins (*14, 38-43, 49, 50, 58, 59*). A similar CoV of likely bat origin also recently

caused Swine Acute Diarrheal Syndrome (SADS) outbreaks and mass mortality of piglets on farms in Guangdong province, China (*46*). Emergence of diseases like SARS, SADS, and now COVID-19 from the same general region strongly indicates a close association between CoVs likely to evolve into pathogens and the wildlife reservoirs where they originate (*14, 38-43*). Bat CoVs show clear global patterns of geographic structure that reflect host distributions, and typically strong co-evolutionary patterns among related hosts (*31, 49, 60, 61*). These phylogeographic factors are also universal determinates of viral sharing among all mammals (*62*). However, predicting broad CoVs jumps (i.e., that lead to spillover and spillback) is difficult because of the wide potential host breadth for many CoVs (*13, 44, 45, 63-67*), and the fact that bats are often asymptomatic reservoirs capable of harboring a diversity of CoV lineages -- obscuring bat-virus association patterns (*31, 49, 50, 61, 68*). Bat-CoV associations remain woefully understudied in temperate-zone NA, despite the large number of bat biologists and virologist working in the US, Mexico, and Canada (*31, 68-70*).

Are viruses like SARS-CoV-2 already widespread in North American bats?

Our preliminary examination of CoV evolutionary lineages and global distribution patterns of the diverse bats they infect suggests that NA bats could be immunologically naïve to infection by viruses like SARS-CoV-2. Alpha and β-CoVs have been detected in bats on most continents, sometimes with both types occurring in the same bat species and individuals (*49, 50, 71*). However, a striking exception to this pattern is the apparent lack of evidence that β-CoVs infect bats of temperate-zone NA. Multiple novel α-CoVs have been detected and described in Nearctic vespertilionid bats of the US and Canada, infecting species living in close contact with humans and in remote wild areas (*68, 70, 72*). Alpha-CoVs of likely bat origin can cause disease in humans and other animals including human α-CoVs NL63 and 229E (*73, 74*). However, emerging infectious diseases like MERS, SARS, SADS, and COVID-19 are caused by β-CoVs. Therefore, scientists have focused great effort on detecting, genotyping, studying the geographic distribution, and host-cell receptor binding of β-CoVs in bats (*49, 50*). SARSr-CoVs of the viral subgenus *Sarbecovirus* that can bind to angiotensin-converting enzyme 2 (ACE2) host-cell receptors of humans and other animals have thus far been detected mostly in species of the Old-World Chiropteran suborder Yinpterochiroptera (Table S1; Fig. 1A; (*11, 31, 49, 50, 75-79*). Two exceptions to this pattern were detection of novel Clade 3 and Clade 1 *Sarbecovirus* (*sensu* (*41*)) in the bat *Chaerephon plicata* (family Molossidae) in China (*80*) and the vespertilionid species *Nyctalus leisleri* cohabiting a Bulgarian cave during autumn with several species of *Rhinolophus* in which other SARS-related β-CoVs were concurrently detected (Fig. 1A; (*81*). β-CoVs of other distinct evolutionary lineages, such as viral subgenera *Hibecovirus* and *Nobecovirus*, also tend to occur mostly in Old-World bat families, with the exception of novel viruses of the latter subgenus detected in two species of *Scotophilus* in Africa (Fig 1B, C; (*31, 41, 49, 50, 77, 82*). Bat β-CoVs of the subgenus *Merbecovirus* (MERS-related lineage) occur in a greater diversity of bat families and across more global regions than others (Fig. 1D; (*49, 60*). These widely distributed viruses can evolve to cause disease in humans and animals (e.g., MERS) and notably appear to be the only bat β-CoVs to diversify among several families of the globally distributed suborder Yangochiroptera (Fig. 2; (*49, 50, 76-78, 83-87*). The several hundred species of extant bats spanning the Americas all belong to the suborder Yangochiroptera, which likely diverged from the Old-World Yinpterochiroptera more than 50 million years ago (Fig. 2; (*88*)). In the Americas, a novel β-CoV of the subgenus *Merbecovirus*

was detected in *Nyctinomops laticaudatus* (family Molossidae), and other distinct lineages in the subgenus *Merbecovirus* were described from *Pteronotus davyii* and *P. personatus* (family Mormoopidae), as well as species of *Artibeus* and *Dermaneura* (family Phyllostomidae) from tropical regions of Mexico (*31, 89, 90*); none of these bat species occur outside of the Neotropics. Successful *in vitro* infection of cells from the Neotropical bat *Artibeus jamaicensis* with MERS-CoV led to experimental infection trials that resulted in virus replication and shedding without obvious clinical signs of disease (*91*). Considering these laboratory findings and detection of only β-CoVs of the subgenus *Merbecovirus* in two exclusively Neotropical bat families (Phyllostomidae & Mormoopidae) and one that is globally distributed (Molossidae), available evidence suggests β-CoVs may have arrived to the New World through South America and have long been evolving in Neotropical bats. β-CoVs of the subgenus *Merbecovirus* are not known to target ACE2 cell receptors, instead using the dipeptidyl peptidase-4 (DPP4/CD26) or possibly other receptors (*41, 92*). Assessing SARS-CoV-2 host range using virus-host receptor binding assays *in silico* and *in vitro* (*14, 41, 92, 93*), together with future experimental infection studies for 'gold standard' confirmation, hold promise to better quantify the potential for NA bat infection. We are not aware of any published detections of β-CoVs in temperate-zone NA vespertilionid bats, although sampling has been limited. Overall, proportionally few studies have looked for CoVs in the approximately 1,400 species of bats occurring across six continents. This sampling deficit limits the inference obtainable by examining known patterns of bat-CoV occurrence and distribution. To our knowledge SARSr-CoVs (*Sarbecovirus spp*; (*41, 77*)) have only been detected in one species of vespertilionid bat in Bulgaria (*81*), a likely transmission from co-roosting *Rhinolophus* sp. bats. This absence of evidence for β-CoVs in temperate-zone bats of NA leaves important gaps in our ability to gauge threats posed by SARS-CoV-2 to bats in the US and Canada.

Figure 1. Global patterns of bats and associated beta-coronaviruses (β-CoVs). A) red-shaded distributions of bat species in which SARS-related β-CoVs of the viral subgenus *Sarbecovirus* were detected; B) pink-shaded distributions of bat species known to host β-CoVs of the subgenus *Hibecovirus*; C) brown-shaded distributions of bats in which β-CoVs of the *Nobecovirus* lineage have been detected; and D) green-shaded distributions of bats known to host MERS-related β-CoVs of the subgenus *Merbecovirus*. Different colors and shade styles within each panel represent different families of bats. See Table S1 for species lists. Maps created using ArcMap (ESRI, Redlands, California, USA) and bat ranges derived from spatial data on terrestrial mammals from the IUCN (https://www.iucnredlist.org/resources/spatial-data-download).

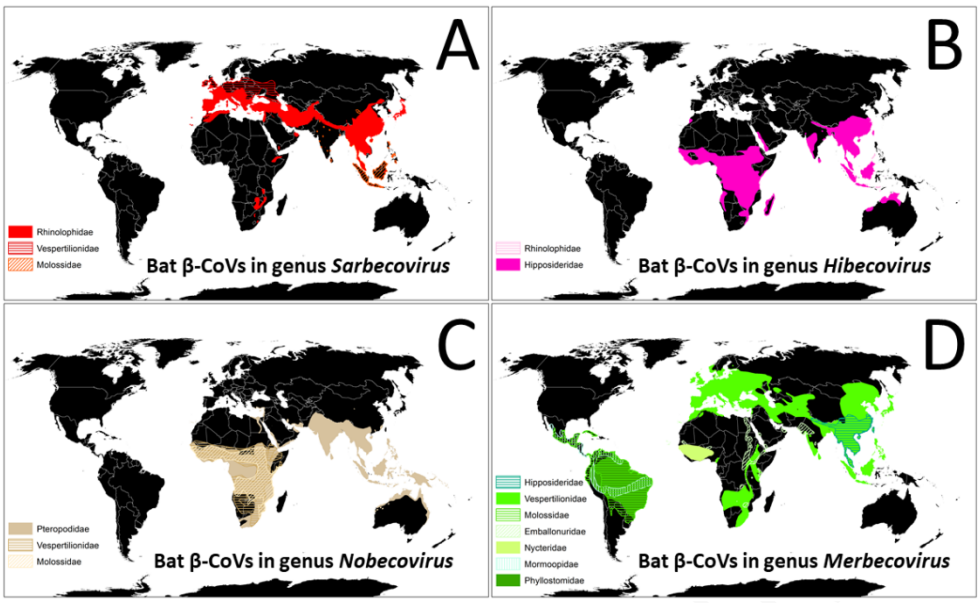
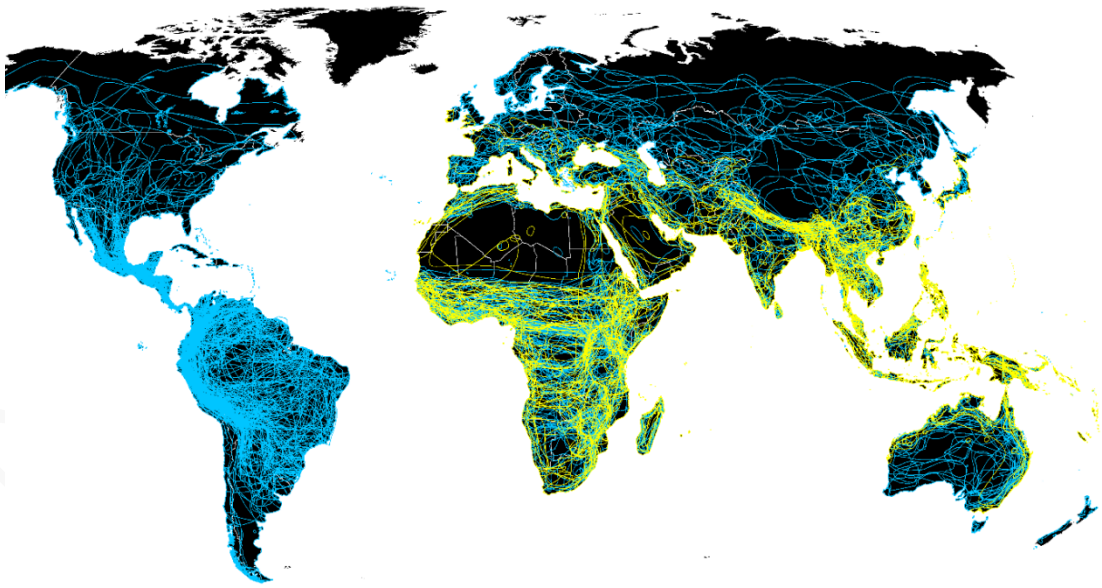


Figure 2. Old-world and new-world bats. Overlapping species distribution outlines of bats in the globally distributed suborder Yangochiroptera (blue) and Old-world Yinpterochiroptera (yellow). Maps created using ArcMap (ESRI, Redlands, California, USA) and bat ranges derived from spatial data on terrestrial mammals from the IUCN (https://www.iucnredlist.org/resources/spatial-data-download).



Proactively connecting the wellbeing of human and bat populations

Scientists have long recognized the risk of disease spillback from humans to bats (*94-96*), but bat researchers in NA did not systematically address such risk prior to WNS**.** Few bat

researchers studied infectious diseases in bats before WNS emerged in 2007 (*69*) and proportionally few disease researchers studied bat pathogens before bats were retrospectively connected to the SARS epidemic (*12, 58, 97*). An often unstated duality of such disease responses is the seemingly contradictory facts that bats are unequivocally ecologically important (*33, 34*), yet also a diverse source of emerging infectious diseases (*6, 50, 97-101*). Factors driving the ecologic success of bats are often the same as those invoked for explaining why bats might host such a diversity of viruses. These factors include characteristics of bat life history (e.g., long-lived, slow reproducing, wide dispersal, multi-species aggregations, daily and seasonal torpor (*97*)), unique physiology for repairing damaged DNA (*102*), unique ability to regulate immune response (*103-105*), and unmatched metabolic range and high body temperatures during flight (*106*). Bats also cryptically come into closer contact with humans than many other types of wildlife, often daily crossing human-wildlife interfaces. An oft-overlooked flip side to abundant evidence that many dangerous human diseases originate from bats is the fact that bats rarely show signs of mass mortality and sickness from these same dangerous pathogens (*20*). Bats cope with viral infection in ways that we do not yet fully comprehend but learning how they do so may reveal important insights to develop therapeutics and ultimately protect human health. *In vitro* and laboratory studies demonstrate that bats can regulate immune response to effectively cope with MERS-CoV and SARS-CoV-2 infection, at least under experimental conditions (*104, 107*). Lack of clear signs of sickness in bats and the cryptic habits of many species also generally inhibit our ability to easily detect spillback of pathogens from human to bat populations, further adding to uncertainty about movement of CoVs among groups. Laboratory findings suggest human viruses like HCoV-NL63 may have historically moved back and forth between human and bat populations multiple times (*74*). SARS-CoV-2 and other CoVs are relatively long for RNA viruses, making them susceptible to recombination and copy errors with resulting functional adaptations (e.g., receptor binding ability, temperature adaptation enzymes)(*108*). CoVs can recombine with functional fragments of other virus families, such as when a bat-derived CoV gained a functional gene from a reovirus (*109*). If spillback of SARS-CoV-2 into NA bats led to the virus becoming more pathogenic to bats, domestic animals, or humans through genetic mixing in a NA bat reservoir host, the public-health and conservation consequences would be severe.

Need for an interdisciplinary disease response

Effectively managing risks of human disease caused by emerging zoonotic pathogens *and* ensuring the health and conservation of potential wildlife reservoirs of those disease agents are not mutually exclusive goals. Research has shown that spillover risk (and probably spillback risk) may be highest in disturbed ecosystems where there is a high frequency of human-wildlife interactions (*2, 110, 111*). Thus, effective bat conservation and management requires understanding both pathogens that cause disease in bats, as well as human activities that present health risks in environments we share with bats. Furthermore, seemingly intuitive reactions to disease risk from wildlife, such as culling infected bat populations, often have negative unintended consequences for the interconnected health of both human and bat populations (*112, 113*). Temperate-zone vespertilionid bats inhabiting human dwellings in US and Canada represent a particularly relevant human-wildlife interface where such actions and potential consequences for disease spillback and spillover may be particularly worth careful consideration. A growing field of 'One Health' or conservation-minded bat virus research studies

have demonstrated the potential for mutual benefit of collaboration between public health, disease, and conservation stakeholders (*95, 112, 114-119*). For example, proper use of personal protective equipment (PPE) including respiratory protection has been adopted by the bat virus research community but by few others studying bats. Assessing the risks of SARS-CoV-2 spillback into NA bats seems like a perfect opportunity to integrate and practically apply lessons learned from prior epizootic and pandemic disease responses, and to tap a growing field of CoV experts studying viral transmission, host range, and natural history. Free-ranging bats are notoriously difficult to study, so scientists researching EIDs can benefit from methods bat researchers have developed for observing, counting, and non-invasively sampling bats (*69, 120*). Bat researchers can learn important biosafety, health monitoring, and laboratory techniques from researchers with expertise in veterinary and medical sciences (*117, 118*).

SARS-CoV-2 alters the *status quo* of bat research, emphasizing the need to carefully weigh risks and benefits of wildlife research in the context of population-altering diseases (*121*). Adopting a precautionary approach in the face of widespread COVID-19 transmission, US and international wildlife organizations have begun advising limiting field research to minimize the risk of humans infecting bats with SARS-CoV-2 until further assessment can be made (*122, 123*). A rapid, quantitative risk assessment and analysis of various mitigation options is an urgent research priority and is currently underway (*122*). One key question is if the proper use of PPE and masks, together with other basic biosafety practices (*124*), during field work can significantly reduce the risk of transmission to bats. In the interim, until new guidelines are established for handling and near-proximity work with bats, important scientific inquiry could continue. Temporarily shifting to 'hands-off' bat research methods in temperate-zone NA seems prudent wherever possible. Examples of such methods applicable to both disease and conservation research include: monitoring echolocation calls to determine the occurrence, distributions, and seasonal/nightly activity patterns of bats (*125-128*); digital imaging methods for counting bats and studying physiology and behaviors in the context of disease and anthropogenic landscape change (*19, 129-134*); methods of safely attaching tracking tags and environmental sensors to bats for multi-month periods (*19, 135*); and sampling guano from below bat roosts to determine bat species and individual identity, population dynamics, and daily or seasonal patterns of bat occupancy and pathogen shedding (*68, 136-139*). Promising areas for innovation include making these 'hands off' field technologies more accessible to a broader global user base, less expensive, easier to use, and scientifically reproducible through open-source hardware, software, and laboratory methods (e.g., (*140-146*)). Assessing the risk of SARS-CoV-2 transmission to NA bats also raises critical gaps in knowledge about bat CoV diversity and distribution, particularly in the New World. Standardized field protocols and probabilistic sampling strategies for monitoring bats and their viruses at a continental scale are needed (www.nabatmonitoring.org; (*147-149*). The currently unknown but potentially high-consequence risk of SARS-CoV-2 transmission and establishment in NA bats warrants precaution. We are at a critical nexus of biosecurity and natural resource conservation. Our actions during this current pandemic could profoundly influence the health of both human and bat populations.

Acknowledgements

We thank Jonathan Sleeman, Tom O'Shea, Jonathan Reichard, Chip Clark, and […] for helpful comments on earlier drafts of this manuscript.

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Table S1. Global patterns of β-CoV associations in bats. Bat species in which β-CoVs were detected, organized by viral subgenera, bat family, and bat suborder. Bats of the suborder Yinpterochiroptera highlighted in yellow and Yangochiroptera in blue.

β-CoV SUBGENERA		BAT SPECIES	BAT FAMILY	REFERENCE	BAT SUBORDER
Sarbecoviruses		*Rhinolophus ferrumequinum*	Rhinolophidae	Anthony et al. 2017	Yinpterochiroptera
	Clade 3	*Rhinolophus sinicus*	Rhinolophidae	Anthony et al. 2017	Yinpterochiroptera
		Rhinolophus macrotis	Rhinolophidae	Tao and Tong 2019	Yinpterochiroptera
		Rhinolophus pearsonii	Rhinolophidae	Tao and Tong 2019	Yinpterochiroptera
		Aselliscus stoliczkanus	Hipposideridae	Tao and Tong 2019	Yinpterochiroptera
		Chaerephon plicatus	Molossidae	Tao and Tong 2019	Yangochiroptera
	Clade 2	*Rhinolophus pusillus*	Rhinolophidae	Tao and Tong 2019	Yinpterochiroptera
		Rhinolophus rex	Rhinolophidae	Wong et al. 2019	Yinpterochiroptera
	Clade 1	*Rhinolophus blasii*	Rhinolophidae	Tao and Tong 2019	Yinpterochiroptera
		Rhinolophus sp. Kenya	Rhinolophidae	Tao and Tong 2019	Yinpterochiroptera
		Nyctalus leisleri	Vespertilionidae	Tao and Tong 2019	Yangochiroptera
Hibecoviruses		*Hipposideros armiger*	Hipposideridae	Anthony et al. 2017	Yinpterochiroptera
		Hipposideros caffer	Hipposideridae	Anthony et al. 2017	Yinpterochiroptera
		Rhinolophus clivosis	Rhinolophidae	Anthony et al. 2017	Yinpterochiroptera
		Hipposideros commersoni	Hipposideridae	Tao and Tong 2019	Yinpterochiroptera
		Rhinolophus creaghi	Rhinolophidae	Anthony et al. 2017	Yinpterochiroptera
		Hipposideros galeritus	Hipposideridae	Anthony et al. 2017	Yinpterochiroptera
		Hipposideros larvatus	Hipposideridae	Anthony et al. 2017	Yinpterochiroptera
		Hipposideros lekaguli	Hipposideridae	Anthony et al. 2017	Yinpterochiroptera
		Hipposideros pratti	Hipposideridae	Tao and Tong 2019	Yinpterochiroptera
		Hipposideros ruber	Hipposideridae	Anthony et al. 2017	Yinpterochiroptera
		Rhinonicteris aurantia	Hipposideridae	Smith et al. 2016	Yinpterochiroptera
β-CoV SUBGENERA		BAT SPECIES	BAT FAMILY	REFERENCE	BAT SUBORDER
Nobecoviruses		*Cynopterus brachyotis*	Pteropodidae	Anthony et al. 2017	Yinpterochiroptera
		Cynopterus horsfieldi	Pteropodidae	Anthony et al. 2017	Yinpterochiroptera
		Cynopterus sphinx	Pteropodidae	Anthony et al. 2017	Yinpterochiroptera
		Dyacopterus spadiceus	Pteropodidae	Anthony et al. 2017	Yinpterochiroptera
		Megaerops niphanae	Pteropodidae	Anthony et al. 2017	Yinpterochiroptera
		Eidolon helvum	Pteropodidae	Anthony et al. 2017	Yinpterochiroptera
		Pteropus alecto	Pteropodidae	Anthony et al. 2017	Yinpterochiroptera
		Pteropus giganteus	Pteropodidae	Anthony et al. 2017	Yinpterochiroptera
		Epomopohorous gambianus	Pteropodidae	Anthony et al. 2017	Yinpterochiroptera
		Epomops franqueti	Pteropodidae	Anthony et al. 2017	Yinpterochiroptera
		Eonycteris spalaea	Pteropodidae	Anthony et al. 2017	Yinpterochiroptera
		Lissonycteris angolensis	Pteropodidae	Anthony et al. 2017	Yinpterochiroptera
		Megaloglossus woermanni	Pteropodidae	Anthony et al. 2017	Yinpterochiroptera
		Micropteropus pusillus	Pteropodidae	Anthony et al. 2017	Yinpterochiroptera
		Rousettus aegyptiacus	Pteropodidae	Anthony et al. 2017	Yinpterochiroptera
		Rousettus amplexicaudatus	Pteropodidae	Anthony et al. 2017	Yinpterochiroptera
		Rousettus leschenaulti	Pteropodidae	Anthony et al. 2017	Yinpterochiroptera
		Hipposideros lekaguli	Hipposideridae	Anthony et al. 2017	Yinpterochiroptera
		Triaenops persicus	Hipposideridae	Anthony et al. 2017	Yinpterochiroptera
		Scotophilus dinganii	Vespertilionidae	Anthony et al. 2017	Yangochiroptera
		Scotophilus leucogaster	Vespertilionidae	Anthony et al. 2017	Yangochiroptera
		Mops condylurus	Molossidae	Anthony et al. 2017	Yangochiroptera

	J	K	L	M	N	O
1						
2	cross-ref					
3	SARS_related_beta_CoV					
4	SARS_related_beta_CoV					
5						
6						
7						
8						
9						
10						
11						
12						
13						
14	SARS_related_betaCoV					
15	Beta_corona_Gabon, Predict_CoV_32, Predict_CoV_43, Predict_CoV_44					
16	Predict_CoV_43					
17						
18	Predict_CoV_51					
19	Predict_CoV_51					
20	BtCoV_hip_KT_Thai					
21	Predict_CoV_22, Predict_CoV_24	put this one in Nobe...see entry in Nobecorviruses				
22						
23	Predict_CoV_20					
24						
25	cross-ref					
26	Predict_CoV_24					
27	Predict_CoV_24					
28	Predict_CoV_24					
29	Phil_Dil1525G2					
30	Predict_CoV_24					
31	Bat_CoV_HKU9, Eidolon_bat_CoV, Kenya_CoV_BtKY56					
32	Betacoronavirus_1, Predict_CoV_67, Predict_CoV_68					
33	Predict_CoV_16, Predict_CoV_17, Betacoronavirus_1					
34	Kenya_CoV_BtKY55, Kenya_CoV_BtKY56					
35	Eidolon_bat_CoV					
36	Bat_CoV_HKU9, Predict_CoV_22					
37	Predict_CoV_30, Predict_CoV_66, Kenya_CoV_BtKY55					
38	Eidolon_bat_CoV, Predict_CoV_2					
39	Kenya_CoV_BtKY55, Kenya_CoV_BtKY56					
40	Bat_CoV_HKU9, Predict_CoV_30, Kenya_CoV_BtKY55, Kenya_CoV_BtKY56, Eidolon_bat_CoV					
41	Bat_CoV_HKU9					
42	Bat_CoV_HKU9					
43	Predict_CoV_22, Predict_CoV_24					
44	Eidolon_bat_CoV					
45	Eidolon_bat_CoV					
46	Kenya_CoV_BtKY56					
47	Predict_CoV_30, Kenya_CoV_BtKY55					

	A	B	C	D	E	F	G	H	I
48	β-CoV SUBGENERA		BAT SPECIES		BAT FAMILY			REFERENCE	BAT SUBORDER
49	*Merbecoviruses*		*Hipposideros armiger*		Hipposideridae			Anthony et al. 2017	Yangochiroptera
50			*Myotis pilosus [ricketti]*		Vespertilionidae			Anthony et al. 2017	Yangochiroptera
51			*Eptesicus isabellinus*		Vespertilionidae			Falcón et al. 2011	Yangochiroptera
52			*Hypsugo savii*		Vespertilionidae			Falcón et al. 2011	Yangochiroptera
53			*Neoromicia zuluensis*		Vespertilionidae			Ithete et al. 2013	Yangochiroptera
54			*Pipistrellus abramus*		Vespertilionidae			Tao and Tong 2019	Yangochiroptera
55			*Pipistrellus coromandra*		Vespertilionidae			Anthony et al. 2017	Yangochiroptera
56			*Pipistrellus hesperidus*		Vespertilionidae			Anthony et al. 2017	Yangochiroptera
57			*Pipistrellus nathusii*		Vespertilionidae			Annan et al. 2013	Yangochiroptera
58			*Pipistrellus pipistrellus*		Vespertilionidae			Anthony et al. 2017	Yangochiroptera
59			*Pipistrellus pygmaeus*		Vespertilionidae			Annan et al. 2013	Yangochiroptera
60			*Tylonycteris pachypus*		Vespertilionidae			Anthony et al. 2017	Yangochiroptera
61			*Vespertilio sinensis [superans]*		Vespertilionidae			Anthony et al. 2017	Yangochiroptera
62			*Ia io*		Vespertilionidae			Anthony et al. 2017	Yangochiroptera
63			*Nyctinomops laticaudatus*		Molossidae			Anthony et al. 2017	Yangochiroptera
64			*Taphozous perforatus*		Emballonuridae			Memish et al. 2013	Yangochiroptera
65			*Nycteris gambiensis*		Nycteridae			Annan et al. 2013	Yangochiroptera
66			*Pteronotus parnelii*		Mormoopidae			Anthony et al. 2017	Yangochiroptera
67			*Pteronotus personatus*		Mormoopidae			Anthony et al. 2017	Yangochiroptera
68			*Artibeus literatus*		Phyllostomidae			Anthony et al. 2017	Yangochiroptera
69			*Artibeus obscurus*		Phyllostomidae			Anthony et al. 2017	Yangochiroptera
70			*Dermaneura phaeotis*		Phyllostomidae			Anthony et al. 2017	Yangochiroptera

	J	K	L	M	N	O
48	cross-ref					
49	Vesper_betaCoV					
50	Predict_CoV_57					
51						
52						
53						
54				á		
55	Predict_CoV_34			ñ		
56	MERS_like_CoV			í		
57						
58	Bat_CoV_HKU5, Predict_CoV_57					
59						
60	Bat_CoV_HKU4					
61	BtVs_betaCoV_SC2013					
62	Vesper_betaCoV					
63	Predict_CoV_9					
64						
65						
66	Predict_CoV_10					
67	Predict_CoV_11					
68	Predict_CoV_11					
69	Predict_CoV_11					
70	Predict_CoV_11					

From: Kevin Olival ecohealthalliance.org>
Sent: Tuesday, April 21, 2020 7:27 AM EDT
To: Kading,Rebekah ; Tigga Kingston
CC: Paul Cryan >
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Thanks Rebekah, thanks Tigga!

Paul and I are revising and will hopefully have a version that includes everyone's feedback soon, by week's end.

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
460 West 34th Street, Suite 1701
New York, NY 10001

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics *and* promote conservation

> On Apr 20, 2020, at 5:27 PM, Kading,Rebekah > wrote:
>
> Hi Paul,
>
> That's very kind of you to offer authorship - its unexpected and very generous of you, but I do appreciate being included! I'm attaching the text with some minor edits/suggests tracked for your consideration. Tigga's comments are great, and I'm glad to hear DeeAnn is involved as well.
>
> Thanks!
> Rebekah
>
> **Rebekah C. Kading, PhD**
> Assistant Professor
> Department of Microbiology Immunology and Pathology
> Colorado State University
> Office:
>
> ---
>
> **From:** Cryan, Paul
> **Sent:** Monday, April 20, 2020 2:04 PM
> **To:** Kingston, Tigga >; Kading,Rebekah >
> **Cc:** ecohealthalliance.org <
> **Subject:** Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats
>
> Hi Rebekah and Tigga,
>
> Thanks for the awesome and quick improvements to the manuscript. I'm assuming you're okay with being co-authors, cause you are now. ☺
>
> I'm working through the comments from everyone now and will get back to you with thoughts about the more strategic and substantive ideas after I've had some time to think about them and catch up with myself.
>
> In the meantime, one easy answer is that I see I created some confusion by citing Tao and Tong for Nyctalus leisleri and Hipposideros pratti in the supplemental table, which were actually reported by Drexler et al. 2010 (attached)...oops, good catch! I'll add country of origin to that table and flesh out the cross-referencing a little better for the next iteration.
>
> And Tigga, thanks for those taxonomy updates! I didn't know about those changes, so thanks for that. DeeAnn is also looking at this and said she'd send a new table of the African pteropodid names, so I'm learning a lot.
>
> Stay tuned and thanks again,
> Paul
>
> Paul Cryan

Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Kingston, Tigga
Sent: Monday, April 20, 2020 11:30 AM
To: Kading,Rebekah Cryan, Paul >
Cc: ecohealthalliance.org
Subject: RE: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

P.S. I looked at the table, and also spotted some things to check in addition to those high-lighted by Rebekah. Perhaps "Region" needs some clarification if it is where the bat was sampled – in the cases below it isn't very representative of the distribution or was impossible

- *Rhinolophus ferrumequinum* is a Eurasian species, just tips into N. Africa
- https://en.wikipedia.org/wiki/Greater_horseshoe_bat

R. sinicus – predominantly Chinese bat -- doesn't get in to Africa
https://en.wikipedia.org/wiki/Chinese_rufous_horseshoe_bat

Taxonomic updates:

FYI *Pteropus giganteus* is no more, it is currently recognized as *P. medius*

Eonycteris spalaea – spelling sp**e**laea

Note that the Hipposiderids have been broken with Rhinonycteridae elevated to family…

family **Rhinonycteridae**. elevated by Foley, *et al*, 2014.[2]
- genus *Cloeotis*
- genus *Brevipalatus*
- genus *Brachipposideros*
- genus *Paratriaenops*
- genus *Rhinonicteris* J.E. Gray, 1847
- genus *Triaenops*

So you might want to update the relevant species.

Best
Tigga

From: Kingston, Tigga
Sent: Monday, April 20, 2020 12:01 PM
To: Kading,Rebekah ; Cryan, Paul >
Cc: ecohealthalliance.org
Subject: RE: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Hi Paul and Kevin

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Hope this helps
Tigga
Xx

From: Kading,Rebekah
Sent: Monday, April 20, 2020 10:40 AM
To: Cryan, Paul >; Kingston, Tigga
Cc: ecohealthalliance.org
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

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More later - thanks again - this is a very nice paper and impressive you put it together so quickly!

Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University
Office:

From: Cryan, Paul >
Sent: Friday, April 17, 2020 11:14 AM
To: Kading,Rebekah >; Kingston, Tigga
Cc: ecohealthalliance.org < >
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Hi Rebekah and Tigga,

Without further adieu, I'm attaching the manuscript draft that Kevin and I put together over the past week and would very much like your input on. Its much leaner and meaner than the rambling draft that went out to the decision-making group last week.

Please take a look if you have the time and consider joining us in trying to get it published somewhere fairly high profile in the coming weeks.

All the best,
Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Kading,Rebekah
Sent: Wednesday, April 15, 2020 8:27 PM
To: Cryan, Paul >; Kingston, Tigga >
Cc: ecohealthalliance.org >
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Oh my goodness Paul! LOL!

Hang in there - you're doing great.

Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University
Office:

From: Cryan, Paul
Sent: Wednesday, April 15, 2020 7:11 PM
To: Kading,Rebekah ; Kingston, Tigga
Cc: ecohealthalliance.org
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Great to know we're on the same path! I'm finding that coordinating and obsessively researching/writing/getting-up-to-speed on a issue are difficult to pull off at the same time!

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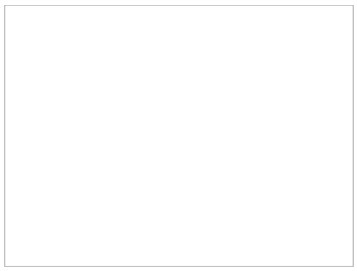

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www.youtube.com

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From: Kading,Rebekah <
Sent: Wednesday, April 15, 2020 8:43 AM
To: Kingston, Tigga ; Cryan, Paul >
Cc: ecohealthalliance.org <
Subject: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

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Take care and talk to you soon -
Rebekah

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From: Kingston, Tigga
Sent: Wednesday, April 15, 2020 7:52 AM
To: Cryan, Paul Kading,Rebekah
Cc: ecohealthalliance.org <
Subject: RE: SARS-CoV-2 spillback risk to North American bats

Hi Paul
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Best wishes
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From: Cryan, Paul
Sent: Tuesday, April 14, 2020 2:16 PM
To: Kingston, Tigga >
Cc: ecohealthalliance.org
Subject: SARS-CoV-2 spillback risk to North American bats

Hi Tigga,

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<Olival et al. bat CoVs 20200417_REVIEW_rck.docx>

From: Kingston, Tigga <
Sent: Monday, April 20, 2020 1:00 PM EDT
To: Kading,Rebekah >; Cryan, Paul
CC: ecohealthalliance.org
Subject: RE: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

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To: Cryan, Paul ; Kingston, Tigga >
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Colorado State University

Office:

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From: Kading,Rebekah
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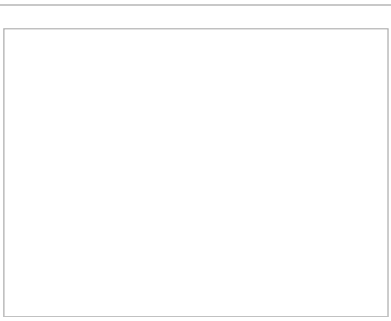

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USGS Fort Collins Science Center

Web Page and Contact Info

From: Coleman, Jeremy T >
Sent: Friday, June 12, 2020 12:12 PM EDT
To: ecohealthalliance.org >; dreeder ; Hume Field >; Charles H Calisher ; Brian R. Amman >; Wang Linfa ; Cryan, Paul Ralph S. Baric ; Blehert, David S Cara Brook < ; Kevin Castle Peter Daszak @ecohealthalliance.org>; epstein ecohealthalliance.org>; wfrick Gilbert, Amy T - APHIS < ; David Hayman >; Ip, Hon S < ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah ; Tigga Kingston >; Lorch, Jeffrey M < ; Ian MENDENHALL PhD alisonpeel >; Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; Reichard, Jonathan D >; Sleeman, Jonathan M >; Daniel Streicker < ; Jonathan S. Towner
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Thanks Kevin

I agree that there's good reason to get the paper out as pre-print. As DeeAnn mentioned, CoV info is coming fast.

Best regards to all,
Jeremy

Jeremy T. H. Coleman, Ph.D.
National White-nose Syndrome Coordinator
Regional Wildlife Disease Biologist
U.S. Fish and Wildlife Service

WHITE-NOSE SYNDROME
RESPONSE TEAM
www.whitenosesyndrome.org

From: Kevin Olival ecohealthalliance
Sent: Friday, June 12, 2020 10:43 AM
To: dreeder ; Hume Field ecohealthalliance.org>; Charles H Calisher >; Brian R. Amman >; Wang Linfa ; Cryan, Paul ; Ralph S. Baric ; Blehert, David S Cara Brook >; Kevin Castle ; Coleman, Jeremy T Peter Daszak ecohealthalliance.org>; Jon Epstein @ecohealthalliance wfrick ; Gilbert, Amy T - APHIS ; David Hayman >; Ip, Hon S >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson >; Kading,Rebekah >; Tigga Kingston ; Lorch, Jeffrey M >; Ian MENDENHALL PhD ; alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina Reichard, Jonathan D Sleeman, Jonathan M ; Daniel Streicker Jonathan S. Towner
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DeeAnn M. Reeder, PhD
Professor
Department of Biology
Bucknell University
Lewisburg, PA 17837

http://deeannreeder.scholar.bucknell.edu

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Thanks for doing the record turn-around! Well done everyone and great leadership Paul and Kevin!
Does anyone have a link to the full CNN documentary? I heard it was great.
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Quick update on our paper — unfortunately got news yesterday that *PNAS* was not interested in this as a Perspectives piece, and rejected our proposal. We are currently pursuing options with editors at *PLOS Pathogens* to see if they want it as a review. Will keep you all posted.

Latest version attached that has cleared CDC and USGS review. We will still aim to get this on BioRxiv, but wanted to wait until we had it cleared first and ideally in review at a journal.

Cheers,
Kevin

<Olival et al. bat CoVs 20200520_v11.3.docx>

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eight Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org
EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

On 12 May 2020, at 10:13 PM, Kevin Olival
ecohealthalliance.org> wrote:

Dear Co-authors,

Attached is the latest, submission ready version of our paper "**Possible risks of SARS-CoV-2 spillover to free-ranging wildlife: a case study of bats**". Thank you all for the last round of invaluable edits and comments. Paul and I have now gone through multiple revisions since you last saw the paper in an attempt to include everyone's feedback; so apologize for the delay in turning this around and moving towards submission.

We started a submission to *Lancet Infectious Diseases*, but after thinking more about the journal's scope and reading other recent reviews that have been published in the journal, Paul and I decided it was not the best fit after all. We instead plan to submit this as a Perspectives article to *PNAS*(https://www.pnas.org/page/authors/purpose-scope). We think *PNAS* is a better fit all around, especially given the US focus of our review. We are currently following up some leads for "sponsorship" of our paper with PNAS which would make it an invited piece. If you have any specific suggestions in this regard, please let me know.

As before, the plan is once we submit (hopefully this week) to *PNAS* we will also post as a pre-print on BioRxiv so it can be viewed and used

immediately. **If there are any objections to this plan or to submit to *PNAS*, please let me know.**
Also, for those that have secured USG approval already, please let me know if these needs to be updated or if you need any more information.

This has been a fantastic exercise in group writing! Big thank you to everyone.

Cheers,
Kevin

<Olival et al. bat CoVs 20200511_V9.1.docx>

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
460 West 34th Street, Suite 1701
New York, NY 10001

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--
DeeAnn M. Reeder, PhD
Professor
Department of Biology
Bucknell University
Lewisburg, PA 17837

http://deeannreeder.scholar.bucknell.edu

Important: This email is confidential and may be privileged. If you are not the intended recipient, please delete it and notify us immediately; you should not copy or use it for any purpose, nor disclose its contents to any other person. Thank you.

From: Coleman, Jeremy T
Sent: Tuesday, May 12, 2020 11:22 AM EDT
To: dreeder ; Baric, Ralph S
CC: Kevin Castle ecohealthalliance.org ; Cryan, Paul ; Brian R. Amman >; Blehert, David S < Cara Brook ; Charles H Calisher ; Peter Daszak ecohealthalliance.org>; epstein ecohealthalliance.org>; Hume Field ecohealthalliance.org>; wfrick >; Gilbert, Amy T - APHIS ; David Hayman ; Ip, Hon S ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson >; Kading,Rebekah ; Tigga Kingston < Lorch, Jeffrey M ; Ian MENDENHALL PhD >; alisonpeel < ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina >; Reichard, Jonathan D ; Sleeman, Jonathan M >; Daniel Streicker ; Jonathan S. Towner >; Wang Linfa >
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PNAS (new plan)

Thanks Kevin and Paul, and nicely done. PNAS sounds good to me.

_____
Jeremy T. H. Coleman, Ph.D.
National White-nose Syndrome Coordinator
Regional Wildlife Disease Biologist
U.S. Fish and Wildlife Service

WHITE-NOSE SYNDROME
RESPONSE TEAM
www.whitenosesyndrome.org

From: DeeAnn Reeder >
Sent: Tuesday, May 12, 2020 10:49 AM
To: Baric, Ralph S
Cc: Kevin Castle ; ecohealthalliance.org ; Cryan, Paul >; Brian R. Amman >; Blehert, David S ; Cara Brook >; Charles H Calisher < ; Coleman, Jeremy T Peter Daszak ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Hume Field ecohealthalliance.org>; wfrick ; Gilbert, Amy T - APHIS ; David Hayman >; Ip, Hon S >; William Karesh < ecohealthalliance.org>; Christine Kreuder Johnson >; Kading,Rebekah Tigga Kingston ; Lorch, Jeffrey M ; Ian MENDENHALL PhD alisonpeel Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; Reichard, Jonathan D Sleeman, Jonathan M ; Daniel Streicker ; Jonathan S. Towner Wang Linfa

Subject: [EXTERNAL] Re: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PNAS (new plan)

Agreed!

On Tue, May 12, 2020 at 10:40 AM Baric, Ralph S wrote:

> PNAS is a good place!
>
> **From:** Kevin Castle
> **Sent:** Tuesday, May 12, 2020 10:22 AM
> **To:** Kevin Olival ecohealthalliance.org>
> **Cc:** Paul Cryan >; Brian R. Amman < >; Baric, Ralph S ; David S Blehert ; Cara Brook ; Charles H Calisher Jeremy Coleman ; Peter Daszak ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Hume Field ecohealthalliance.org>; Winifred F Frick, Ph.D.

>; Gilbert, Amy T - APHIS < >; David Hayman ; Hon S Ip < ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson < Kading,Rebekah ; Tigga Kingston >; Lorch, Jeffrey M >; Ian MENDENHALL PhD >; alisonpeel Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; DeeAnn Reeder < ; Jonathan D Reichard >; Jonathan M Sleeman ; Daniel Streicker Jonathan S. Towner Wang Linfa
Subject: Re: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PNAS (new plan)

Thanks Kevin and Paul, et al.!
K

On Tue, May 12, 2020 at 8:13 AM Kevin Olival ecohealthalliance.org> wrote:

> Dear Co-authors,
>
> **Attached is the latest, submission ready version of our paper**"**Possible risks of SARS-CoV-2 spillover to free-ranging wildlife: a case study of bats**". Thank you all for the last round of invaluable edits and comments. Paul and I have now gone through multiple revisions since you last saw the paper in an attempt to include everyone's feedback; so apologize for the delay in turning this around and moving towards submission.
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> Cheers,
> Kevin
>
> **Kevin J. Olival, PhD**
> *Vice President for Research*
>
> EcoHealth Alliance
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> New York, NY 10001
>
> www.ecohealthalliance.org
> EcoHealth Alliance develops science-based solutions to prevent pandemics *and* promote conservation

--
Kevin T. Castle, DVM, MS
Wildlife Veterinary Consulting, LLC
840 Sundance Dr.
Livermore, CO 80536

--
DeeAnn M. Reeder, PhD
Professor
Department of Biology
Bucknell University

Lewisburg, PA 17837

http://deeannreeder.scholar.bucknell.edu

From: Cryan, Paul
Sent: Thursday, September 13, 2018 11:35 AM EDT
To: Megan Hudson >
CC: Jon Epstein ecohealthalliance.org>; Kading,Rebekah ; Vivek Kapur >; Kingston, Tigga ; Kevin Olival ecohealthalliance.org>; raina.plowright Catalino Demetria ; Stokes, Martha M CIV (US) >; Katie Leahy >; Aleman, Nicki D CTR DTRA J3-7 (US) ; Becker, Stephen M CTR DTRA J3-7 (US)

Subject: Re: [EXTERNAL] Reminder: BOHRN November IMED Meeting Invitation
Attachment(s): "image001.png","image002.png","image002.png"

Hi Megan,

Regrettably, I'm not going to be able to make it to Austria for the BOHRN meeting. A couple of research projects I'm overseeing are bleeding into the late autumn and early winter here in Colorado and I need to stay put to keep them on track. Please keep me in the loop and let me know if there ways I can somehow help or participate remotely.

Thanks,
Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info
ORCID

On Mon, Sep 10, 2018 at 7:45 AM Megan Hudson > wrote:

> All,
>
> As a reminder, please respond NLT **14 September** if you are able to attend the BOHRN/IMED Meeting in Vienna on 8-12 November 2018. The BOHRN meeting will be held 8-9 November.
>
> We are looking for nominations to grow the BOHRN network, please send any nominations of subject matter experts or other participants who would be beneficial to this discussion **no later than Today, 10 September 2018**.
>
> IMED will take place 9 – 12 November at the Hilton Vienna. The 2018 IMED will focus on innovation and changes in political and societal responses to outbreaks. The theme of IMED aligns with our overall BOHRN objectives and we encourage all BOHRN members to stay and participant in the conference.
>
> **We need you to confirm your attendance to BOHRN and IMED NLT 14 September.**
>
> v/r,
>
> Megan
>
> **Megan Hudson**
>
> *Task Lead* | Global Systems Engineering
>
> 6303 Little River Turnpike #208
>
> Alexandria, VA 22312
>
> http://globalsyseng.com

Travel instructions:

Please contact Nicki Alemar **NLT 14 September 2018** if you intend to travel; you will likely need to provide her with your passport information, to and from destinations, and travel dates. CBEP's logistics support coordinators will work with you to secure plane reservations. Please note that they try to work with your preferences, but must remain within the boundaries of the Department of Defense regulations for travel.

From: Megan Hudson
Date: Thursday, September 6, 2018 at 10:54
To: "cryanp " >, ecohealthalliance.org" , "rebekah.kading " , "vkapur >, "tigga.kingston " < >, @ecohealthalliance.org" , "dreeder , "raina.plowright " "ian.mendenhall " , "c_demetria " <c_demetria
Cc: "Stokes, Martha M CIV (US)" Katie Leahy >, "Aleman, Nicki D CTR DTRA PARTNERSHIP AND INSP (US)" <nicki.d.aleman , "Becker, Stephen M CTR DTRA J3-7 (US)"
Subject: BOHRN November IMED Meeting Invitation

All,

On behalf of Dr. Marty Stokes you are receiving this email, as part of a save the date to attend our BOHRN Steering Committee meeting and International Meeting on Emerging Diseases and Surveillance (IMED) 8 – 12 November 2018 in Vienna, Austria.

Our meeting will take place on 8 – 9 November (hotel/meeting location TBD). The BOHRN steering committee meeting will aim to meet the objectives the group identified in Saskatoon. The following objectives were suggested based on your survey responses:

1. Prioritizes funding needs based on working groups' characterization of gaps and needs, to help organize and develop funding initiatives; and
2. Analyze progress of action plans and their yields establishing collaborate and sustainable projects

To facilitate these objectives, we will be asking each working group to present their progress. The progress updates for each working group are imperative to the outcomes for this meeting.

As discussed during the June BOHRN meeting, an objective of this meeting is to develop our outreach and populate working groups. Please send any nominations of subject matter experts or other participants who would be beneficial to this discussion **no later than 10 September 2018**.

IMED will take place 9 – 12 November at the Hilton Vienna. The 2018 IMED will focus on innovation and changes in political and societal responses to outbreaks. The theme of IMED aligns with our overall BOHRN objectives and we encourage all BOHRN

members to stay and participant in the conference. **Therefore, we need you to confirm your attendance to BOHRN and IMED NLT 14 September.**

v/r,

Megan

Megan Hudson

Task Lead | Global Systems Engineering

6303 Little River Turnpike #208

Alexandria, VA 22312

http://globalsyseng.com

Travel instructions:

Please contact Nicki Alemar **NLT 14 September 2018** if you intend to travel; you will likely need to provide her with your passport information, to and from destinations, and travel dates. CBEP's logistics support coordinators will work with you to secure plane reservations. Please note that they try to work with your preferences, but must remain within the boundaries of the Department of Defense regulations for travel.

From: Kevin Olival cohealthalliance.org>
Sent: Tuesday, June 16, 2020 11:31 AM EDT
To: Kendra Phelps ecohealthalliance.org>; Raina Plowright < ; Paul Cryan >; Wang Linfa dreedel ; Hume Field ecohealthalliance.org>; Charles H Calisher Brian R. Amman Ralph S. Baric >; David S Blehert ; Cara Brook >; Kevin Castle Jeremy Coleman < ; Peter Daszak ecohealthalliance.org>; epstein ecohealthalliance.org>; wtrick Gilbert, Amy T - APHIS >; David Hayman >; Hon S Ip ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah >; Tigga Kingston Lorch, Jeffrey M < Ian MENDENHALL PhD alisonpee >; Jonathan D Reichard >; Jonathan M Sleeman >; Daniel Streicker ; Jonathan S. Towner
Subject: Re: [EXTERNAL] SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Most memorable line from the whole CNN piece: Dan Riskin describing how awesome mother bats are using the analogy of "attaching a jumper cable to his nipple with a 50 pound weight and going for a jog". :-) Seriously though, I think they did a great job balancing the conservation and disease messaging, and great to see so many of our coauthors featured! Kudos to Peter, Jon, Cara, Ralph, and Linfa…

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

> On Jun 16, 2020, at 10:59 AM, Kendra Phelps ecohealthalliance.org> wrote:
>
> Agreed, great job Kevin and Paul for the quick turnaround.
>
> The CNN special can be viewed on www.cnn.com/go, click on "Shows" to the left-side of the screen and the special should be an option at the top of the screen (or one scroll to the right). I think you need a cable subscription to log-in to view though.
>
> Cheers,
> Kendra
>
> **Kendra Phelps, PhD**
> *Research Scientist*
>
> EcoHealth Alliance
> 520 Eighth Avenue, Ste. 1200
> New York, NY 10018
>
> www.ecohealthalliance.org
>
> ***EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.***
>
> > On Jun 16, 2020, at 10:48 AM, Raina Plowright wrote:
> >
> > Thanks for doing the record turn-around! Well done everyone and great leadership Paul and Kevin!
> > Does anyone have a link to the full CNN documentary? I heard it was great.
> > Raina
> >
> > > On Jun 16, 2020, at 8:40 AM, Cryan, Paul > wrote:
> > >
> > > That was one of those unforgettable moments for me watching many of you on the CNN special...in my opinion you all came off very well! Congrats!
> > >
> > > Paul
> > >
> > > Paul Cryan
> > > Research Biologist
> > > USGS Fort Collins Science Center
> > >
> > > Web Page and Contact Info
> > >
> > > ---
> > >
> > > **From:** Wang Linfa
> > > **Sent:** Monday, June 15, 2020 11:22 PM
> > > **To:** ecohealthalliance.org ; dreedel Hume Field ecohealthalliance.org>; Charles H Calisher ; Kevin Castle Coleman, Jeremy T Peter Daszak ecohealthalliance.org>; Jon Epstein @ecohealthalliance.org>; wtrick < Gilbert, Amy T - APHIS ; David Hayman >; Ip, Hon S William Karesh ecohealthalliance.org>; Christine Kreuder Johnson
> > >
> > > alisonpeel Kendra Phelps ecohealthalliance.org>; Plowright, Raina Reichard, Jonathan D ; Sleeman, Jonathan M Daniel Streicker Jonathan S. Towner
> > >
> > > **Cc:** Cryan, Paul
> > > **Subject:** [EXTERNAL] RE: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)
> > >
> > > Thanks Kevin and Paul for doing a great job so quickly.
> > >
> > > I guess the CNN documentary yesterday also made this a hot (hotter) topic now and the editor may want to have "a ride on the bat wings" to get it out asap!
> > >
> > > Fingers crossed.
> > >
> > > LF
> > >
> > > ***Linfa (Lin-Fa) WANG, PhD FTSE***
> > > **Professor & Director**
> > > **Programme in Emerging Infectious Disease**
> > > **Duke-NUS Medical School,**
> > > **8 College Road, Singapore 169857**
> > >
> > > ---
> > >
> > > **From:** Kevin Olival ecohealthalliance.org>
> > > **Sent:** Tuesday, 16 June 2020 1:19 PM
> > > **To:** DeeAnn Reeder >; Hume Field ecohealthalliance.org>; Charles H Calisher < Brian R. Amman ; Wang Linfa < ; Ralph S. Baric ; David S Blehert ; Cara Brook

Kevin Castle >; Jeremy Coleman >; Peter Daszak ecohealthalliance.org>; Jon Epstein @ecohealthalliance.org>; Winifred F Frick, Ph.D. < ; Gilbert, Amy T - APHIS David Hayman Hon S Ip >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson >; Kading,Rebekah >; Tigga Kingston < >; Lorch, Jeffrey M ; Ian Mendenhall alisonpee ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina >; Jonathan D Reichard ; Jonathan M Sleeman >; Daniel Streicker < >; Jonathan S. Towner <

Cc: Paul Cryan
Subject: Re: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

- External Email -

Hi Team,

Funny thing, bioRxiv actually rejected us! Apparently they don't take "reviews".

In any case we got **very positive reviews back from *PLoS Pathogens*** today, and the revised ms was just resubmitted (<24 hour turnaround). Woohooo! Finger's crossed that the editors turn it around again quickly and we can see this published soon.

Attached is the cover letter, response to reviewers, and the resubmitted version of ms.

Cheers,
Kevin and Paul

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org
EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

On Jun 12, 2020, at 10:43 AM, Kevin Oliva ecohealthalliance.org> wrote:

Dear all,

We successfully submitted to bioRxiv yesterday and it's currently in "review" with the editorial staff and should be posted within 48 hours. Big thanks to Paul for getting the final USGS approvals and ms formatting in place.

Hume and Charlie, I understand your very valid and "traditional" concerns here, there's a lot of riff-raff out there on pre-print servers and hence why we have the peer-review system. Nonetheless, given that there are other similar reviews being posted at the moment and the timeliness of this given the USGS/USFW Risk Assessment out last week, etc., would be best to get this out there while we're still in review at PLOS.

Best,
Kevin

Kevin J. Olival, PhD
Vice President for Research

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520 Eighth Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org
EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

On Jun 12, 2020, at 8:24 AM, DeeAnn Reeder > wrote:

Thanks all - I am in support of bioRxrv for this paper (although I don't systematically use it - in this fast moving CoV environment, for some papers I think it is a very good option).

Cheers - DeeAnn

On Thu, Jun 11, 2020 at 7:22 PM Hume Fielc ecohealthalliance.org> wrote:

> Thanks Kevin.. no prob, tho philosophically I'm with Charlie!
>
> Hume
>
> On Fri., 12 Jun. 2020, 1:23 am , wrote:
>
> > No significant objections about the manuscript but I am not crazy about pre-print servers or their purpose. I am not only old, I am a traditionalist. Lots of crap being sent out as pre-print servers that wind up not being acceptable – or withdrawn.
> >
> > Charlie
> >
> > ---
> > **From:** Amman, Brian R. (CDC/DDID/NCEZID/DHCPP)
> > **Sent:** Thursday, June 11, 2020 8:05 AM
> > **To:** Kevin Olival ecohealthalliance.org>; Wang Linfa < ; Paul Cryan Ralph S. Baric >; David S Blehert >; Cara Brook >; Charles H Calisher >; Kevin Castle <ce >; Jeremy Coleman >; Peter Daszak ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Hume Field ecohealthalliance.org>; Winifred F Frick, Ph.D. ; Gilbert, Amy T - APHIS >; David Hayman >; Hon S Ip >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson >; Kading,Rebekah ; Tigga Kingston >; Lorch, Jeffrey M ; Ian MENDENHALL PhD ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina >; DeeAnn Reeder ; Jonathan D Reichard ; Jonathan M Sleeman < Daniel Streicker < >; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)
> >
> > **Subject:** RE: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)
> >
> > Thanks Kevin!
> >
> > ---
> > **From:** Kevin Olival @ecohealthalliance.org>
> > **Sent:** Thursday, June 11, 2020 9:43 AM
> > **To:** Wang Linfa ; Paul Cryan < ; Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) ; Ralph S. Baric David S Blehert >; Cara Brook < u>; Charles H Calisher < >; Kevin Castle Jeremy Coleman ; Peter Daszak ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Hume Field cohealthalliance.org>; Winifred F Frick, Ph.D. >; Gilbert, Amy T - APHIS < ; David Hayman ; Hon S Ip >; William Karesh @ecohealthalliance.org>; Christine Kreuder Johnson < ; Kading,Rebekah

Tigga Kingston Lorch, Jeffrey M ; Ian MENDENHALL PhD >;alisonpee ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina DeeAnn Reeder >; Jonathan D Reichard >; Jonathan M Sleeman Daniel Streicker >; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)

Subject: Re: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Dear all,

Update on our ms. It was submitted to PLOS Pathogens on June 2nd (you should have all received an email from the journal confirming this) and it is currently under review.

We are in the final stages of USGS approval to also submit to bioRxiv (pre-print server), and expect to finalize that and post it on bioRxiv in the next 24 hours. *Please let me know if there are any objections.*

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

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520 Eight Avenue, Suite 1201
New York, NY 10018

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EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

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> Hi Folks,
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> Quick update on our paper — unfortunately got news yesterday that *PNAS* was not interested in this as a Perspectives piece, and rejected our proposal. We are currently pursuing options with editors at *PLOS Pathogens* to see if they want it as a review. Will keep you all posted.
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> Latest version attached that has cleared CDC and USGS review. We will still aim to get this on BioRxiv, but wanted to wait until we had it cleared first and ideally in review at a journal.
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> Cheers,
> Kevin
>
> <Olival et al. bat CoVs 20200520_v11.3.docx>
>
> **Kevin J. Olival, PhD**
> *Vice President for Research*
>
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> > **Kevin J. Olival, PhD**
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--
DeeAnn M. Reeder, PhD
Professor
Department of Biology
Bucknell University
Lewisburg, PA 17837

http://deeannreeder.scholar.bucknell.edu

From: Cara Brook
Sent: Tuesday, June 16, 2020 2:16 PM EDT
To: Christine Kreuder Johnson
CC: Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Raina Plowright >; Paul Cryan ; Wang Linfa dreedel Hume Field ecohealthalliance.org>; Charles H Calisher Brian R. Amman >; Ralph S. Baric >; David S Blehert ; Kevin Castle < ; Jeremy Coleman < ; Peter Daszak cohealthalliance.org>; epstein ecohealthalliance.org>; wfrick Gilbert, Amy T - APHIS >; David Hayman >; Hon S Ip ; William Karesh @ecohealthalliance.org>; Kading,Rebekah Tigga Kingston >; Lorch, Jeffrey M Ian MENDENHALL PhD alisonpeel Jonathan D Reichard >; Jonathan M Sleeman Daniel Streicker ; Jonathan S. Towner
Subject: Re: [EXTERNAL] SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Agreed on all the kudos! Thanks to Kevin and Paul for pulling this together and including us all!

Cheers,
Cara

—
Cara E. Brook
Miller Postdoctoral Fellow
Department of Integrative Biology
University of California, Berkeley
carabrook.github.io

On Tue, Jun 16, 2020 at 10:36 AM Christine Kreuder Johnson wrote:

> That analogy was the best; bat mothers rock!
>
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Department of Biology
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Lewisburg, PA 17837

http://deeannreeder.scholar.bucknell.edu

Important: This email is confidential and may be privileged. If you are not the intended recipient, please delete it and notify us immediately; you should not copy or use it for any purpose, nor disclose its contents to any other person. Thank you.

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Professor
Department of Biology
Bucknell University
Lewisburg, PA 17837

http://deeannreeder.scholar.bucknell.edu

Important: This email is confidential and may be privileged. If you are not the intended recipient, please delete it and notify us immediately; you should not copy or use it for any purpose, nor disclose its contents to any other person. Thank you.

From: Kendra Phelps ecohealthalliance.org>
Sent: Tuesday, June 16, 2020 10:59 AM EDT
To: Raina Plowright
CC: Paul Cryan >; Wang Linfa >; ecohealthalliance.org >; dreedel ; Hume Field ecohealthalliance.org>; Charles H Calisher >; Brian R. Amman Ralph S. Baric ; Blehert, David S ; Cara Brook >; Kevin Castle >; Coleman, Jeremy T >; Peter Daszak ecohealthalliance.org>; epstein ecohealthalliance.org>; wfrick Gilbert, Amy T - APHIS >; David Hayman ; Ip, Hon S >; William B. Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah >; Tigga Kingston Lorch, Jeffrey M ; Ian Mendenhall ; alisonpee ; Reichard, Jonathan D >; Sleeman, Jonathan M ; Daniel Streicker Jonathan S. Towner
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Cheers,
Kendra

Kendra Phelps, PhD
Research Scientist

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200
New York, NY 10018

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

On Jun 16, 2020, at 10:48 AM, Raina Plowright wrote:

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Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

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Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
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Tel:

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Hi Folks,

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Latest version attached that has cleared CDC and USGS review. We will still aim to get this on BioRxiv, but wanted to wait until we had it cleared first and ideally in review at a journal.

Cheers,
Kevin

<Olival et al. bat CoVs 20200520_v11.3.docx>

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This has been a fantastic exercise in group writing! Big thank you to everyone.

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Ditto here! Thanks for turning this around so quickly - nice to get such positive feedback from the reviewers!

Ditto also on the CNN special - which was really put together well! I was tickled that they included my "panda bat" - one of you must have turned them on to this lovely beastie!

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From: Kingston, Tigga
Sent: Wednesday, August 26, 2020 6:13 PM EDT
To: Guzal Masharipova >; martha.m.stokes.civ < ; Kading,Rebekah >; Katie Leahy >
CC: jamechia.d.hoyle.ctr >; epstein ecohealthalliance.org>
Subject: RE: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

Hi Guzal,
Thanks for clarifying the password situation (I was only going partially mad then -- possible I never had that password, rather than I'd forgotten it (more often the case)).
Yes let's get rid of the login feature for now, and meet Friday 10 CT. I'd prefer Zoom as I've not yet used MS Teams. I imagine this will be mostly a "scoping" meeting, with practical changes to follow.

Best wishes
Tigga

-----Original Message-----
From: Guzal Masharipova
Sent: Wednesday, August 26, 2020 5:42 PM
To: Kingston, Tigga ; martha.m.stokes.civ >; Kading,Rebekah ; Katie Leahy

Cc: jamechia.d.hoyle. >; epstein ecohealthalliance.org>
Subject: Re: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

Hi Tigga,

We're behind the scenes right now talking to Squarespace, and there were never any profiles created with usernames/passwords. Whenever you see a "login" button on the website, it leads you to a page with a single password entry space - this was a universal password that we set to hide some pages so only certain people could access them. An outcome of Phuket was to add an interactive map and chat feature that would need assigned logins / passwords to protect the information – but we were not able to get approvals to move forward with that next phase. This is still a likely objective for the network. However, since those pages are as of now blank, I suggest we get rid of the "login" feature altogether to get rid of the confusion.

If you wanted to update website content/bios/pages, I am happy to offer the Squarespace administrative login info that lets you change/make edits to the entire website. It's pretty intuitive, but I'll be available to make those changes for you or provide tech support if you wanted to go in yourself. We can also do a screen-sharing scenario during our call and I can live edit - I am flexible. __

Friday 10 - noon CT / 11 - 1 EST works with me. Does a Teams call invitation work or do you prefer Zoom?

Thank you,
GUZAL MASHARIPOVA | Task Lead
Global Systems Engineering, LLC

On 8/26/20, 3:39 PM, "Kingston, Tigga" < wrote:

Dear Guzal
That's great to hear!

Most immediate -- I've forgotten my login password and there's no way to reset, and I'd like to be able to get behind the login. Is it possible to reset my password behind the scenes and send me a new one? I think Rebekah will need one too.

Rebekah and I plan to meet tomorrow, and then think it would be helpful to talk with you virtually on Friday or Monday, if you have the time. Our current options are
Friday -- 10-noon CT
Monday 10-11 CT.

But we can try and free up other slots if those don't work.

Best wishes
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-----Original Message-----
From: Guzal Masharipova >
Sent: Wednesday, August 26, 2020 1:10 PM
To: martha.m.stokes. ; Kading,Rebekah < ; Katie Leahy ; Kingston, Tigga

. < ; epstein ecohealthalliance.org>
Subject: Re: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

Hi everyone,

I now have the administrative rights for the BOHRN website from Squarespace. I apologize about the delay; it was a little confusing because of the login requirement on the landing page. This was initially installed because we intended to add geographic information of BOHRN members that we didn't want the public to have access to without permission. However, that information was never set up so we may want to consider removing the login feature of the website altogether.

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I look forward to helping out.

Best regards,
GUZAL MASHARIPOVA | Task Lead
Global Systems Engineering, LLC

On 8/26/20, 10:50 AM, "Stokes, Martha M CIV (USA)" wrote:

Hi Rebekah,

Thanks so much!

Best,
Marty

-----Original Message-----

From: Kading,Rebekah >
Sent: Wednesday, August 26, 2020 10:45 AM
To: Stokes, Martha M CIV (USA) ; Katie Leahy ; Kingston, Tigga
Cc: Hoyle, Jamechia D CTR (USA) Guzal Mashar ipova epstein ecohealthalliance.org>
Subject: Re: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

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Rebekah

Rebekah C. Kading, PhD

Assistant Professor

Department of Microbiology Immunology and Pathology

Colorado State University

Office:

From: Stokes, Martha M CIV (USA) >
Sent: Wednesday, August 26, 2020 8:26 AM
To: Kading,Rebekah Katie Leahy ; Kingston, Tigga >
Cc: Hoyle, Jamechia ecohealthalliance.org>
Subject: RE: [Non-DoD Source] Re. [External Sender] RE: BOHRN Status, publication

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Subject: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

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Global Systems Engineering, LLC

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>

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From: "Kingston, Tigga"
Date: Tuesday, August 25, 2020 at 1:51 PM
To: "martha.m.stokes " >
Cc: Katie Leahy , jamechia.d.hoyle >, Guzal Masharipova ,
"Kading,Rebekah" pstein econ ch
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Marty

Martha M Stokes, PhD

Southeast Asia Regional Science Manager

Biological Threat Reduction Program (BTRP)

From: "Kingston, Tigga"

Date: Monday, August 24, 2020 at 5:09 PM

To: "martha.m.stokes

Cc: Katie Leahy , "jamechia.d.hoyle. < <
Guzal Masharipova <
>, "Kading,Rebekah" < > >, Jon Epstein

Subject: [External Sender] BOHRN Status, publication

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All the best

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From: Kingston, Tigga
Sent: Wednesday, August 26, 2020 3:39 PM EDT
To: Guzal Masharipova ; martha.m.stokes < >; Kading,Rebekah >; Katie Leahy

CC: jamechia.d.hoyle epstein
Subject: RE: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

Dear Guzal
That's great to hear!

Most immediate -- I've forgotten my login password and there's no way to reset, and I'd like to be able to get behind the login. Is it possible to reset my password behind the scenes and send me a new one? I think Rebekah will need one too.

Rebekah and I plan to meet tomorrow, and then think it would be helpful to talk with you virtually on Friday or Monday, if you have the time. Our current options are
Friday -- 10-noon CT
Monday 10-11 CT.

But we can try and free up other slots if those don't work.

Best wishes
Tigga

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From: Guzal Masharipova >
Sent: Wednesday, August 26, 2020 1:16 PM
To: martha.m.stokes >; Kading,Rebekah ; Katie Leahy < Kingston, Tigga >
Cc: jamechia.d.hoyle. ; epstein ecohealthalliance.org>
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Subject: Re: [Non-DoD Source] Re tatus, publication

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epstein @ecohealt il
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Southeast Asia Regional Science Manager

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Thanks so much!

Best,

Marty

Martha M Stokes, PhD

Southeast Asia Regional Science Manager

Biological Threat Reduction Program (BTRP)

From: "Kingston, Tigga" >

Date: Monday, August 24, 2020 at 5:09 PM

To: "martha.m.stokes > >

Cc: Katie Leahy > >, "jamechia.d.hoyle.
: >, Guzal Masharipova < >,
Kading,Rebekah > >, Jon Epstein ecohealthalliance.org < caution-
mailto: ec

Subject: [External Sender] BOHRN Status, publication

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All the best

Tigga

From: Kingston, Tigga
Sent: Wednesday, August 26, 2020 10:47 AM EDT
To: Kading,Rebekah < >; Stokes, Martha M CIV (USA) I>; Katie Leahy >
CC: Hoyle, Jamechia D CTR (USA) Guzal Masharipova ; epstein < ecohealthalliance.org>
Subject: RE: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

Hi Everyone
Guzal, do please let us know when you are comfortable with the website. Great to have your support.
Best
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Assistant Professor

Department of Microbiology Immunology and Pathology

Colorado State University

Office:

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KATIE LEAHY | Director, Science Engagement

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From: Guzal Masharipova >
Sent: Wednesday, August 26, 2020 4:42 PM EDT
To: Kingston, Tigga < ; martha.m.stokes.civ ; Kading,Rebekah >; Katie Leahy

CC: jamechia.d.hoyle.ctr epstein ecohealthalliance.org>
Subject: Re: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

Hi Tigga,

We're behind the scenes right now talking to Squarespace, and there were never any profiles created with usernames/passwords. Whenever you see a "login" button on the website, it leads you to a page with a single password entry space - this was a universal password that we set to hide some pages so only certain people could access them. An outcome of Phuket was to add an interactive map and chat feature that would need assigned logins / passwords to protect the information – but we were not able to get approvals to move forward with that next phase. This is still a likely objective for the network. However, since those pages are as of now blank, I suggest we get rid of the "login" feature altogether to get rid of the confusion.

If you wanted to update website content/bios/pages, I am happy to offer the Squarespace administrative login info that lets you change/make edits to the entire website. It's pretty intuitive, but I'll be available to make those changes for you or provide tech support if you wanted to go in yourself. We can also do a screen-sharing scenario during our call and I can live edit - I am flexible. __

Friday 10 - noon CT / 11 - 1 EST works with me. Does a Teams call invitation work or do you prefer Zoom?

Thank you,
GUZAL MASHARIPOVA | Task Lead
Global Systems Engineering, LLC
A Certified HUBZone Company

On 8/26/20, 3:39 PM, "Kingston, Tigga" wrote:

Dear Guzal
That's great to hear!

Most immediate -- I've forgotten my login password and there's no way to reset, and I'd like to be able to get behind the login. Is it possible to reset my password behind the scenes and send me a new one? I think Rebekah will need one too.

Rebekah and I plan to meet tomorrow, and then think it would be helpful to talk with you virtually on Friday or Monday, if you have the time. Our current options are
Friday -- 10-noon CT
Monday 10-11 CT.

But we can try and free up other slots if those don't work.

Best wishes
Tigga

-----Original Message-----
From: Guzal Masharipova >
Sent: Wednesday, August 2
To: martha.m.stokes.civ >; Kading,Rebekah Katie Leahy >; Kingston, Tigga
Cc: jamechia.d.hoyle.ctr >; epstein ecohealthalliance.org>
Subject: Re: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

Hi everyone,

I now have the administrative rights for the BOHRN website from Squarespace. I apologize about the delay; it was a little confusing because of the login requirement on the landing page. This was initially installed because we intended to add geographic information of BOHRN members that we didn't want the public to have access to without permission. However, that information was never set up so we may want to consider removing the login feature of the website altogether.

Please let me know how you'd like to proceed - I'm happy to make changes based on updates you send me over email or I can set up a virtual meeting for us as well.

I look forward to helping out.

Best regards,
GUZAL MASHARIPOVA | Task Lead
Global Systems Engineering, LLC

On 8/26/20, 10:50 AM, "Stokes, Martha M CIV (USA)" < wrote:

Hi Rebekah,

Thanks so much!

Best,
Marty

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From: Kading,Rebekah <
Sent: Wednesday, August 26, 2020 10:45 AM
To: Stokes, Martha M CIV (USA) ; Katie Leahy ; Kingston, Tigga
Cc: Hoyle, Jamechia D CTR (USA) Guzal Masharipova ; epstein ecohealthalliance.org>
Subject: Re: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

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Assistant Professor

Department of Microbiology Immunology and Pathology

Colorado State University

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To: Kingston, Tigga ; martha.m.stokes.civ >
Cc: jamechia.d.hoyle Guzal Masharipova ; Kading,Rebekah epstein ecohealthalliance.org>
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Subject: Re: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

Hi everyone,

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To: Kading,Rebekah >; Guzal Masharipova < >; martha.m.stokes.civ ; Katie Leahy >
Cc: jamechia.d.hoyle.ctr ; epstein ecohealthalliance.org>
Subject: RE: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

Yep me too

From: Kading,Rebekah >
Sent: Thursday, August 27, 2020 9:25 AM
To: Guzal Masharipova >; Kingston, Tigga < ; martha.m.stokes.civ < >; Katie Leahy <
Cc: jamechia.d.hoyle ; epstein ecohealthalliance.org>
Subject: Re: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

Got it - talk to you all then!
Rebekah

Rebekah C. Kading, PhD

Assistant Professor

Department of Microbiology Immunology and Pathology

Colorado State University

From: Guzal Masharipova < >
Sent: Wednesday, August 26, 2020 9:41 PM
To: Kading,Rebekah >; Kingston, Tigga >; martha.m.stokes Katie Leahy <
Cc: jamechia.d.hoyle epstein ecohealthalliance.org>
Subject: Re: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

GSE is inviting you to a scheduled Zoom meeting.

Topic: BOHRN Website Sync
Time: Aug 28, 2020 11:00 AM Eastern Time (US and Canada)

Join Zoom Meeting
https://us02web.zoom.us/j/82783798548

Meeting ID: 827 8379 8548
One tap mobile
+13017158592,,82783798548# US (Germantown)
+13126266799,,82783798548# US (Chicago)

Dial by your location
+1 301 715 8592 US (Germantown)
+1 312 626 6799 US (Chicago)
+1 646 876 9923 US (New York)
+1 253 215 8782 US (Tacoma)
+1 346 248 7799 US (Houston)
+1 408 638 0968 US (San Jose)
+1 669 900 6833 US (San Jose)
Meeting ID: 827 8379 8548
Find your local number: https://us02web.zoom.us/u/kcdoc3Cg7Q

GUZAL MASHARIPOVA | ***Task Lead***
Global Systems Engineering, LLC
A Certified HUBZone Company
www.globalsyseng.com
(571) 355-4706

GLOBAL SYSTEMS ENGINEERING

85 S. Bragg Street, Suite 300 | Alexandria, VA 22312

From: "Kading,Rebekah"
Date: Wednesday, August 26, 2020 at 10:30 PM
To: "Kingston, Tigga" < Guzal Masharipova martha.m.stokes.civ" >, Katie Leahy >
Cc: "jamechia.d.hoyle.ctr" , epstein ecohealthalliance.org>
Subject: Re: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

Thank you Guzal! Friday at 10am Central on Zoom works for me too. Looking forward to the discussion, and thank you again for your help!
Best,
Rebekah

Rebekah C. Kading, PhD

Assistant Professor

Department of Microbiology Immunology and Pathology

Colorado State University

From: Kingston, Tigga
Sent: Wednesday, August 26, 2020 4:13 PM
To: Guzal Masharipova ; martha.m.stokes.civ < ; Kading,Rebekah Katie Leahy <
Cc: jamechia.d.hoyle epstein ecohealthalliance.org>
Subject: RE: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

Hi Guzal,
Thanks for clarifying the password situation (I was only going partially mad then -- possible I never had that password, rather than I'd forgotten it (more often the case)).
Yes let's get rid of the login feature for now, and meet Friday 10 CT. I'd prefer Zoom as I've not yet used MS Teams. I imagine this will be mostly a "scoping" meeting, with practical changes to follow.

Best wishes
Tigga

-----Original Message-----
From: Guzal Masharipova
Sent: Wednesday, August 26, 2020 3:42 PM
To: Kingston, Tigga < martha.m.stokes.civ < Kading,Rebekah Katie Leahy
Cc: jamechia.d.hoyle >; epstein ecohealthalliance.org>
Subject: Re: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

Hi Tigga,

We're behind the scenes right now talking to Squarespace, and there were never any profiles created with usernames/passwords. Whenever you see a "login" button on the website, it leads you to a page with a single password entry space - this was a universal password that we set to hide some pages so only certain people could access them. An outcome of Phuket was to add an interactive map and chat feature that would need assigned logins / passwords to protect the information – but we were not able to get approvals to move forward with that next phase. This is still a likely objective for the network. However, since those pages are as of now blank, I suggest we get rid of the "login" feature altogether to get rid of the confusion.

If you wanted to update website content/bios/pages, I am happy to offer the Squarespace administrative login info that lets you change/make edits to the entire website. It's pretty intuitive, but I'll be available to make those changes for you or provide tech support if you wanted to go in yourself. We can also do a screen-sharing scenario during our call and I can live edit - I am flexible. __

Friday 10 - noon CT / 11 - 1 EST works with me. Does a Teams call invitation work or do you prefer Zoom?

Thank you,
GUZAL MASHARIPOVA | Task Lead
Global Systems Engineering, LLC
A Certified HUBZone Company

On 8/26/20, 3:39 PM, "Kingston, Tigga" wrote:

Dear Guzal
That's great to hear!

Most immediate -- I've forgotten my login password and there's no way to reset, and I'd like to be able to get behind the login. Is it possible to reset my password behind the scenes and send me a new one? I think Rebekah will need one too.

Rebekah and I plan to meet tomorrow, and then think it would be helpful to talk with you virtually on Friday or Monday, if you have the time. Our current options are
Friday -- 10-noon CT
Monday 10-11 CT.

But we can try and free up other slots if those don't work.

Best wishes
Tigga

-----Original Message-----
From: Guzal Masharipova
Sent: Wednesday, August 26, 2020 1:16 PM
To: martha.m.stokes ; Kading,Rebekah >; Katie Leahy >; Kingston, Tigga
Cc: jamechia.d.hoyle epstein ecohealthalliance.org>
Subject: Re: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

Hi everyone,

I now have the administrative rights for the BOHRN website from Squarespace. I apologize about the delay; it was a little confusing because of the login requirement on the landing page. This was initially installed because we intended to add geographic information of BOHRN members that we didn't want the public to have access to without permission. However, that information was never set up so we may want to consider removing the login feature of the website altogether.

Please let me know how you'd like to proceed - I'm happy to make changes based on updates you send me over email or I can set up a virtual meeting for us as well.

I look forward to helping out.

Best regards,
GUZAL MASHARIPOVA | Task Lead
Global Systems Engineering, LLC
A Certified HUBZone Company

On 8/26/20, 10:50 AM, "Stokes, Martha M CIV (USA)" > wrote:

Hi Rebekah,

Thanks so much!

Best,
Marty

-----Original Message-----
From: Kading,Rebekah
Sent: Wednesday, August 26, 2020 10:43 AM
To: Stokes, Martha M Katie Leahy >; Kingston, Tigga <
Cc: Hoyle, Jamechia D ; Guzal Masharipova >; epstein ecohealthalliance.org>
Subject: Re: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

Hi Marty - yes of course, here you go! This is the version that came back for us to revise. (Stefanie Campbell has also recently put this through BTRP clearance, as a heads up.) Thanks!
Rebekah

Rebekah C. Kading, PhD

Assistant Professor

Department of Microbiology Immunology and Pathology

Colorado State University

From: Stokes, Martha M CIV (USA)
Sent: Wednesday, August 26, 2020 8:28 AM
To: Kading,Rebekah ; Katie Leahy ; Kingston, Tigga
Cc: Hoyle, Jamechia D) ; Guzal Masharipova < >; epstein ecohealthalliance.org>
Subject: RE: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

Hi Rebekah,

Is there any way we could get a draft of the manuscript? We would maintain confidentiality and keep it close hold.

Thanks so much.

Best,
Marty

-----Original Message-----
From: Kading,Rebekah <
Sent: Tuesday, August 25, 2020 3:04 PM
To: Katie Leahy Kingston, Tigga ; Stokes, Martha M CIV (USA)
Cc: Hoyle, Jamechia D CTR (USA) >; Guzal Masharipova ; epstein ecohealthalliance.org>
Subject: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

---

Hi Katie, Marty, and Guzal -

Just chiming in to say hello and THANK YOU for the quick response and support for this effort! This is all great to hear, and I think we have a fantastic opportunity with this paper to provide another way to invigorate and draw attention to BOHRN. As Tigga and I were discussing the reviewer's suggestion, we basically converged on "Hey, BOHRN has already done all of this!" So it is wonderful to hear that we can move forward together to use this paper to direct people to BOHRN, which is where the rubber will hit the road. Looking forward to moving this forward, and we'll keep in touch with the revised manuscript. Thanks!

Best,
Rebekah :-)

Rebekah C. Kading, PhD

Assistant Professor

Department of Microbiology Immunology and Pathology

Colorado State University

From: Katie Leahy
Sent: Tuesday, August 25, 2020 11:54 AM
To: Kingston, Tigga martha.m.stokes
Cc: jamechia.d.hoyle >; Guzal Masharipova < >; Kading,Rebekah >; epstein ecohealthalliance.org>
Subject: Re: [External Sender] RE: BOHRN Status, publication

Hi, Tigga. Guzal (copied) should be able to help. I can make sure she has all the passwords; give us a day to make sure all the links are active. I talked with her today about it and she is ready to support in any way.

V/r,

Katie Leahy

KATIE LEAHY | Director, Science Engagement

Global Systems Engineering, LLC

A Certified HUBZone Company

From: "Kingston, Tigga"
Date: Tuesday, August 25, 2020 at 1:51 PM
To: "martha.m.stokes.civ"
Cc: Katie Leahy >, "jamechia.d.hoyle Guzal Masharipova >, "Kading,Rebekah" Jon Epstein ecohealthalliance.org>
Subject: [External Sender] RE: BOHRN Status, publication

Dear Marty

Thanks for the speedy response and support! Great to hear of the documentation efforts and continued commitment.

The lynchpin to everything that we'd like to do is the BOHRN website - is there a webmaster, or can one be allocated, so that we can host content, build membership, post some of the materials that have been developed.

Best

Tigga

From: Stokes, Martha M
Sent: Tuesday, August 25, 2020 8:45 AM
To: Kingston, Tigga
Cc: Katie Leahy Hoyle, Jamechia D CTR (USA) < Guzal Masharipova ; Kading,Rebekah >; Jon Epstein ecohealthalliance.org>
Subject: RE: BOHRN Status, publication

Hi Tigga,

Congratulations on having your piece accepted (with revisions, as always)! I would really appreciate you adding detail about BOHRN and highlighting the network's efforts. All of the positive outcomes you mention are well noted and align with our goals and objectives, which remain steadfast.

The current situation has certainly created unexpected challenges for all our work, but we're adapting, and want to ensure that we continue moving forward and position the network to pick up where it left off last summer, once things return to a more normal environment. In the meantime, we'll do what we are able virtually.

Let us know what you need to support this. Katie and I, along with our teams, recently updated a huge amount of documentation, reports, participant lists, etc. for BOHRN and other our TRNs for the incoming BTRP Director, in order to deposit it on our internal database, so it should be very easy to provide whatever you need. Just let us know how we can help.

Thanks so much!

Best,

Marty

Martha M Stokes, PhD

Southeast Asia Regional Science Manager

Biological Threat Reduction Program (BTRP)

From: "Kingston, Tigga" _> >

Date: Monday, August 24, 2020 at 5:09 PM

To: "martha.m.stokes < >

Cc: Katie Leahy >, "jamechia.d.hoyle >, Guzal Masharipova >, "Kading,Rebekah" _> >, Jon Epstein ecohealthalliance.org < >

Subject: [External Sender] BOHRN Status, publication

Dear Marty,

Rebekah Kading and I wrote a perspectives piece that is in revision for PLOS Biology. It calls for greater integration of ecologists/virologists (hmm, sounds familiar) and builds on analysis of a publication coauthor network. We conceptualized this at BORHN meetings and consider it a true BOHRN output, supporting BOHRN's message.

One of the reviewers specified some simple, but concrete actions that they would like to see in the revision. These actions closely ally with things we've begun at BOHRN (e.g., mission statement, contact lists of researchers). We would really like to be able to respond using BOHRN's infrastructure as it would be a good fit and would draw substantial attention to BOHRN and help boost the distributed membership and get us more on the map. The reviewer called for a mission statement, a list of who is doing what, and other simple things that could easily be integrated into the BOHRN website.

Currently, we refer to BOHRN in the acknowledgements, but have been reluctant to feature the network too centrally because we are unsure of its status and stability. It would be great to move forward with BOHRN featured more prominently, but we could do with some clarity of where things are heading. At minimum we need support of the website as that is where we will be directing people. Currently people can't join, or reset passwords etc, and we would need to work with someone on updates supporting these simple collations of information.

We have a bit less than a month to turn this around and get our revision in, so it would be great to hear your thoughts. I hope we can talk soon. I am now free fairly consistently between 10 am-Noon Mo-Thursday. I have other windows here and there as well.

All the best

Tigga

From: Stokes, Martha M
Sent: Wednesday, August 26, 2020 10:47 AM EDT
To: Kading,Rebekah ; Katie Leahy <k >; Kingston, Tigga
CC: Hoyle, Jamechia D < Guzal Masharipova >; epstein ecohealthalliance.org>
Subject: RE: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

Hi Rebekah,

Thanks so much!

Best,
Marty

-----Original Message-----
From: Kading,Rebekah
Sent: Wednesday, August 26, 2020 10:43 AM
To: Stokes, Martha M <m Katie Leahy < ; Kingston, Tigga <
Cc: Hoyle, Jamechia D) ; Guzal Masharipova ; epstein ecohealthalliance.org>
Subject: Re: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

All active links contained in this email were disabled. Please verify the identity of the sender, and confirm the authenticity of all links contained within the message prior to copying and pasting the address to a Web browser.

Hi Marty - yes of course, here you go! This is the version that came back for us to revise. (Stefanie Campbell has also recently put this through BTRP clearance, as a heads up.) Thanks!
Rebekah

Rebekah C. Kading, PhD

Assistant Professor

Department of Microbiology Immunology and Pathology

Colorado State University

From: Stokes, Martha M
Sent: Wednesday, August
To: Kading,Rebekah ; Katie Leahy ; Kingston, Tigga >
Cc: Hoyle, Jamechia D CIV (USA) >, Guzal Masharipova , epstein ecohealthalliance.org>
Subject: RE: [Non-DoD Source] Re Status, publication

Hi Rebekah,

Is there any way we could get a draft of the manuscript? We would maintain confidentiality and keep it close hold.

Thanks so much.

Best,
Marty

-----Original Message-----
From: Kading,Rebekah <
Sent: Tuesday, August
To: Katie Leahy Kingston, Tigga ; Stokes, Martha M
Cc: Hoyle, Jamechia D Guzal Masharipova epstein ecohealthalliance.org>
Subject: [Non-DoD Sour E , publication

All active links contained in this email were disabled. Please verify the identity of the sender, and confirm the authenticity of all links contained within the message prior to copying and pasting the address to a Web browser.

Hi Katie, Marty, and Guzal -

Just chiming in to say hello and THANK YOU for the quick response and support for this effort! This is all great to hear, and I think we have a fantastic opportunity with this paper to provide another way to invigorate and draw attention to BOHRN. As Tigga and I were discussing the reviewer's suggestion, we basically converged on "Hey, BOHRN has already done all of this!" So it is wonderful to hear that we can move forward together to use this paper to direct people to BOHRN, which is where the rubber will hit the road. Looking forward to moving this forward, and we'll keep in touch with the revised manuscript. Thanks!

Best,
Rebekah :-)

Rebekah C. Kading, PhD

Assistant Professor

Department of Microbiology Immunology and Pathology

Colorado State University

From: Katie Leahy
Sent: Tuesday, Aug
To: Kingston, Tigga ; martha.m.stokes.
Cc: jamechia.d.hoyle. ; Guzal Masharipova ; Kading,Rebekah ; epstein
ecohealthalliance.org>
Subject: Re: [External Sender] RE: BOHRN Status, publication

Hi, Tigga. Guzal (copied) should be able to help. I can make sure she has all the passwords; give us a day to make sure all the links are active. I talked with her today about it and she is ready to support in any way.

V/r,

Katie Leahy

KATIE LEAHY | Director, Science Engagement

Global Systems Engineering, LLC

A Certified HUBZone Company

From: "Kingston, Tigga"
Date: Tuesday, August 25, 2020 at 1:31 PM
To: "martha.m.stokes "
Cc: Katie Leahy , jamechia.d.hoyle Guzal Masharipova ,
"Kading,Rebekah" , Jon Epstein econearthalliance.org>
Subject: [Externa blication

Dear Marty

Thanks for the speedy response and support! Great to hear of the documentation efforts and continued commitment.

The lynchpin to everything that we'd like to do is the BOHRN website - is there a webmaster, or can one be allocated, so that we can host content, build membership, post some of the materials that have been developed.

Best

Tigga

From: Stokes, Martha M
Sent: Tuesday, August 25, 2020 8:45 AM
To: Kingston, Tigga
Cc: Katie Leahy Hoyle, Jamechia D Guzal Masharipova
Kading,Rebekah Epstein econearthalliance.org>
Subject: RE: BOHRN status, publication

Hi Tigga,

Congratulations on having your piece accepted (with revisions, as always)! I would really appreciate you adding detail about BOHRN and highlighting the network's efforts. All of the positive outcomes you mention are well noted and align with our goals and objectives, which remain steadfast.

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Let us know what you need to support this. Katie and I, along with our teams, recently updated a huge amount of documentation, reports, participant lists, etc. for BOHRN and other our TRNs for the incoming BTRP Director, in order to deposit it on our internal database, so it should be very easy to provide whatever you need. Just let us know how we can help.

Thanks so much!

Best,

Marty

Martha M Stokes, PhD

Southeast Asia Regional Science Manager

Biological Threat Reduction Program (BTRP)

From: "Kingston, Tigga" <

Date: Monday, August 24, 2020 at 5:09 PM

To: "martha.m.stokes

Cc: Katie Leahy > >, "jamechia.d.hoyle.

Kading,Rebekah Jon Epstein

ecohealthalliance.org

Subject: [External Sender] BOHRN Status, publication

Dear Marty,

Rebekah Kading and I wrote a perspectives piece that is in revision for PLOS Biology. It calls for greater integration of ecologists/virologists (hmm, sounds familiar) and builds on analysis of a publication coauthor network. We conceptualized this at BORHN meetings and consider it a true BOHRN output, supporting BOHRN's message.

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All the best

Tigga

From: Brooks, Lance R
Sent: Thursday, February 01, 2018 12:29 AM EST
To: Wade Abel
CC: Katie Leahy >; Newman, Carl I
Lancaster, Mary J Lewis, Christopher R
>; Kading,Rebekah ; DeeAnn Reeder
Paul Cryan >; Vivek Kapur < >; Gavin James Smith
>; Tigga Kingston ; Ian Mendenhall
Tamar Kutateladze Keti Sidamonidze Lela
Urushadze >; Joram Buza Catalino Demetria
Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>;
cryan.paul ; Stokes, Martha M Simmi Ghai
Supaporn Wacharapluesadee < cnkisinga
>
Subject: Re: [Non-DoD Source] Re: Afternoon Session
Attachment(s): "image001.png"

Hi Wade, et al,

Transport is not arranged for this evening. Everyone is on their own. Most are within walking distance.

Regards,
Lance

Division Chief, CBEP
CTR, DTRA

On Feb 1, 2018, at 11:53, Wade Abel > wrote:

Dear Katie
Just to find out if you could please remain us or give us more info about the transport arrangement for the diner invitation by the Ambassador this evening.
Kind regards

Wade

On 30 Jan 2018 1:15 pm, "Katie Leahy"
< > > wrote:

> All,
>
> Here are slides to start filling out for the afternoon session.
>
> V/r,
>
> Katie Leahy
>
> ---
>
> **From:** Katie Leahy <
> **Date:** Tuesday, January 30, 2018 at 10:30 AM
> **To:** "lance.r.brooks "
> >, "Newman, Carl I CIV DTRA
> J3-7 (US)" >, "Lancaster, Mary J
> CIV (US)" > >,
> "christopher.r.lewis > "

> >, "Kading,Rebekah"
>, DeeAnn Reeder
> >, "Cryan, Paul"
< > >, Vivek Kapur
>, Gavin James Smith
< > >, Tigga Kingston
> >,
"abelwade < "
>, Ian Mendenhall

"tamar_kutateladze <
> >, Keti Sidamonidze
>, Lela Urushadze
joram.buza
"

"c_demetria h
>, Kevin Olival
ecohealthalliance.org > >, Jon Epstein
ecohealthalliance.org > >, Jason Rao
>,
"cryan.paul "
> >

Cc: "Stokes, Martha M CIV (US)"
> >, Simmi Ghai
> >, S Wacharapluesadee
> >

Subject: NEW SLIDES

Here are the working group slides that were live-edited for your use in break-out groups.

V/r,

Katie Leahy

From: Katie Leahy
Date: Monday, January 29, 2018 at 9:01 PM
To:

>, "Kading,Rebekah"

"

>,
"c_demetria "
> >, Kevin Olival
ecohealthalliance.org < > >, Jon Epstein
ecohealthalliance.org < > >, Jason Rao

> >,
"cryan.paul

Cc: "Stokes, Martha M CIV (US)"
> >, Simmi Ghai
> >, S Wacharapluesadee
>

Subject: Update to the BPERNet Slides

Hi, everyone! We made a couple changes to the slides for tomorrow. Nothing substantive, just our approach to conducting the brief-out discussions and the order of a couple of the initial slides.

A reminder again to please be in the lobby at 0745, the bus will depart for Chulalongkorn promptly at 0800.

V/r,

Katie Leahy

From: Katie Leahy <
Date: Monday, January 29, 2018 at 10:28 AM
To: "lance.r.brooks <
> >, "Newman, Carl I CIV DTRA
J3-7 (US)" > >, "Lancaster, Mary J
CIV (US)" > >,
"christopher.r.lewis < > "
< > >, "Kading,Rebekah"
> >, DeeAnn Reeder
< >, "Cryan, Paul"
>, Vivek Kapur
< >, Gavin James Smith
Tigga Kingston
< >,
"abelwade "
> >, Ian Mendenhall
>,
"tamar_kutateladze "
>, Keti Sidamonidze
> >, Lela Urushadze
>, "joram.buza
> "

"c_demetria > "
>, Kevin Olival
ecohealthalliance.org > >, Jon Epstein
ecohealthalliance.org > >
Cc: "Stokes, Martha M CIV (US)"
>, Simmi Ghai
> >, S Wacharapluesadee
>

Subject: BPERNet: Transportation Times and Other Useful Information (30 and 31 January 2017)

Hello, everyone! Welcome to Bangkok. On behalf of the Executive Committee (Dr. Martha Stokes and Dr. Mary Lancaster), we are so pleased that you are able to join us this week for our BPERNet planning meeting and other PMAC activities.

Please use this email as your resource for information regarding transportation, logistics, and other coordinating information for 30 January – 31 January.

30 January – BPERNet Meeting at Chulalongkorn Hospital

1. **The bus will depart from the Renaissance Hotel promptly at 0800** ; please be in the lobby for head count at 0745
2. We will provide coffee and light refreshment during the meeting; you will take lunch at one of the many canteen options at the hotel; please bring about 200 - 300 thai baht (~10 USD) for lunch

31 January – PMAC / BPERNet Field Trip

1. **The bus will depart from the Renaissance Hotel promptly at 0630** ; please be in the lobby for head count at 0615; please make sure that you are on time, as we are caravanning with a delegation from the Centara Hotel and will receive a police escort to move us quickly through traffic
2. We will provide a box breakfast for the bus ride
3. Please make sure that you dress appropriately for this field trip; we strongly suggest covered shoes and loose, comfortable clothing; in addition to this mode of dress we also suggest that you bring accompaniments for spending a day outdoors amongst bat roosts; such as:
    a. Hat
    b. Sunscreen
    c. Sunglasses
    d. Bug spray
    e. Water bottle

We will provide information regarding the Ambassador's reception at the close of tomorrow's meeting.

Again, we are so excited to have you all here. Please do not hesitate to reach out to me or Megan Hudson (copied) if you have any questions.

V/r,

Katie Leahy

Katie Leahy

Program Manager| Global Systems Engineering

6303 Little River Turnpike, Suite 208

Alexandria, VA 22305

Caution-http://globalsyseng.com < Caution-http://globalsyseng.com/ >

From: Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US)
Sent: Tuesday, August 14, 2018 7:24 AM EDT
To: Kading,Rebekah >; Kingston, Tigga ; Megan Hudson ; nisreen.hmoud@rss.jo ; joram.buza cryanp ; c demetria epstein ; vkapur ; kityrob tamar kutateladze ; ian.mendenhal ; oliva ; dreeder >; ksidamonidze >; gavin.smith ; l.urushadze ; spwa ; abelwade >; raina.plowright >
CC: Stokes, Martha M CIV (US) >; Katie Leahy >; Becker, Stephen M CTR DTRA J3-7 (US) Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) >
Subject: RE: [Non-DoD Source] Re: Draft Executive Summary and Website Materials

Hi all,
Thank you Tigga and Rebekah for the inputs and reminders about academic calendar constraints. We'll keep this in mind when arranging meeting opportunities in the future. We've been aiming BOHRN meetings as side events at existing conferences/meetings, so may not be able to completely mitigate the issue, but we can certainly take academic calendars into account as we make plans.

Cheers,
Mary

Mary Lancaster, PhD
Cooperative Biological Engagement Program
Defense Threat Reduction Agency
Ft. Belvoir, VA

**NOTICE: Nothing in this email is intended to constitute contractual direction or impact currently negotiated cost, price, or schedule contained within the contract. If the contractor believes there is an impact, the contractor must disregard that portion of the communication and contact the contracting officer for direction.

-----Original Message-----
From: Kading,Rebekah
Sent: Monday, August 13, 2018 11:55 PM
To: Kingston, Tigga >; Megan Hudson ; nisreen.hmouc joram.buza ; cryanp ; c demetria ; epstein ; vkapur ; kityrob tamar kutateladze ian.mendenhall ; ecohealthalliance.org; dreeder ; ksidamonidze ; gavin.smith ; l.urushadze ; spwa ; abelwade ; plowright
Cc: Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) <mary.j.lancaster >; Stokes, Martha M CIV (US) >; Katie Leahy Becker, Stephen M CTR DTRA J3-7 (US)
raft Executive Summary and Website Mat

All active links contained in this email were disabled. Please verify the identity of the sender, and confirm the authenticity of all links contained within the message prior to copying and pasting the address to a Web browser.

Hi Tigga and everyone,

Yes, that is challenge for me as well. I am not involved in the Georgia meeting, but have made arrangements regarding class coverage so I could travel to Vienna if we proceed with that meeting in Nov. I also would not have been able to get away for both meetings though. January, after the semester is over, is generally better timing for me too. There was a December meeting option as well, which unfortunately for me would fall during the last week of classes so I couldn't get away for that, but if that works better for the majority of the steering committee perhaps we should reconsider it?

Kind regards,

Rebekah

Rebekah C. Kading, PhD

Assistant Professor

Department of Microbiology Immunology and Pathology

Colorado State University

From: Kingston, Tigga
Sent: Saturday, August 11, 2018 5:26:09 AM
To: Megan Hudson; nisreen.hmouc ; joram.buza ; cryanp ; c_demetria ecohealthalliance.org; Kading,Rebekah; vkapur kityrob tamar_kutateladze ian.mendenhall ecohealthalliance.org; dreeder .edu; ksidamonidze ; gavin.smith@ ; l.urushadze ; spwa , abelwade ; raina.plowright
Cc: Lancaster CIV DTRA PARTN (US); Stokes M CIV e Leahy; Bec phen M CTR DTRA J3-
Subject: RE: Draft Executive Summary and Website Materials

Hi Megan

Just trying to unpack the plans this fall, and have been reading through the Exec summary. Essentially a lot of BOHRN are going to Georgia and you propose an additional meeting in Austria a couple of months later?

I don't want to second guess what you all decided on in Canada, but is there any chance the second meeting (currently scheduled for November) could be when the fall semester is over (i.e. early-mid December through mid January)? As I'm on the WABnet Steering Committee I have committed to the Georgia meeting, but it is challenging to get release for multiple trips during the academic semester, particularly for same entities. I am probably not the only one running into this problem or similar

Thanks for your consideration,

Tigga

From: Megan Hudson
Sent: Friday, July 13, 2018 11:02 AM
To: nisreen.hmouc ; joram.buza ; cryanp ; c demetria ; ecohealthalliance.org; rebekah.kading ; vkapur ; Kingston, Tigga ; kityrob ; tamar_kutateladze ian.mendenhall ; ecohealthalliance.org;

dreeder ; ksidamonidze gavin.smith ; l.urushadze ; spwa ; abelwade raina.plowright
Cc: Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) ; Stokes, Martha M CIV (US) ; Katie Leahy
; Becker, Stephen M CTR DTR
Subject: Draft Executive Summary and Website Materials

All,

Please find the draft report from our BOHRN meeting 20-21 June. This report includes an executive summary, action items, participant list, working group outcomes, and your research quad charts.

We ask that you provide constructive comments (e.g., content changes) no later than 18 July. It is our intent to adjudicate and incorporate any comments to then publish a final report.

In addition, you will find an updated version of the website map here (Caution-https://docs.google.com/document/d/1x5GdAKEPpKXTol9utZiYvaGoXNtOQsyTdlub1WvN0tk/edit?usp=sharing < Caution-https://na01.safelinks.protection.outlook.com/?url=https%3A%2F%2Fdocs.google.com%2Fdocument%2Fd%2F1x5GdAKEPpKXTol9utZiYvaGoXNtOQsyTdlub1WvN0tk%2Fedit%3Fusp%3Dsharing&data=02%7C01%7Ctigga.kingston%40ttu.edu%7C0435a45a4 >). Each page has the title of the website page and the content, make edits, as you see fit, to the language to help us better develop the website.

As a reminder, we will be adding individual bios to the website. If you have not already done so, you may submit your information here:Caution-https://www.surveymonkey.com/r/BPMTG2T < Caution-https://na01.safelinks.protection.outlook.com/?url=https%3A%2F%2FCaution-www.surveymonkey.com%2Fr%2FBPMTG2T&data=02%7C01%7Ctigga.kingston%40ttu.edu%7C0435a45a40304498aaf808d5e8d9f2f3%7C178a51bf8b2049ffb65556245d5c173c%7C0%7C0%7C636670946451753 >

You will find the report contains softened language to add a more conservationist view point, please review the language within the report and on the website.

v/r,

Megan

Megan Hudson

Task Lead| Global Systems Engineering

6303 Little River Turnpike #208

Alexandria, VA 22312

From: Prof. Joram Buza >
Sent: Thursday, August 03, 2017 2:14 AM EDT
To: Sander, William E CTR (US) >; Katie Leahy ;
kityrob >; ian.mendenhall ;
joram.buza >; vkapur ;
ecohealthalliance.org >; ecohealthalliance.org
>; Kading,Rebekah >; lelincdc
; l.urushadze ; tamar_kutateladze
; spwa >; abelwade
; c_demetria >; tigga.kingston
; cryanp ; dreeder < >;
gavin.smith
CC: Lancaster, Mary J CIV (US) >; Gamboa, Omar Maj USAF DTRA J3-7 (US)
l>; Sander, William E CTR (US) ; Caitlin Devaney

Subject: RE: [Non-DoD Source] RE: GBA Products and Action Items

Dear Sander,
I am in agreement with the name ;Bat-associated Pathogen and Ecology Research Network (BPERN). My vote goes for the "Participatory Epidemiology Network for Animal and Public Health (PENAPH)" conference that will be held in Thailand in January 2018.

Regards,

Buza

-----Original Message-----
From: Sander, William E CTR (US)
Sent: Monday, July 31, 2017 4:59 PM
To: Prof. Joram Buza
Cc: Lancaster, Mary J CIV (US)
Subject: RE: [Non-DoD Source] RE: GBA Products and Action Items

Thanks, Buza. I will get you added shortly. Let us know if you have any edits for the documents sent along.

Best,
Will

-----Original Message-----
From: Prof. Joram Buza
Sent: Monday, July 31, 2017 8:22 AM
To: Sander, William E CTR (US)
Cc: Lancaster, Mary J CIV (US) >
Subject: RE: [Non-DoD Source] RE: GBA Products and Action Items

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Dear Sander,
Many greetings. I arrived safely back in Tanzania. Thanks so much for the support.

As per your request, I have registered in the APAN:

My username is: joram.buza

Regards,

Buza

-----Original Message-----
From: Sander, William E CTR (US)
Sent: Friday, July 28, 2017 3:48 P
To: Kingston, Tigga; DeeAnn Reeder; Jon Epstein
Cc: Wade Abel; l.urushadze ; rebekah.kading ; c_demetria
spwa ; Lancaster, Mary J CIV (US); Stokes, Martha M CIV (US); gavin.smith ;
nisreen.nmoud ; Caitlin Devaney; joram.buza ; Gamboa, Omar Maj USAF DTRA J3-7 (US);
Katie Leahy; vkapur ; lelincdc ; kityrob ; ian.mendenhall ;
ecohealthalliance.org; tamar_kutateladze ; cryanp
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Hi Tigga,
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Cc: Wade Abel ; l.urushadze ; rebekah.kading
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nisreen.hmoud ; Caitlin Devaney >; Sander, William E CTR (US)
; joram.buza@nm-aist Gamboa, Omar Maj USAF DTRA J3-7 (US)
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lelincoc ; kityrob ; ian.mendenhall ; ecohealthalliance.org;
tamar_kutateladze cryanp
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For all the reasons pointed out by DeeAnn, I too like:

Research Alliance for Bat-borne Emerging Zoonoses

(RABEZ)

Best wishes

Tigga

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Sent: Thursday, July 27, 2017 11:47 PM
To: Jon Epstein ecohealthalliance.org>
Cc: Wade Abel >; l.urushadze ; rebekah.kading ;
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Stokes, Martha M CIV (US) >; gavin.smith Kingston, Tigga
nisreen.hmoud ; Caitlin Devaney < ;
Sander, William E CTR (US) >; joram.buza Gamboa, Omar Maj
USAF DTRA J3-7 (US) ; Katie Leahy >;
vkapur ; lelin ; ian.me
ecohealthalliance.org; tamar_kutateladze ; cryanp
Subject: Re: GBA Products and Action Items

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Thanks, DeeAnn

On Jul 28, 2017 3:42 AM, "Jon Epstein" ecohealthalliance.org < Caution- > wrote:

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(RABEZ)

Cheers,

Jon

Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
New York

(e) ecohealthalliance.org <

On Jul 25, 2017 9:18 AM, "Katie Leahy" > wrote:

Note: this email is best viewed in HTML

Greetings, GBA Steering Committee!

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    b. Participatory Epidemiology Network for Animal and Public Health (PENAPH) - 10-12 January 2018, Chiang Mei, ThailandCaution-Caution-https://penaph.net/second-penaph-conference-participatory-approaches-in-animal-health-public-health-one-health-and-ecohealth/ < Caution-Caution-https://penaph.net/second-penaph-conference-participatory-approaches-in-animal-health-public-health-one-health-and-ecohealth/ >
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3. We need nominations for co-chairs, seek your suggestions; we will plan to release nominees in one week from now for vote.

Katie Leahy

Program Manager| Global Systems Engineering

5881 Leesburg Pike, Suite 506

Baileys Crossroads, VA 22041

Caution-Caution-http://globalsyseng.com < Caution-Caution-http://globalsyseng.com/ >

From: Lancaster, Mary J
Sent: Friday, July 28, 2017 12:02 PM EDT
To: Jon Epstein ecohealthalliance.org>; Kingston, Tigga < >
CC: DeeAnn Reeder >; Wade Abel ; l.urushadze ; Kading,Rebekah < >; c_demetria >; spwa Stokes, Martha M CIV (US) ; gavin.smith >; nisreen.hmoud ; Caitlin Devaney >; Sander, William E CTR (US) >; joram.buza >; Gamboa, Omar Maj USAF DTRA J3-7 (US) >; Katie Leahy ; vkapur ; lelincdc ; kityrob >; ian.mendenhall >; ecohealthalliance.org ; tamar_kutateladze <tamar kutateladze ; cryanp ; Lancaster, Mary J CIV (US) >
Subject: RE: [Non-DoD Source] Re: GBA Products and Action Items

On the off-chance that we might find something interesting which is non-viral, what about Bat-associated Pathogen and Ecology Research Network? That would yield the BPER Network or BPERN as acronyms.

Mary Lancaster, PhD
Cooperative Biological Engagement Program
Defense Threat Reduction Agency

-----Original Message-----
From: Jon Epstein ecohealthalliance.org]
Sent: Friday, July 28, 2017 11:50 AM
To: Kingston, Tigga
Cc: DeeAnn Reeder wade Abel ; l.urushadze ; rebekah.kading c demetria spwa Lancaster, Mary J CIV (US) Stokes, Martha M CIV (US) ; gavin.smith ; nisreen.hmoud ; Caitlin Devaney >; Sander, William E CTR (US) ; joram.buza ; Gamboa, Omar Maj USAF DTRA J3-7 (US) ; Katie Leahy ; vkapur ; lelincdc ; kityrob ; ian.mendenhall ecohealthalliance.org; tamar_kutateladze ; cryanp
Subject: [Non-DoD Source] Re: GBA Products and Action Items

My RABEZ suggestion was slightly tongue-in-cheek. In retrospect, I worry that it might be outwardly confusing to others if we become the "Rabies network" when we won't actually be doing much with rabies. With sensitivity to the bat conservation community, I suggest the "Bat Viral Ecology Research Network" or something along that line.

Cheers,
Jon

On Fri, Jul 28, 2017 at 8:19 AM, Kingston, Tigga > > wrote:

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(RABEZ)

Best wishes

Tigga

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Sent: Thursday, July 27, 2017 11:47 PM
To: Jon Epstein ecohealthalliance.org >
Cc: Wade Abel < >; t.urushadze < ; rebekah.kading ; c_demetria
> ; spwa < caution-mailto:spwa > ; Lancaster, Mary J CIV (US) > >; Stokes, Martha M CIV (US) > >;
gavin.smith < ; Kingston, Tigga >; nisreen.hmoud ; Caitlin Devaney :caitlin.devaney@ > >; Sander, William E CTR (US) joram.buza < > ; Gamboa, Omar Maj USAF DTRA J3-7 (US) >; Katie Leahy >; vkapur > ;
felincac ; kityrok ; ian.mendenhall < ; ecohealthalliance.org < ;
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Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
New York

(e) ecohealthalliance.org

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Program Manager| Global Systems Engineering

5881 Leesburg Pike, Suite 506

Baileys Crossroads, VA 22041

Caution-http://globalsyseng.com < Caution-http://globalsyseng.com/ >

--

JonathanH. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street - 17th floor
New York, NY 10001

web: ecohealthalliance.org < Caution-http://www.ecohealthalliance.org/ >

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Sent: Friday, July 28, 2017 8:48 AM EDT
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1. We need suggestions for a next meeting and would like your suggestions; we will plan to release all options to the group in one week from now for vote. Here are some suggestions to get us started:
    a. International Congress on Pathogens at the Human and Animal Interface (ICOPHAI) 7-9 November 2017, Doha, QatarCaution-https://icophai.org/ < Caution-https://icophai.org/ >
    b. Participatory Epidemiology Network for Animal and Public Health (PENAPH) – 10-12 January 2018, Chiang Mei, ThailandCaution-https://penaph.net/second-penaph-conference-participatory-approaches-in-animal-health-public-health-one-health-and-ecohealth/ < Caution-https://penaph.net/second-penaph-conference-participatory-approaches-in-animal-health-public-health-one-health-and-ecohealth/ >
    c. Others??

2. We need suggestions for Network names and would like your suggestions; we will plan to release the options to the group in one week from now for vote. Here are some suggestions to get us started:

a. Global Alliance for Bat-borne Pathogens (GABP)
b. Global Bat Pathogen Disease Network (GBPDN)
c. Bat Alliance Trust Disease Network (BAT-DN)
d. Others??

3. We need nominations for co-chairs, seek your suggestions; we will plan to release nominees in one week from now for vote.

Katie Leahy

Program Manager| Global Systems Engineering

5881 Leesburg Pike, Suite 506

Baileys Crossroads, VA 22041

Caution-http://globalsyseng.com < Caution-http://globalsyseng.com/ >

From: Sander, William E CTR (US) >
Sent: Friday, June 30, 2017 10:07 AM EDT
To: Katie Leahy
CC: kityob >; ian.mendenhall >; Prof. Joram Buza ; Vivek Kapur ; Kevin Olival, PhD ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; gavin.smith Kading,Rebekah ; lelincdc ; l.urushadze >; tamar_kutateladze >; spwa >; abelwade ; c demetria ; Kingston, Tigga < ; nisreen.hmoud >; cryanp ; dreeder >; Lancaster, Mary J CIV (US) ; Stokes, Martha M CIV (US) ; Gamboa, Omar Maj USAF DTRA J3-7 (US) < >; Caitlin Devaney
Subject: RE: [Non-DoD Source] Re: Global Bat Alliance Steering Committee meeting - info

Hi all,
If we can, we would like to meet right at 12PM today after the last morning session where the reception was last night for a picture!

We neglected to take a group photo of the Global Bat Alliance SC yesterday and would love to have us come together to do this today. Please spread the word as not everyone will check their e-mail.

Best,
Will Sander

-----Original Message-----
From: Katie Leahy]
Sent: Thursday, June 29, 2017 10:10 AM
To: Sander, William E CTR (US) >
Cc: kityob ; ian.mendenhall ; Prof. Joram Buza < >; Vivek Kapur ; Kevin Olival, PhD ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; gavin.smith ; Kading,Rebekah ; lelincdc ; l.urushadze tamar_kutateladze ; spwa ; abelwade ; c_demetr Kingston, Tigga >; nisreen.hmoud ; cryanp ; dreede Lancaster, Mary J CIV (US) ; Stokes, Martha M CIV (US) ; Gamboa, Omar Maj USAF DTRA J3-7 (US) >; Caitlin Devaney >
Subject: [Non-DoD Source] Re: Global Bat Alliance Steering Committee meeting - info

All active links contained in this email were disabled. Please verify the identity of the sender, and confirm the authenticity of all links contained within the message prior to copying and pasting the address to a Web browser.

_____

Hi, everyone. A quick reminder on behalf of Mary and Marty:

Our meeting this morning will be held in Room 142, in the University Center for the Arts. This is thesame building where the conference will be held.

V/r,

Katie Leahy

Sent from my iPhone

On Jun 27, 2017, at 14:27, Sander, William E CTR (US)
: > > wrote:

On behalf of Mary Lancaster and Marty Stokes, we're excited to convene the first in-person meeting of the Steering Committee for the Global Bat Alliance.

As friendly reminders of what to expect:

- Convene on Thursday, June 29th, in room 142 of the University Center for the Arts (same building as the conference)
- Start at 9:30AM local time (room will be open by 9AM)
- Working lunch (lunch provided) - vegetarian option included
- Plan to end the meeting at 2:30PM local time

- For those of you calling in, we will get that information to you within the next day.

I have attached again our agenda as well as the Terms of Reference for Trusted Agents for your reference and review.

If you have any questions, do not hesitate to reach out to any of us in the CC line. The number below is my cell phone.

Best,

Will Sander, DVM, MPH, DACVPM, PMP
Veterinary Specialist
Booz Allen Hamilton
CTR A&AS Support Contractor

<TORFTA_GBA_v10.docx>

<GBA Meeting Overview_29June2017_v2.docx>

From: Stokes, Martha M CIV (US)
Sent: Monday, May 15, 2017 9:05 AM EDT
To: Kevin Olival, PhD ecohealthalliance.org>; Leahy, Catharine (US) Lancaster, Mary J CIV (US) >; Sander, William E CTR (US) Joram Buza >; Vivek Kapur ; Jon Epstein gavin.smith ; Ian MENDENHALL PhD kityrob >; Devaney, Caitlin (US) < Kading,Rebekah
Subject: RE: [Non-DoD Source] Re: UPDATE: Global Bat Alliance Network (convened on behalf of CBEP)

Kevin,

Wonderful, thanks so much.

Good call this morning, and thank you to all who were able to join. We'll send out action items and notes quickly so we can move forward on developing a clear and useful agenda for the Fort Collins meeting.

Best,
Marty

-----Original Message-----
From: Kevin Olival, PhD
Sent: Monday, May 15, 2017 8:59 AM
To: Leahy, Catharine (US) ; Lancaster, Mary J CIV (US) >; Stokes, Martha M CIV (US) >; Sander, William E CTR (US) >; Joram Buza < >; Vivek Kapur ; Jon Epstein ; gavin.smith ; Ian MENDENHALL PhD ; kityrob ; Devaney, Caitlin (US) ; Rebekah.Kading
Subject: [Non-DoD Source] Re: UPDATE: Global Bat Alliance Network (convened on behalf of CBEP)

Dear all,

As mentioned, here is Tigga's book chapter on global bat conservation networks that I mentioned. The chapter is available for free download, as is the whole book!

Caution-http://link.springer.com/chapter/10.1007%2F978-3-319-25220-9_17 < Caution-http://link.springer.com/chapter/10.1007%2F978-3-319-25220-9_17 >

Cheers,
Kevin

Kevin J. Olival, PhD
Associate Vice President for Research

EcoHealth Alliance
460 West 34th Street - 17th floor
New York, NY 10001

On May 15, 2017, at 7:00 AM, Leahy, Catharine (US) > wrote:

<Bat meeting notes 9Feb2017.docx>

From: Ian Mendenhall >
Sent: Monday, May 29, 2017 12:41 AM EDT
To: Devaney, Caitlin (US)
CC: Stokes, Martha M CIV (US) ; Kevin Olival, PhD ecohealthalliance.org>; Leahy, Catharine (US) < ; Lancaster, Mary J CIV (US) ; Sander, William E CTR (US) ; joram buza ; Vivek Kapur ; Gavin James Smith >; kityrob >; katie.leahy >; caitlin.devaney >; Kading,Rebekah ; Jon Epstein

Subject: Re: [Non-DoD Source] Re: UPDATE: Global Bat Alliance Network (convened on behalf of CBEP)

Hi Caitlin,

I'm on vacation in the states and may or may not attend. I'll let you know closer to the dates, but if you could send me the call details, that would be great.

Best,
Ian

From: Jon Epstein @ecohealthalliance.org>
Date: Thursday, 25 May 2017 10:21 am
To: "Kading,Rebekah" >
Cc: "Devaney, Caitlin (US)" >, Marty Stokes >, "Kevin Olival, PhD" < "Leahy, Catharine (US)" "Lancaster, Mary J CIV (US)" , "Sander, William E CTR (US)" , joram buza >, Vivek Kapur < Gavin James Smith Ian Mendenhall "kityrob " , "katie.leahy < >, "caitlin.devaney " >
Subject: Re: [Non-DoD Source] Re: UPDATE: Global Bat Alliance Network (convened on behalf of CBEP)

works for me as well.
-Jon

On Thu, May 25, 2017 at 12:48 PM, Kading,Rebekah < > wrote:

> Hi Caitlin,
>
> Thank you - this date and time works for me.
>
> Best regards,
>
> Rebekah
>
> **Rebekah C. Kading, PhD**
>
> Assistant Professor
>
> Department of Microbiology Immunology and Pathology
>
> Colorado State University
>
> Office:
>
> ---
>
> **From:** Devaney, Caitlin (US)
> **Sent:** Thursday, May 25, 2017 10:42:06 AM
> **To:** Stokes, Martha M CIV (US); Kevin Olival, PhD; Leahy, Catharine (US); Lancaster, Mary J CIV (US); Sander, William E CTR (US); Joram Buza; Vivek Kapur; Jon Epstein; gavin.smith ; Ian MENDENHALL PhD; kityrob ; Kading,Rebekah; katie.leahy caitlin.devaney
>
> **Subject:** RE: [Non-DoD Source] Re: UPDATE: Global Bat Alliance Network (convened on behalf of CBEP)
>
> All,
>
> It looks like the best date and time for the next GBA steering committee planning call will be 7 June at 0900 U.S. EST. Please let us know if you will not be able to make this date and time. A calendar invitation will follow with call-in information.

Additionally, before the 7 June call we will send out a draft (Terms of Reference for Trusted Agents) TORFTA for your review. Please take a look at this document, and provide any feedback that you may have, as we will plan to work towards a consensus on the TORFTA during the call. We will plan to finalize the TORFTA when we meet in-person during the 29 June meeting in Fort Collins.

v/r,
Caitlin Devaney

Caitlin Devaney
Global Security Programs
Cubic Global Defense
5695 King Centre Drive
Alexandria, VA 22315

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From: Devaney, Caitlin (US)
Sent: Monday, May 15, 2017 3:21 PM
To: 'Stokes, Martha M CIV (US)'; Kevin Olival, PhD; Leahy, Catharine (US); Lancaster, Mary J CIV (US); Sander, William E CTR (US); Joram Buza; Vivek Kapur; Jon Epstein; gavin.smith Ian MENDENHALL PhD; kityrob Rebekah.Kading
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Thank you,
Caitlin Devaney

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Global Security Programs
Cubic Global Defense
5695 King Centre Drive
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Marty

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From: Kevin Olival, PhD ecohealthalliance.org]

Sent: Monday, May 15, 2017 8:59 AM

To: Leahy, Catharine (US) >; Lancaster, Mary J CIV (US) Stokes, Martha M CIV (US) ; Sander, William E CTR (US) < >; Joram Buza ; Vivek Kapur >; Jon Epstein ecohealthalliance.org >; gavin.smith ; Ian MENDENHALL PhD >; kityrob ; Devaney, Caitlin (US) < Rebekah.Kading

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Cheers,

Kevin

Kevin J. Olival, PhD

Associate Vice President for Research

EcoHealth Alliance

460 West 34th Street – 17th floor

New York, NY 10001

On May 15, 2017, at 7:00 AM, Leahy, Catharine (US) > wrote:

<Bat meeting notes 9Feb2017.docx>

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

web: ecohealthalliance.org

Twitter: @epsteinjon

-

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

From: Jon Epstein ecohealthalliance.org>
Sent: Thursday, May 25, 2017 1:21 PM EDT
To: Kading,Rebekah <
CC: Devaney, Caitlin (US) >; Stokes, Martha M CIV (US) ;
Kevin Olival, PhD ecohealthalliance.org>; Leahy, Catharine (US) Lancaster, Mary
J CIV (US) Sander, William E CTR (US) < joram buza
Vivek Kapur < gavin.smith
Ian MENDENHALL PhD >; kityrob < >;
katie.leahy ; caitlin.devaney

Subject: Re: [Non-DoD Source] Re: UPDATE: Global Bat Alliance Network (convened on behalf of CBEP)

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> Hi Caitlin,
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>
> Rebekah
>
> **Rebekah C. Kading, PhD**
>
> Assistant Professor
>
> Department of Microbiology Immunology and Pathology
>
> Colorado State University

From: Devaney, Caitlin (US)
Sent: Thursday, May 25, 2017 10:42:06 AM
To: Stokes, Martha M CIV (US); Kevin Olival, PhD; Leahy, Catharine (US); Lancaster, Mary J CIV (US); Sander, William E CTR (US); Joram Buza; Vivek Kapur; Jon Epstein; gavin.smith ; Ian MENDENHALL PhD; kityrob ;
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v/r,
Caitlin Devaney

Caitlin Devaney
Global Security Programs
Cubic Global Defense
5695 King Centre Drive
Alexandria, VA 22315

w: globalsecurity.cubic.com

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From: Devaney, Caitlin (US)
Sent: Monday, May 15, 2017 3:21 PM
To: 'Stokes, Martha M CIV (US)'; Kevin Olival, PhD; Leahy, Catharine (US); Lancaster, Mary J CIV (US); Sander, William E CTR (US); Joram Buza;
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Thank you,
Caitlin Devaney

Caitlin Devaney
Global Security Programs
Cubic Global Defense
5695 King Centre Drive
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w: globalsecurity.cubic.com

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Sent: Monday, May 15, 2017 9:06 AM
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Best,

Marty

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Sent: Monday, May 15, 2017 8:59 AM

To: Leahy, Catharine (US) >; Lancaster, Mary J CIV (US) < I>; Stokes, Martha M CIV (US) ; Sander, William E CTR (US) ; Joram Buza < Vivek Kapur >; Jon Epstein ecohealthalliance.org >; gavin.smith ; Ian MENDENHALL PhD >; kityrob ; Devaney, Caitlin (US) < ; Rebekah.Kading

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Cheers,

Kevin

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EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

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<Bat meeting notes 9Feb2017.docx>

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Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

web: ecohealthalliance.org

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Subject: RE: [Non-DoD Source] Re: UPDATE: Global Bat Alliance Network (convened on behalf of CBEP)
Attachment(s): "GBA Planning Meeting Notes_15 MAY 17.pdf"

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Cheers,

Kevin

Kevin J. Olival, PhD

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460 West 34th Street – 17th floor

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<Bat meeting notes 9Feb2017.docx>

Global Bat Alliance Steering Committee | Planning Meeting Notes
0800 US EST 15 MAY 2017

ATTENDEES

- Dr. Marty Stokes (CBEP)
- Dr. Will Sander (CBEP)
- Ms. Katie Leahy (Cubic Global Defense)
- Ms. Caitlin Devaney (Cubic Global Defense)
- Dr. Ian Mendenhall (Duke-NUS)
- Dr. Vivek Kapur (Penn State University)
- Dr. Jon Epstein (EcoHealth Alliance)
- Dr. Kevin Olival (EcoHealth Alliance)

ACTION ITEMS

Task	Responsible	Due Date
Nominate additional GBA Steering Committee members	ALL	Rolling; interim status check during next planning meeting ~5-9 June
Gather information on neglected research areas (countries/ regions, specific diseases, specific areas) for GBA database	ALL	Rolling; interim status check during next planning meeting ~5-9 June
Gather and share information on other groups and projects, that may be underfunded, inactive or unconnected	ALL	Rolling; interim status check during next planning meeting ~5-9 June
Identify all stakeholders, and different categories in order to determine engagement routes, overlaps and appropriate integration mechanisms	ALL	Rolling; interim status check during next planning meeting ~5-9 June
Review and provide feedback on Draft Terms of Reference for the GBA Steering Committee	ALL	By next planning meeting ~5-9 June

AGENDA

Introductions

- Dr. Marty Stokes facilitated the introductions of all Global Bat Alliance (GBA) Steering Committee planning meeting attendees, as well as introductions for steering committee members who were unable to make the call.

Review of Global Bat Alliance Mission and Scope

- The overall goal of the GBA is to bring together people and organizations that seek to reduce the threat of infectious disease, with specific goals to:
    - Foster inter-regional collaborations with a focus on bat disease surveillance and bat ecology and migration
    - Identify and engage stakeholder community
    - Identify and address knowledge gaps through research projects and training activities
    - Identify opportunities to mitigate risks by applying knowledge gained
- The intent of the GBA is to develop sustainable capabilities within partner countries.
- Ultimately, the GBA Steering Committee will need more distributed, cross-disciplinary representation.
    - Current GBA Steering Committee members should explore current contacts and affiliations in order to start identifying these individuals. Of particular importance will be those with ties to both research and policy.

Discussion of upcoming meeting at Fort Collins in June

- Prior to the meeting, the GBA Steering Committee members should start gathering information on (1) neglected research areas, and (2) other related groups and projects, which will be collated into a database.
    - This will assist in further identifying missing information, and defining decisions that will need to be made in terms of critical research needs and next steps.

Discussion of infrastructure and organization of the network

- A formal structure for the GBA Steering Committee, such as a Terms of Reference (TOR), is important to guide activities such as: convening, oversight processes, and in order to create metrics for success.
- A TOR is also critical to allow for equitable and fair competition for funding, internal and external to the GBA Steering Committee.
- A draft TOR for the GBA Steering Committee will be sent out to the group for edits and review.
- The GBA should work to identify all stakeholders, and categories of stakeholders, and then determine how best to formalize those engagements.
    - A formal mechanism might be required to integrate the GBA with existing groups, such as a Memorandum of Understanding or Memorandum of Agreement.
- The GBA Steering Committee should be perceived solely as facilitators of building sustainable capacities. As such, the TOR should include a system of rotating membership, and a clear scope of membership.
- There could be utility in having a pure conservationist on the GBA Steering Committee.

Discussion of output and mentorship goals for the network

- Holding more meetings like the one that will occur next month in Fort Collins, but on a regional scale, could serve to identify additional key researchers, prioritize GBA efforts, and build awareness of the GBA.
- The GBA will explore convening regional meetings, and possibly linking them to other external bat meetings.
- The GBA can leverage the efforts of existing groups such as SEABRC, Bat Conservation Africa, and possibly some of the PREDICT work as well.

Next Steps

- The next planning meeting call will be at 0900 US EST during the week of 5-9 June.
- The next planning meeting call will focus on:
    - Creating an agenda for the Fort Collins meeting
    - Reviewing the current draft of the Steering Committee Terms of Reference
    - Status updates on the listed action items.

From: Devaney, Caitlin (US)
Sent: Thursday, May 25, 2017 12:42 PM EDT
To: Stokes, Martha M CIV (US) < ; Kevin Olival, PhD ecohealthalliance.org>; Leahy, Catharine (US) ; Lancaster, Mary J CIV (US) < Sander, William E CTR (US) ; Joram Buza Vivek Kapur >; Jon Epstein ecohealthalliance.org>; gavin.smith Ian MENDENHALL PhD kityrob@ ; Kading,Rebekah ; katie.leahy@ < ; caitlin.devaney

Subject: RE: [Non-DoD Source] Re: UPDATE: Global Bat Alliance Network (convened on behalf of CBEP)

All,

It looks like the best date and time for the next GBA steering committee planning call will be 7 June at 0900 U.S. EST. Please let us know if you will not be able to make this date and time. A calendar invitation will follow with call-in information.

Additionally, before the 7 June call we will send out a draft (Terms of Reference for Trusted Agents) TORFTA for your review. Please take a look at this document, and provide any feedback that you may have, as we will plan to work towards a consensus on the TORFTA during the call. We will plan to finalize the TORFTA when we meet in-person during the 29 June meeting in Fort Collins.

v/r,
Caitlin Devaney

Caitlin Devaney
Global Security Programs
Cubic Global Defense
5695 King Centre Drive
Alexandria, VA 22315

w: globalsecurity.cubic.com

-----Original Message-----
From: Devaney, Caitlin (US)
Sent: Monday, May 15, 2017 3:21 PM
To: 'Stokes, Martha M CIV (US)'; Kevin Olival, PhD; Leahy, Catharine (US); Lancaster, Mary J CIV (US); Sander, William E CTR (US); Joram Buza; Vivek Kapur; Jon Epstein; gavin.smith ; Ian MENDENHALL PhD; kityrob ; Rebekah.Kading@
Subject: RE: [Non-DoD Source] Re: UPDATE: Global Bat Alliance Network (convened on behalf of CBEP)

All,

Attached please find notes and action items from today's GBA planning meeting call. We will get started on some of the action items, which we will send to the group for comment. This will include a draft agenda for our 29 June meeting at Fort Collins, and the draft Terms of Reference for the Steering Committee.

We will also send out a calendar invitation for our next planning call. Please visit the following link: PollEv.com/gbaplanning and select the best date/time that works for your schedule, during the first week of June.

Thank you,
Caitlin Devaney

Caitlin Devaney
Global Security Programs
Cubic Global Defense
5695 King Centre Drive

w: globalsecurity.cubic.com

-----Original Message-----
From: Stokes, Martha M CIV (US)
Sent: Monday, May 15, 2017 9:06 AM
To: Kevin Olival, PhD; Leahy, Catharine (US); Lancaster, Mary J CIV (US); Sander, William E CTR (US); Joram Buza; Vivek Kapur; Jon Epstein; gavin.smith ; Ian MENDENHALL PhD; kityrob ; Devaney, Caitlin (US); Rebekah.Kading
Subject: RE: [Non-DoD Source] Re: UPDATE: Global Bat Alliance Network (convened on behalf of CBEP)

Kevin,

Wonderful, thanks so much.

Good call this morning, and thank you to all who were able to join. We'll send out action items and notes quickly so we can move forward on developing a clear and useful agenda for the Fort Collins meeting.

Best,

Marty

-----Original Message-----

From: Kevin Olival, PhD ecohealthalliance.org]

Sent: Monday, May 15, 2017 8:59 AM

To: Leahy, Catharine (US) < ; Lancaster, Mary J CIV (US)
Stokes, Martha M CIV (US) ; Sander, William E CTR (US)
>; Joram Buza >; Vivek Kapur < ; Jon Epstein
econealthalliance.org>; gavin.smith Ian MENDENHALL PhD ;
Kityrob Devaney, Caitlin (US) Rebekah.Kading

Subject: [Non-DoD Source] Re: UPDATE: Global Bat Alliance Network (convened on behalf of CBEP)

_____

Dear all,

As mentioned, here is Tigga's book chapter on global bat conservation networks that I mentioned. The chapter is available for free download, as is the whole book!

Caution-https://urldefense.proofpoint.com/v2/url?u=http-3A__link.springer.com_chapter_10.1007-252F978-2D3-2D319-2D25220-2D9-5F17&d=DwIGaQ&c=zUSW9Sw6oKY41zSJbj5J3w&r=q3-bqrVcX8tMM0pJCuF-6hCthhszKVXjqAumC3t65V4&m=bRoMgqohipNm6xLuJ0skY9StYccu2_Yz4GX5HnIjXNU&s=jokhkk_Yq9FAsOcmSpb-MTAQpwo_sQHdiO9rCBmjeSI&e= < Caution-https://urldefense.proofpoint.com/v2/url?u=http-3A__link.springer.com_chapter_10.1007-252F978-2D3-2D319-2D25220-2D9-5F17&d=DwIGaQ&c=zUSW9Sw6oKY41zSJbj5J3w&r=q3-bqrVcX8tMM0pJCuF-6hCthhszKVXjqAumC3t65V4&m=bRoMgqohipNm6xLuJ0skY9StYccu2_Yz4GX5HnIjXNU&s=jokhkk_Yq9FAsOcmSpb-MTAQpwo_sQHdiO9rCBmjeSI&e= >

Cheers,

Kevin

Kevin J. Olival, PhD

Associate Vice President for Research

EcoHealth Alliance

460 West 34th Street - 17th floor

New York, NY 10001

)

Caution-www.ecohealthalliance.org < Caution-https://urldefense.proofpoint.com/v2/url?u=http-

3A__www.ecohealthalliance.org_&d=DwIGaQ&c=zUSW9Sw6oKY41zSJbj5J3w&r=q3-bqrVcX8tMM0pJCuF-6hCthhszKVXjqAumC3t65V4&m=bRoMgqohipNm6xLuJ0skY9StYccu2_Yz4GX5HnIjXNU&s=3fYejJJAbn2OdDfdvqsBMiCfjca1ahGM1X_emMlEjuk&e=
>

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

On May 15, 2017, at 7:00 AM, Leahy, Catharine (US) <
wrote:

<Bat meeting notes 9Feb2017.docx>

From: Kingston, Tigga >
Sent: Tuesday, February 13, 2018 9:59 AM EST
To: Katie Leahy ; lance.r.brooks ; Newman, Carl I CIV DTRA J3-7 (US) ; Lancaster, Mary J CIV (US) >; christopher.r.lewis >; Kading,Rebekah >; DeeAnn Reeder >; Cryan, Paul ; Vivek Kapur >; Gavin James Smith >; abelwade ; Ian Mendenhall ; tamar_kutateladze >; Keti Sidamonidze ; Lela Urushadze >; joram.buza ; c_demetria >; Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; cryan.paul
CC: Stokes, Martha M CIV (US) >; Simmi Ghai ; S Wacharapluesadee
Subject: RE: Afternoon Session

Katie
Could you share (or share again) the final slides we put together for the afternoon session – these were the ones we presented to the group. Possibly they were sent out before, but I can't find them.
Thank you
Tigga

From: Katie Leahy
Sent: Tuesday, January 30, 2018 12:15 AM
To: lance.r.brooks ; Newman, Carl I CIV DTRA J3-7 (US) >; Lancaster, Mary J CIV (US) >; christopher.r.lewis Kading,Rebekah >; DeeAnn Reeder ; Cryan, Paul ; Vivek Kapur ; Gavin James Smith >; Kingston, Tigga >; abelwade Ian Mendenhall >; tamar_kutateladze Keti Sidamonidze ; Lela Urushadze >; joram.buza c_demetria ; Kevin Olival ecohealthalliance.org>; Jon Epstein @ecohealthalliance.org>; cryan.paul
Cc: Stokes, Martha M CIV (US) < ; Simmi Ghai ; S Wacharapluesadee

Subject: Afternoon Session

All,

Here are slides to start filling out for the afternoon session.

V/r,

Katie Leahy

From: Katie Leahy
Date: Tuesday, January 30, 2018 at 10:30 AM
To: "lance.r.brooks " , "Newman, Carl I CIV DTRA J3-7 (US)" , "Lancaster, Mary J CIV (US)" , "christopher.r.lewis " , "Kading,Rebekah" >, DeeAnn Reeder >, "Cryan, Paul" , Vivek Kapur , Gavin James Smith , Tigga Kingston , "abelwade " >, Ian Mendenhall "tamar_kutateladze " >, Keti Sidamonidze , Lela Urushadze >, "joram.buza " "c_demetria " < >, Kevin Olival ecohealthalliance.org>, Jon Epstein ecohealthalliance.org>, Jason Rao , "cryan.paul "

Cc: "Stokes, Martha M CIV (US)" Simmi Ghai , S Wacharapluesadee >
Subject: NEW SLIDES

Here are the working group slides that were live-edited for your use in break-out groups.

V/r,

Katie Leahy

From: Katie Leahy
Date: Monday, January 29, 2018 at 9:01 PM
To: "lance.r.brooks " , "Newman, Carl I CIV DTRA J3-7 (US)" , "Lancaster, Mary J CIV (US)" , "christopher.r.lewis >, "Kading,Rebekah" , DeeAnn Reeder >, "Cryan, Paul" >, Vivek

Kapur >, Gavin James Smith , Tigga Kingston >, "abelwade , Ian Mendenhall "tamar_kutateladze " >, Keti Sidamonidze >, Lela Urushadze >, "joram.buza " "c_demetria " , Kevin Olival ecohealthalliance.org>, Jon Epstein ecohealthalliance.org>, Jason Rao , "cryan.paul " >
Cc: "Stokes, Martha M CIV (US)" , Simmi Ghai , S Wacharapluesadee
Subject: Update to the BPERNet Slides

Hi, everyone! We made a couple changes to the slides for tomorrow. Nothing substantive, just our approach to conducting the brief-out discussions and the order of a couple of the initial slides.

A reminder again to please be in the lobby at 0745, the bus will depart for Chulalongkorn promptly at 0800.

V/r,

Katie Leahy

From: Katie Leahy >
Date: Monday, January 29, 2018 at 10:28 AM
To: "lance.r.brooks " >, "Newman, Carl I CIV DTRA J3-7 (US)" , "Lancaster, Mary J CIV (US)" , "christopher.r.lewis " , "Kading,Rebekah" >, DeeAnn Reeder >, "Cryan, Paul" >, Vivek Kapur >, Gavin James Smith >, Tigga Kingston >, "abelwade , Ian Mendenhall "tamar_kutateladze " >, Keti Sidamonidze , Lela Urushadze >, "joram.buza " "c_demetria " >, Kevin Olival ecohealthalliance.org>, Jon Epstein ecohealthalliance.org>
Cc: "Stokes, Martha M CIV (US)" , Simmi Ghai < , S Wacharapluesadee
Subject: BPERNet: Transportation Times and Other Useful Information (30 and 31 January 2017)

Hello, everyone! Welcome to Bangkok. On behalf of the Executive Committee (Dr. Martha Stokes and Dr. Mary Lancaster), we are so pleased that you are able to join us this week for our BPERNet planning meeting and other PMAC activities.

Please use this email as your resource for information regarding transportation, logistics, and other coordinating information for 30 January – 31 January.

30 January – BPERNet Meeting at Chulalongkorn Hospital

1. **The bus will depart from the Renaissance Hotel promptly at 0800** ; please be in the lobby for head count at 0745
2. We will provide coffee and light refreshment during the meeting; you will take lunch at one of the many canteen options at the hotel; please bring about 200 - 300 thai baht (~10 USD) for lunch

31 January – PMAC / BPERNet Field Trip

1. **The bus will depart from the Renaissance Hotel promptly at 0630** ; please be in the lobby for head count at 0615; please make sure that you are on time, as we are caravanning with a delegation from the Centara Hotel and will receive a police escort to move us quickly through traffic
2. We will provide a box breakfast for the bus ride
3. Please make sure that you dress appropriately for this field trip; we strongly suggest covered shoes and loose, comfortable clothing; in addition to this mode of dress we also suggest that you bring accompaniments for spending a day outdoors amongst bat roosts; such as:
    a. Hat
    b. Sunscreen
    c. Sunglasses
    d. Bug spray
    e. Water bottle

We will provide information regarding the Ambassador's reception at the close of tomorrow's meeting.

Again, we are so excited to have you all here. Please do not hesitate to reach out to me or Megan Hudson (copied) if you have any questions.

V/r,

Katie Leahy

Katie Leahy
Program Manager | Global Systems Engineering
6303 Little River Turnpike, Suite 208
Alexandria, VA 22305

http://globalsyseng.com

From: Wade Abel
Sent: Wednesday, January 31, 2018 11:53 PM EST
To: Katie Leahy >
CC: Brooks, Lance R CIV DTRA J3-7 (US) ; Newman, Carl I CIV DTRA J3-7 (US) >; Lancaster, Mary J CIV DTRA J3-7 (US) >; christopher.r.lewis >; Kading,Rebekah >; DeeAnn Reeder >; Paul Cryan >; Vivek Kapur ; Gavin James Smith ; Tigga Kingston ; Ian Mendenhall ; Tamar Kutateladze Keti Sidamonidze ; Lela Urushadze ; Joram Buza ; Catalino Demetria Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; cryan.paul ; Stokes, Martha M CIV (US) ; Simmi Ghai >; Supaporn Wacharapluesadee ; cnkisinga >
Subject: Re: Afternoon Session

Dear Katie
Just to find out if you could please remain us or give us more info about the transport arrangement for the diner invitation by the Ambassador this evening.
Kind regards

Wade

On 30 Jan 2018 1:15 pm, "Katie Leahy" wrote:

> All,
>
> Here are slides to start filling out for the afternoon session.
>
> V/r,
>
> Katie Leahy

From: Katie Leahy >
Date: Tuesday, January 30, 2018 at 10:30 AM
To: "lance.r.brooks >, "Newman, Carl I CIV DTRA J3-7 (US)" "Lancaster, Mary J CIV (US)" , "christopher.r.lewis " >, "Kading,Rebekah" >, DeeAnn Reeder >, "Cryan, Paul" , Vivek Kapur >, Gavin James Smith >, Tigga Kingston , "abelwade " , Ian Mendenhall "tamar_kutateladze " , Keti Sidamonidze , Lela Urushadze >, "joram.buza " "c_demetria " >, Kevin Olival ecohealthalliance.org>, Jon Epstein ecohealthalliance.org >, Jason Rao >, "cryan.paul " >
Cc: "Stokes, Martha M CIV (US)" Simmi Ghai , S Wacharapluesadee
Subject: NEW SLIDES

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V/r,

Katie Leahy

From: Katie Leahy
Date: Monday, January 29, 2018 at 9:01 PM
To: "lance.r.brooks " , "Newman, Carl I CIV DTRA J3-7 (US)" "Lancaster, Mary J CIV (US)" "christopher.r.lewis >, "Kading,Rebekah" , DeeAnn Reeder , "Cryan, Paul" >, Vivek Kapur >, Gavin James Smith , Tigga Kingston >, "abelwade " >, Ian Mendenhall , "tamar_kutateladze " < >, Keti Sidamonidze >, Lela Urushadze >, "joram.buza " "c_demetria " >, Kevin Olival ecohealthalliance.org>, Jon Epstein ecohealthalliance.org >, Jason Rao , "cryan.paul " >
Cc: "Stokes, Martha M CIV (US)" Simmi Ghai Wacharapluesadee >
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V/r,

Katie Leahy

From: Katie Leahy
Date: Monday, January 29, 2018 at 10:28 AM
To: "lance.r.brooks " , "Newman, Carl I CIV DTRA J3-7 (US)" , "Lancaster, Mary J CIV (US)" "christopher.r.lewis " >, "Kading,Rebekah" <Rebekah.Kading , DeeAnn Reeder >, "Cryan, Paul" < >, Vivek Kapur >, Gavin James Smith >, Tigga Kingston >, "abelwade " >, Ian Mendenhall "tamar_kutateladze " >, Keti Sidamonidze >, Lela Urushadze >, "joram.buza " "c_demetria " >, Kevin Olival ecohealthalliance.org>, Jon Epstein ecohealthalliance.org >
Cc: "Stokes, Martha M CIV (US)" < , Simmi Ghai S Wacharapluesadee
Subject: BPERNet: Transportation Times and Other Useful Information (30 and 31 January 2017)

Hello, everyone! Welcome to Bangkok. On behalf of the Executive Committee (Dr. Martha Stokes and Dr. Mary Lancaster), we are so pleased that you are able to join us this week for our BPERNet planning meeting and other PMAC activities.

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    b. Sunscreen
    c. Sunglasses
    d. Bug spray
    e. Water bottle

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Again, we are so excited to have you all here. Please do not hesitate to reach out to me or Megan Hudson (copied) if you have any questions.

V/r,

Katie Leahy

Katie Leahy

Program Manager | Global Systems Engineering

6303 Little River Turnpike, Suite 208

Alexandria, VA 22305

http://globalsyseng.com

From: Kevin Olival ecohealthalliance.org>
Sent: Monday, September 14, 2020 8:29 PM EDT
To: Kading,Rebekah
Subject: Re: Bat One Health Research Network Directory - request to join!

Signed up!

-Kevin

On Sep 14, 2020, at 12:30 PM, Kading,Rebekah wrote:

Dear BOHRN colleagues,

Oh my goodness, what a year it has been! We hope this message finds you all healthy and safe. While the pandemic has taken many of us on various detours from our usual routine and research over the past six months, we all have been very busy responding to this pandemic in myriad ways. In many cases, BOHRN network members have found ourselves working together on various initiatives, which has been exciting. We are looking forward to the time when we can interact in person again at conferences and at future BOHRN meetings. Thank you SO MUCH for all your efforts during this challenging time!

Tigga and I are writing to you today with a BOHRN-related update and a **specific action request to participate in a BOHRN membership directory (more details below)**.

The context: One of the positive outcomes of months of quarantine in Texas (Tigga) and Colorado (Rebekah) -- is that we followed up in a tangible way on one of the key challenges identified during our BORHN meetings: addressing the polarization of the bat ecology and infectious disease research communities. We have written a Perspectives piece, currently in review at PLOS Biology, which reports the results of a bibliometric analysis of co-author relationships among bat researchers between 1950 and 2019. This analysis identified a division between ecology- and infectious disease disciplines from the perspective of co-authored interdisciplinary journal articles (no surprise there!). However, our fields have done a good job at converging over issues that have presented a common mission, such as white nose syndrome. SARS-CoV-2 has provided a similar common ground for us to rally around as far as the risk this virus poses to both human and bat health. The editors and reviewers have challenged us to take steps that will actually lead to productive outcomes and interdisciplinary collaborations. Hence, we are very excited to engage directly with BOHRN and build on the infrastructure that has already been put into place by DTRA-BTRP.

Action item: In the immediate-term, **our goal is build a searchable membership directory housed within the BOHRN website.** This will enable members to connect with each other, learn more about what others are doing, and recruit people to the various working groups that BOHRN has established. DTRA and Global Systems Engineering have graciously and expeditiously revamped the website to enable this specific functionality. **How this works**: interested stakeholders will set up a member login on the BOHRN website as well as a member profile that will be visible to other members after logging in. **Members will benefit** from being able to search the directory for colleagues in complementary research areas, and receive information disseminated by BOHRN regarding opportunities and meetings. All of the information you enter will be accessible only to other members.

Steps we're asking you to take:

1. Go to https://www.bohrn.net
2. Click on "Join"
3. Create an account, fill out your profile
4. Check the boxes to affirm that you agree with having your information visible to others within the member page, and with the BOHRN mission statement (provided)
5. Click "Continue" to be brought to the Members page.
6. Your profile will automatically be entered into the directory, butthis may take a few hours to sync and be visible on the website.
7. From the Members page you should be able to view other member profiles as well as search the directory.

Thanks so much, and please don't hesitate to reach out to us if you have any questions. We look forward staying in contact and growing the BOHRN network together.

Kind regards,

Rebekah and Tigga

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Robert Kityo
Sent: Friday, June 15, 2018 1:53 PM EDT
To: Megan Hudson
CC: nisreen.hmoud >; joram.buza
c_demetria ; Kading,Rebekah
tamar_kutateladze >; dreeder ;
ksidamonidze ; l.urushadze ;
spwa abelwade ; ecohealthalliance.org
>; ian.mendenhall ;
ecohealthalliance.org ; vkapur Katie Leahy
>; Gano Cohen, Kelsey A CTR DTRA J3-7 (US) ;
Stokes, Martha M CIV (US) Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US)

Subject: Re: BOHRN Meeting Agenda and Materials 20 - 21 June

Dear Megan Hudson
I pray that all in the mailing list are in good health.
Today was a public holiday in Uganda (and I think all of East Africa and beyond). By close of business yesterday the information I had from the Canadian Embassy (Tanzania office where Visas for Ugandan applicants are processed) was that my Visa was "being processed@. Therefore I don't have have one yet.
My last hope is that I get back my passport on Monday from Tanzania with a visa. I requested that my travel plans be moved to the 19th June therefore. If the Visa comes through, I will only be able to arrive in Canada late on the 20th and therefore will be unable to attend business on the 20th June. I shall fill the ResearchQuard and return it in the hope that I shall make the trip and therefore be able to talk about it on the 21st if the schedule will permit for this.
I shall give an update on Monday if I receive back my passport from Dar-er salaam with the Visa.
Best regards
Robert Kityo

Kityo Robert M (PhD)
Makerere University
College of Natural Sciences
School of BioSciences
Department of Zoology, Entomology and Fisheries Sciences

On Thu, Jun 14, 2018 at 9:31 PM, Megan Hudson > wrote:

> All,
>
> The final agenda for our BOHRN 20 – 21 June meeting is attached. Our meeting will be held in the Garden South Meeting Room at the Hilton Garden Inn in Saskatoon (90 22 St. E, Saskatoon, SK S7K 3X6, Canada).
>
> From our discussions in January we built in time to discuss your current research, as part of this event's agenda. In order to maintain time for BOHRN discussions, we are asking for you to fill out the attached quad chart. Quad charts are designed to give a quick overview of information. Therefore, please don't try to fit all of your research into the boxes, just important points or conclusions you would like to provide to the group. **Please review and fill in the quad chart prior to our meeting, and plan on presenting your chart in 5 minutes during the first day**.
>
> We are requesting that you email your quad chart back **NLT Monday, 18 June**. Attached are instructions and a blank quad chart. Be advised that we will only project one slide, therefore all information must fit within the attached chart provided.
>
> Let us know if you have any questions regarding any of the documents. **As a reminder we will need a completed quad chart from you NLT 18 June.** We look forward to seeing everyone next week in Canada.
>
> Thank you,
>
> Megan

Megan Hudson

Task Lead | Global Systems Engineering

6303 Little River Turnpike #208

Alexandria, VA 22312

http://globalsyseng.com

From: Kingston, Tigga
Sent: Tuesday, August 25, 2020 1:50 PM EDT
To: Stokes, Martha M CIV (USA)
CC: Katie Leahy >; Hoyle, Jamechia D CTR (USA) ; Guzal Masharipova <guzal. ; Kading,Rebekah >; epstein ecohealthalliance.org>
Subject: RE: BOHRN Status, publication

Dear Marty
Thanks for the speedy response and support! Great to hear of the documentation efforts and continued commitment.

The lynchpin to everything that we'd like to do is the BOHRN website – is there a webmaster, or can one be allocated, so that we can host content, build membership, post some of the materials that have been developed.

Best
Tigga

From: Stokes, Martha M CIV (USA) < >
Sent: Tuesday, August 25, 2020 8:45 AM
To: Kingston, Tigga >
Cc: Katie Leahy Hoyle, Jamechia D CTR (USA) Guzal Masharipova Kading,Rebekah < Jon Epstein ecohealthalliance.org>
Subject: RE: BOHRN Status, publication

Hi Tigga,

Congratulations on having your piece accepted (with revisions, as always)! I would really appreciate you adding detail about BOHRN and highlighting the network's efforts. All of the positive outcomes you mention are well noted and align with our goals and objectives, which remain steadfast.

The current situation has certainly created unexpected challenges for all our work, but we're adapting, and want to ensure that we continue moving forward and position the network to pick up where it left off last summer, once things return to a more normal environment. In the meantime, we'll do what we are able virtually.

Let us know what you need to support this. Katie and I, along with our teams, recently updated a huge amount of documentation, reports, participant lists, etc. for BOHRN and other our TRNs for the incoming BTRP Director, in order to deposit it on our internal database, so it should be very easy to provide whatever you need. Just let us know how we can help.

Thanks so much!

Best,
Marty

Martha M Stokes, PhD
Southeast Asia Regional Science Manager
Biological Threat Reduction Program (BTRP)

From: "Kingston, Tigga" >
Date: Monday, August 24, 2020 at 5:09 PM
To: "martha.m.stokes.civ"
Cc: Katie Leahy "jamechia.d.hoyle.ctr" , Guzal Masharipova "Kading,Rebekah" >, Jon Epstein ecohealthalliance.org>
Subject: [External Sender] BOHRN Status, publication

Dear Marty,

Rebekah Kading and I wrote a perspectives piece that is in revision for PLOS Biology. It calls for greater integration of ecologists/virologists (hmm, sounds familiar) and builds on analysis of a publication coauthor network. We conceptualized this at

BORHN meetings and consider it a true BOHRN output, supporting BOHRN's message.

One of the reviewers specified some simple, but concrete actions that they would like to see in the revision. These actions closely ally with things we've begun at BOHRN (e.g., mission statement, contact lists of researchers). We would really like to be able to respond using BOHRN's infrastructure as it would be a good fit and would draw substantial attention to BOHRN and help boost the distributed membership and get us more on the map. The reviewer called for a mission statement, a list of who is doing what, and other simple things that could easily be integrated into the BOHRN website.

Currently, we refer to BOHRN in the acknowledgements, but have been reluctant to feature the network too centrally because we are unsure of its status and stability. It would be great to move forward with BOHRN featured more prominently, but we could do with some clarity of where things are heading. At minimum we need support of the website as that is where we will be directing people. Currently people can't join, or reset passwords etc, and we would need to work with someone on updates supporting these simple collations of information.

We have a bit less than a month to turn this around and get our revision in, so it would be great to hear your thoughts. I hope we can talk soon. I am now free fairly consistently between 10 am-Noon Mo-Thursday. I have other windows here and there as well.

All the best

Tigga

From: Stokes, Martha M CIV (USA)
Sent: Tuesday, August 25, 2020 9:44 AM EDT
To: Kingston, Tigga
CC: Katie Leahy >; Hoyle, Jamechia D CTR (USA) ; Guzal Masharipova ; Kading,Rebekah ; epstein <epstein
Subject: RE: BOHRN Status, publication

Hi Tigga,

Congratulations on having your piece accepted (with revisions, as always)! I would really appreciate you adding detail about BOHRN and highlighting the network's efforts. All of the positive outcomes you mention are well noted and align with our goals and objectives, which remain steadfast.

The current situation has certainly created unexpected challenges for all our work, but we're adapting, and want to ensure that we continue moving forward and position the network to pick up where it left off last summer, once things return to a more normal environment. In the meantime, we'll do what we are able virtually.

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Thanks so much!

Best,
Marty

Martha M Stokes, PhD
Southeast Asia Regional Science Manager
Biological Threat Reduction Program (BTRP)

From: "Kingston, Tigga" >
Date: Monday, August 24, 2020 at 5:09 PM
To: "martha.m.stokes.civ"
Cc: Katie Leahy , "jamechia.d.hoyle.ctr" >, Guzal Masharipova , "Kading,Rebekah" , Jon Epstein ecohealthalliance.org>
Subject: [External Sender] BOHRN Status, publication

Dear Marty,

Rebekah Kading and I wrote a perspectives piece that is in revision for PLOS Biology. It calls for greater integration of ecologists/virologists (hmm, sounds familiar) and builds on analysis of a publication coauthor network. We conceptualized this at BORHN meetings and consider it a true BOHRN output, supporting BOHRN's message.

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We have a bit less than a month to turn this around and get our revision in, so it would be great to hear your thoughts. I hope we can talk soon. I am now free fairly consistently between 10 am-Noon Mo-Thursday. I have other windows here and there as well.

All the best

Tigga

From: Tamar Kutateladze >
Sent: Wednesday, July 24, 2019 6:08 AM EDT
To: Paul Cryan ; Catalino Demetria Kading,Rebekah ; Kingston, Tigga ; Robert Kityo ; Ian MENDENHALL PhD Kevin Olival, PhD ecohealthalliance.org>; DeeAnn Reeder ; Keti Sidamonidze >; Gavin Smith Lela Urushadaze ; Jon Epstein ecohealthalliance.org>
CC: Katie Leahy >; Stokes, Martha M. ; Megan Hudson >
Subject: Re: BOHRN steering committee - preparation for data discussion

Dear Jon,

This is to inform you, that I did not receive the invitation to participate this meeting.

Yours sincerely,

Tamar

Tamar Kutateladze,MD, PhD.

R. Lugar Center for Public Health Research
National Center for Disease Control & Public Health

On Tuesday, July 23, 2019, 3:02:20 AM GMT+4, Jon Epstein ecohealthalliance.org> wrote:

Dear BOHRN Steering Committee Members,
As part of our poliolab@ncdc.ge Marty and Katie would like us to discuss data curation and data standardization for BOHRN projects. The plan is to begin the discussion during the SC meeting, and then have a broader discussion, on day three, with the full group. On Sunday, Noam Ross from EHA will present some specific ideas around data standardization to kick start the discussion, focusing on how we might approach developing a common database or data collection standard that can be used across BOHRN projects to facilitate broader analyses. Noam works with Kevin on the PREDICT Modeling & Analytics team and has substantial experience with data management and curation.

We'll also discuss whether and how we might want to make existing datasets available to the BOHRN network, to create opportunities for scientists to leverage them to develop new projects or perform new analyses. For this part, Marty has requested that we come prepared with a list or description of datasets, (e.g. those already published) that we have in hand that could be made available to the BOHRN network.

If you have any questions, don't hesitate to reach out to Katie Leahy Marty, or me. I look forward to seeing you all in Phuket soon.

Safe travels.

Cheers,
Jon

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street, Ste. 1701

New York, NY 10001

web: ecohealthalliance.org

Twitter:

EcoHealth Alliance leads cutting-edge scientific research into the critical connections between human and wildlife health and delicate ecosystems. With this science, we develop solutions that prevent pandemics and promote conservation.

From: Lela Urushadze
Sent: Tuesday, July 23, 2019 7:48 AM EDT
To: Jon Epstein ecohealthalliance. ; Wade Abel ; Nisreen Alhmoud >; joram buza >; Paul Cryan < Catalino Demetria >; Kading,Rebekah ; Kingston, Tigga Robert Kityo Ian MENDENHALL PhD Kevin Olival, PhD ecohealthalliance.org>; Plowright, Raina < >; Tamar Kutateladze ; DeeAnn Reeder >; Keti Sidamonidze >; Gavin Smith Supaporn Wacharapluesadee

CC: Katie Leahy >; Stokes, Martha M. >; Megan Hudson

Subject: Re: BOHRN steering committee - preparation for data discussion

Dear Jon

Thank you for the information
We will prepare list of published datasets, as you suggetsed, from Georgian side.

Regards
Lela

From: Jon Epstein ecohealthalliance.org>
Sent: Tuesday, July 23, 2019 03:01:43
To: Wade Abel; Nisreen Alhmoud; joram buza; Paul Cryan; Catalino Demetria; Kading,Rebekah; Kingston, Tigga; Robert Kityo; Ian MENDENHALL PhD; Kevin Olival, PhD; Plowright, Raina; Tamar Kutateladze; DeeAnn Reeder; Keti Sidamonidze Gmail; Gavin Smith; Lela Urushadze; Supaporn Wacharapluesadee
Cc: Katie Leahy; Stokes, Martha M.; Megan Hudson
Subject: BOHRN steering committee - preparation for data discussion

Dear BOHRN Steering Committee Members,
As part of our upcoming meeting, Marty and Katie would like us to discuss data curation and data standardization for BOHRN projects. The plan is to begin the discussion during the SC meeting, and then have a broader discussion, on day three, with the full group. On Sunday, Noam Ross from EHA will present some specific ideas around data standardization to kick start the discussion, focusing on how we might approach developing a common database or data collection standard that can be used across BOHRN projects to facilitate broader analyses. Noam works with Kevin on the PREDICT Modeling & Analytics team and has substantial experience with data management and curation.

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If you have any questions, don't hesitate to reach out to Katie Leahy Marty, or me. I look forward to seeing you all in Phuket soon.

Safe travels.

Cheers,
Jon

--
Jonathan H. Epstein DVM, MPH, PhD
Vice President for Science and Outreach
EcoHealth Alliance
460 West 34th Street, Ste. 1701
New York, NY 10001

From: Wade Abel >
Sent: Monday, July 22, 2019 10:40 PM EDT
To: Jon Epstein ecohealthalliance.org>
CC: Nisreen Alhmoud ; Joram Buza >; Paul Cryan >; Catalino Demetria < Kading,Rebekah >; Kingston, Tigga Robert Kityo ; Ian MENDENHALL PhD ; Kevin Olival, PhD ecohealthalliance.org> Plowright, Raina ; Tamar Kutateladze ; DeeAnn Reeder >; Keti Sidamonidze >; Gavin Smith Lela Urushadaze >; Supaporn Wacharapluesadee ; Katie Leahy ; Stokes, Martha M. < ; Megan Hudson >
Subject: Re: BOHRN steering committee - preparation for data discussion

Sound perfect. Looking forward to it!

Regards
Wade

On Tue, 23 Jul 2019, 00:02 Jon Epstein, ecohealthalliance.org> wrote:

> Dear BOHRN Steering Committee Members,
> As part of our upcoming meeting, Marty and Katie would like us to discuss data curation and data standardization for BOHRN projects. The plan is to begin the discussion during the SC meeting, and then have a broader discussion, on day three, with the full group. On Sunday, Noam Ross from EHA will present some specific ideas around data standardization to kick start the discussion, focusing on how we might approach developing a common database or data collection standard that can be used across BOHRN projects to facilitate broader analyses. Noam works with Kevin on the PREDICT Modeling & Analytics team and has substantial experience with data management and curation.
>
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>
> If you have any questions, don't hesitate to reach out to Katie Leahy Marty, or me. I look forward to seeing you all in Phuket soon.
>
> Safe travels.
>
> Cheers,
> Jon

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street, Ste. 1701

New York, NY 10001

web: ecohealthalliance.org

From: Keti Sidamonidze
Sent: Friday, March 23, 2018 2:54 AM EDT
To: Megan Hudson
CC: nisreen.hmoud ; joram.buza
cryanp >; c demetria >;
ecohealthalliance.org >; Kading,Rebekah
vkapur ; tigga.kingston ; kityrob
; tamar kutateladze ; ian.mendenhall
; ecohealthalliance.org ;
dreeder gavin.smith ;
l.urushadze ; spwa ; abelwade
; Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) >;
Gano Cohen, Kelsey A CTR DTRA J3-7 (US) ; Katie Leahy
Stokes, Martha M CIV (US) Becker, Stephen M CTR
DTRA J3-7 (US)
Subject: Re: BOHRN Steering Committee/One Health Congress Meeting

Dear Megan,
Thank you for the information.
I confirm attendance at the meeting.
Regards,
- Keti

On Thu, Mar 22, 2018 at 9:46 PM, Megan Hudson > wrote:

> All,
>
> You are receiving this email, as part of a save the date to attend our BOHRN Steering Committee meeting and the 5th International One Health Congress (OHC) in Saskatoon, Canada.
>
> Our meeting will take place on 20-21 June (location TBD, though likely at the Hilton Garden Inn). The agenda and travel information for this two day event will follow shortly. The OHC will take place 22-25 June.
>
> On behalf of Dr. Marty Stoke and Dr. Mary Lancaster, CBEP will provide funding your travel and registration to the OHC and BOHRN Planning Meeting. While the OHC is not required it would be a good opportunity for networking on behalf of BOHRN. CBEP will be paying for OHC attendance next week. **Therefore, we need you to confirm your attendance to the OHC NLT tomorrow 23 March.** However, please note if regulations for DoD travel are not met by the specified due date, funding for the conference and travel will not be provided.
>
> Please respond with your availability to attend the meeting NLT 23 March.
>
> v/r,
>
> Megan
>
> **Megan Hudson**
>
> *Task Lead* | Global Systems Engineering
>
> 6303 Little River Turnpike #208
>
> Alexandria, VA 22312
>
> http://globalsyseng.com
>
>

--
Keti Sidamonidze, MD
Senior Specialist, Department of Virology, Molecular Biology and Genome Research,
R.G. Lugar Center for Public Health Research,National Center for Disease Control & Public Health
9 M. Asatiani st, Tbilisi 0177, Georgia

From: Prof. Joram Buza >
Sent: Thursday, March 22, 2018 9:56 PM EDT
To: Megan Hudson <
CC: nisreen.hmoud ; cryanp c _demetria ; ecohealthalliance.org ; Kading,Rebekah ; vkapur ; tigga.kingston ; kityrob >; tamar kutateladze ; ian.mendenhall ; ecohealthalliance.org >; dreeder >; ksidamonidze ; gavin.smith ; l.urushadze < >; spwa >; abelwade ; Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) ; Gano Cohen, Kelsey A CTR DTRA J3-7 (US) < >; Katie Leahy ; Stokes, Martha M CIV (US) ; Becker, Stephen M CTR DTRA J3-7 (US) >
Subject: Re: BOHRN Steering Committee/One Health Congress Meeting

Dear Megan
This is to confirm that I will attend the Saskatoon meeting in June.

Buza

On Mar 22, 2018 20:46, "Megan Hudson" > wrote:

> All,
>
> You are receiving this email, as part of a save the date to attend our BOHRN Steering Committee meeting and the 5th International One Health Congress (OHC) in Saskatoon, Canada.
>
> Our meeting will take place on 20-21 June (location TBD, though likely at the Hilton Garden Inn). The agenda and travel information for this two day event will follow shortly. The OHC will take place 22-25 June.
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> Please respond with your availability to attend the meeting NLT 23 March.
>
> v/r,
>
> Megan
>
> **Megan Hudson**
>
> *Task Lead* | Global Systems Engineering
>
> 6303 Little River Turnpike #208
>
> Alexandria, VA 22312
>
> http://globalsyseng.com
>
>

From: Tamar Kutateladze
Sent: Friday, March 23, 2018 5:05 AM EDT
To: nisreen.hmoud ; cryanp ; c_demetria >; ecohealthalliance.org ; Kading,Rebekah ; vkapur ; kityrob ; ian.mendenhall ecohealthalliance.org >; dreeder ksidamonidze ; gavin.smith ; l.urushadze ; spwa >; abelwade >; Megan Hudson
CC: Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) ; Gano Cohen, Kelsey A CTR DTRA J3-7 (US) ; Katie Leahy >; Stokes, Martha M CIV (US) >; Becker, Stephen M CTR DTRA J3-7 (US) >
Subject: Re: BOHRN Steering Committee/One Health Congress Meeting

Dear Megan,

Thanks for information.

I confirm my attendance to the meeting and one health congress.

Yours Sincerely,
Tamar

Tamar Kutateladze,

MD, PhD,Department of Virology, MolecularBiology and Genome Research,
R. Lugar Center for Public Health Research
National Center for Disease Control & Public Health

On Thursday, March 22, 2018, 9:46:06 PM GMT+4, Megan Hudson > wrote:

All,

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Please respond with your availability to attend the meeting NLT 23 March.

v/r,

Megan

Megan Hudson

Task Lead | Global Systems Engineering

6303 Little River Turnpike #208

Alexandria, VA 22312

http://globalsyseng.com

From: c_demetria >
Sent: Thursday, March 22, 2018 9:28 PM EDT
To: Megan Hudson >; nisreen.hmoud
joram.buza ; cryanp >;
ecohealthalliance.org ; Kading,Rebekah
vkapur ; tigga.kingston ; kityrob
>; tamar_kutateladze ; ian.mendenhall
; ecohealthalliance.org
dreeder ksidamonidze ;
gavin.smith l.urushadze ;
spwa ; abelwade
CC: Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) ; Gano Cohen, Kelsey
A CTR DTRA J3-7 (US) >; Katie Leahy >; Stokes, Martha
M CIV (US) >; Becker, Stephen M CTR DTRA J3-7 (US)

Subject: RE: BOHRN Steering Committee/One Health Congress Meeting

Hi Megan,

I confirm my attendance to the meeting and one health congress.

Sincerely,

Sent from my Samsung Galaxy smartphone.

-------- Original message --------
From: Megan Hudson <
Date: 3/23/18 1:46 AM (GMT+08:00)
To: nisreen.hmoud , joram.buza , cryanp , c_demetria ,
ecohealthalliance.org, rebekah.kading , vkapur , tigga.kingston
kityrob , tamar_kutateladze , ian.mendenhall , ecohealthalliance.org,
dreeder , ksidamonidze , gavin.smith , l.urushadze ,
spwa , abelwade
Cc: "Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US)" , "Gano Cohen,
Kelsey A CTR DTRA J3-7 (US)" , Katie Leahy
"Stokes, Martha M CIV (US)" "Becker, Stephen M CTR DTRA J3-7 (US)"

Subject: BOHRN Steering Committee/One Health Congress Meeting

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Please respond with your availability to attend the meeting NLT 23 March.

v/r,

Megan

Megan Hudson

Task Lead | Global Systems Engineering

6303 Little River Turnpike #208

Alexandria, VA 22312

http://globalsyseng.com

From: Katie Leahy
Sent: Monday, November 05, 2018 4:07 PM EST
To: Wade Abel <
CC: Nisreen Alhmoud ; Joram Buza ; Tigga Kingston >; Robert Kityo >; Supaporn Wacharapluesadee ; wanda.markotter ; pilotdovih >; abubasha ; meryem.lemrani ; wava ; Catalino Demetria ; paalviola ecohealthalliance.org ; Jon Epstein ecohealthalliance.org>; Kading,Rebekah ; sara.b >; sarabumrungsri ; julianas >; wiantoro ; benjamin_lee pipat ; vudinhthong >; iroro.tanshi ; benneth.obitte Julius Lutwama ; jit ; astghik.ghazaryan ; ioseb.natradze >; Keti Sidamonidze >; Lela Urushadaze ; mariano.sanchez-lockhart farlowscience ; payscue bbrooks ; docshusmitadutta shahanajshanc ; aril ; eric.laing.ctr stsang ; bhbird ; ahandel ; tgoldstein Stokes, Martha M CIV (US) >; stephen.m.becker ; Megan Hudson ; Jason Hudson >; Chris Russell
Subject: Re: BOHRN Vienna Materials

Dear Abel,

Am for all.

V/r,

Katie Leahy

Sent from my iPhone

On Nov 5, 2018, at 16:01, Wade Abel wrote:

> Dear Katie,
>
> Thanks for the kind information. Do you mean AM or PM on the 2 time indicated below: "08 November at 0700 (for 1-hr) in the Ambrosius Room prior to the workshop; for those of you staying at the Hilton, the van will pick you up on the first day at 0620" ?.
>
> kr
>
> On Mon, 5 Nov 2018 at 19:44, Katie Leahy > wrote:
>
> > Hi, everyone! Attached to this email, you will find the BOHRN Vienna Participant Guide. This guide has all the information you will need for the workshop (objectives, agenda, and logistics instructions). We have additionally included strategy maps that outline the four major research interest areas of BOHRN, which were developed during three strategy mapping sessions prior to this workshop. Also attached to this email you will find a series of slides that provide a visual accompaniment for the research areas described in the participant guide. This will be explained more in-depth during the workshop; however, it should give you a good idea about the scope and bounds of the network.
> >
> > A quick reminder that we begin our registration for the workshop on 08 November at 0730 in the Imlauer Hotel outside the Ambrosius Room on the ground floor.
> >
> > For members of the BOHRN Steering Committee, we will hold an internal meeting on 08 November at 0700 (for 1-hr) in the Ambrosius Room prior to the workshop; for those of you staying at the Hilton, the van will pick you up on the first day at 0620.
> >
> > Please let us know if you have any questions. We look forward to seeing you all in Vienna!
> >
> > V/r,

Katie Leahy

Katie Leahy

Director of Science Engagement | Global Systems Engineering

6303 Little River Turnpike #208

Alexandria, VA 22312

http://globalsyseng.com

--

Dr Abel WADE
Director of the National Veterinary Laboratory (LANAVET) annex in Yaounde, and Head of the diagnostic & Research laboratory
Ministry of Livestock, Fisheries and Animal Industries (MINEPIA)
OIE focal point for laboratories in Cameroon
Visiting lecturer,University of Yaounde 1-Cameroon
Member of American Biological Safety Association (ABSA) and Cameroon Biosafety Association (CamBsA)
Yaounde-Cameroon

www.lanavet.com; www.minepia.org.cm

From: Katie Leahy >
Sent: Wednesday, February 14, 2018 2:49 PM EST
To: Kingston, Tigga < >
CC: Tamar Kutateladze >; Kading,Rebekah >; DeeAnn Reeder >; Cryan, Paul >; Vivek Kapur ; Gavin James Smith >; abelwade >; Ian Mendenhall ; Keti Sidamonidze Lela Urushadze >; c_demetria ; Jon Epstein ecohealthalliance.org>; cryan.paul ; S Wacharapluesadee >; Kevin Olival ecohealthalliance.org>; Stokes, Martha M CIV (US) ; Lancaster, Mary J CIV (US) >; Megan Hudson m>
Subject: Re: BPERNet Read-out
Attachment(s): "image001.png"

Tigga,

They are included in the report; Annex C.

V/r,

Katie Leahy

Sent from my iPhone

On Feb 14, 2018, at 14:36, Kingston, Tigga wrote:

> Thanks Katie
> Could you also share the slides from the final session? It would be good to cross match our intent with the write-up
> Thanks
> Tigga
>
> ---
>
> **From:** Katie Leahy
> **Sent:** Wednesday, February 14, 2018 8:46 AM
> **To:** Tamar Kutateladze ; Kading,Rebekah >; DeeAnn Reeder ; Cryan, Paul Vivek Kapur Gavin James Smith ; abelwade ; Ian Mendenhall Keti Sidamonidze ; Lela Urushadze >; c_demetria ; Jon Epstein < ecohealthalliance.org>; cryan.paul ; Kingston, Tigga >; S Wacharapluesadee ; Kevin Olival ecohealthalliance.org>
> **Cc:** Stokes, Martha M CIV (US) < Lancaster, Mary J CIV (US) ; Megan Hudson < >
> **Subject:** BPERNet Read-out
>
> All,
>
> Please find the draft report from our meeting last week. This report includes an executive summary, action items, participant list, working group outcomes, lessons learned from your feedback, and the original slides from the end-of-day brief-out.
>
> We ask that you provide constructive comments (e.g., content changes) no later than 20 February 2018. It is our intent to adjudicate and incorporate any comments with Mary and Marty and then publish a final report on 22 February 2018.
>
> Also, thank you, to everyone who provided feedback via the survey monkey poll. We will be incorporating all of your comments into our meetings going forward.
>
> V/r,
>
> Katie Leahy
>
> 
> **Katie Leahy**
> *Program Manager* | Global Systems Engineering
> 6303 Little River Turnpike, Suite 208
> Alexandria, VA 22305
>
> http://globalsyseng.com

From: Kingston, Tigga <
Sent: Wednesday, February 14, 2018 2:36 PM EST
To: Katie Leahy Tamar Kutateladze >; Kading,Rebekah >; DeeAnn Reeder >; Cryan, Paul >; Vivek Kapur >; Gavin James Smith ; abelwade >; Ian Mendenhall ; Keti Sidamonidze >; Lela Urushadze ; c_demetria Jon Epstein ecohealthalliance.org>; cryan.paul ; S Wacharapluesadee Kevin Olival ecohealthalliance.org>
CC: Stokes, Martha M CIV (US) ; Lancaster, Mary J CIV (US) ; Megan Hudson
Subject: RE: BPERNet Read-out

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Thanks
Tigga

From: Katie Leahy
Sent: Wednesday, February 14, 2018 8:46 AM
To: Tamar Kutateladze ; Kading,Rebekah ; DeeAnn Reeder >; Cryan, Paul >; Vivek Kapur ; Gavin James Smith ; abelwade Ian Mendenhall Keti Sidamonidze ; Lela Urushadze >; c_demetria Jon Epstein ecohealthalliance.org>; cryan.paul ; Kingston, Tigga ; S Wacharapluesadee ; Kevin Olival ecohealthalliance.org>
Cc: Stokes, Martha M CIV (US) ; Lancaster, Mary J CIV (US) ; Megan Hudson
Subject: BPERNet Read-out

All,

Please find the draft report from our meeting last week. This report includes an executive summary, action items, participant list, working group outcomes, lessons learned from your feedback, and the original slides from the end-of-day brief-out.

We ask that you provide constructive comments (e.g., content changes) no later than 20 February 2018. It is our intent to adjudicate and incorporate any comments with Mary and Marty and then publish a final report on 22 February 2018.

Also, thank you, to everyone who provided feedback via the survey monkey poll. We will be incorporating all of your comments into our meetings going forward.

V/r,

Katie Leahy

Katie Leahy
Program Manager | Global Systems Engineering
6303 Little River Turnpike, Suite 208
Alexandria, VA 22305

http://globalsyseng.com

From: Kingston, Tigga >
Sent: Wednesday, February 14, 2018 2:50 PM EST
To: Katie Leahy >
CC: Tamar Kutateladze Kading,Rebekah ; DeeAnn Reeder < ; Cryan, Paul >; Vivek Kapur ; Gavin James Smith ; abelwade ; Ian Mendenhall >; Keti Sidamonidze Lela Urushadze c_demetria < Jon Epstein ecohealthalliance.org>; cryan.paul >; S Wacharapluesadee ; Kevin Olival ecohealthalliance.org>; Stokes, Martha M CIV (US) Lancaster, Mary J CIV (US) >; Megan Hudson >
Subject: RE: BPERNet Read-out

Awesome, thanks!!

From: Katie Leahy
Sent: Wednesday, February 14, 2018 1:49 PM
To: Kingston, Tigga
Cc: Tamar Kutateladze ; Kading,Rebekah >; DeeAnn Reeder Cryan, Paul ; Vivek Kapur < >; Gavin James Smith abelwade Ian Mendenhall ; Keti Sidamonidze ; Lela Urushadze ; c_demetria Jon Epstein ecohealthalliance.org>; cryan.paul S Wacharapluesadee >; Kevin Olival ecohealthalliance.org>; Stokes, Martha M CIV (US) < >; Lancaster, Mary J CIV (US) ; Megan Hudson
Subject: Re: BPERNet Read-out

Tigga,

They are included in the report; Annex C.

V/r,

Katie Leahy

Sent from my iPhone

On Feb 14, 2018, at 14:36, Kingston, Tigga > wrote:

> Thanks Katie
> Could you also share the slides from the final session? It would be good to cross match our intent with the write-up
> Thanks
> Tigga
>
> ---
>
> **From:** Katie Leahy
> **Sent:** Wednesday, February 14, 2018 8:46 AM
> **To:** Tamar Kutateladze >; Kading,Rebekah ; DeeAnn Reeder < >; Cryan, Paul >; Vivek Kapur >; Gavin James Smith < >; abelwade ; Ian Mendenhall Keti Sidamonidze Lela Urushadze ; ; Jon Epstein < ecohealthalliance.org>; cryan.paul Kingston, Tigga ; S Wacharapluesadee ; Kevin Olival ecohealthalliance.org>
> **Cc:** Stokes, Martha M CIV (US) ; Lancaster, Mary J CIV (US) ; Megan Hudson >
> **Subject:** BPERNet Read-out
>
> All,
>
> Please find the draft report from our meeting last week. This report includes an executive summary, action items, participant list, working group outcomes, lessons learned from your feedback, and the original slides from the end-of-day brief-out.
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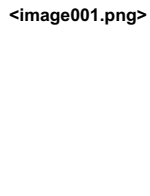
> Also, thank you, to everyone who provided feedback via the survey monkey poll. We will be incorporating all of your comments into our meetings going forward.
>
> V/r,
>
> Katie Leahy



Katie Leahy
Program Manager | Global Systems Engineering
6303 Little River Turnpike, Suite 208
Alexandria, VA 22305

http://globalsyseng.com

From: Jon Epstein ecohealthalliance.org>
Sent: Wednesday, December 13, 2017 7:33 AM EST
To: Katie Leahy >
CC: Keti Sidamonidze Robert Kityo ; Ian Mendenhall ; Joram Buza ; Vivek Kapur >; Kevin Olival ecohealthalliance.org>; Kading,Rebekah >; Lela Urushadaze Lela Urushadaze ; Tamar Kutateladze Supaporn Wacharapluesadee ; Abel Wade <a ; Catalino Demetria < ; Tigga Kingston >; Paul Cryan >; DeeAnn Reeder >; Gavin Smith ; Nisreen Alhmoud ; Stokes, Martha M CIV (US) >; Megan Hudson < Lancaster, Mary J CIV (US) >; Aleman, Nicki D CTR DTRA J3-7 (US)

Subject: Re: BPERNet Side Meeting / PMAC

Thanks Katie.

Do you know the timing of our side meeting at Chula?

Cheers,
Jon

Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
New York

On Dec 12, 2017 10:41 AM, "Katie Leahy" > wrote:

> All,
>
> By now you should have received a letter of invitation from the PMAC Organizing Committee. Please log-on and sign up to the sessions that you can attend. Our side meeting will be on the 30th at Chula Hospital. If you have confirmed attendance with us, then you should have already contacted Nicki Aleman (copied). If not, and you require travel assistance, please email me and her.
>
> CBEP is still covering your air travel, transport to and from the airport, and hotel arrangements, so please ignore those instructions in your PMAC invitation.
>
> Please let me know if you have any questions.
>
> V/r,
>
> Katie Leahy

Katie Leahy

Program Manager | Global Systems Engineering

6303 Little River Turnpike, Suite 208

Alexandria, VA 22305

http://globalsyseng.com

From: Jon Epstein ecohealthalliance.org>
Sent: Wednesday, November 01, 2017 6:31 PM EDT
To: Katie Leahy
CC: Robert Kityo >; Ian MENDENHALL PhD >; Joram Buza Vivek Kapur < >; Kevin Olival ecohealthalliance.org>; Kading,Rebekah >; Lela Urushadaze ; Lela Urushadaze ; Tamar Kutateladze < Supaporn Wacharapluesadee ; Abel Wade >; Catalino Demetria < ; Tigga Kingston >; Paul Cryan ; DeeAnn Reeder < Gavin Smith < >; Nisreen Alhmoud ; Stokes, Martha M CIV (US) >; Lancaster, Mary J CIV (US) Flegler, Ayanna J CTR (US) >
Subject: Re: BPERNet Update and Meeting Date

Thank you, Katie. I'll look forward to seeing everyone there.

Cheers,
Jon

Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
New York

On Nov 1, 2017 4:53 PM, "Katie Leahy" > wrote:

> Dear BPERNet Steering Committee Members,
>
> After careful consideration of the size and scope of PENAPH and increased travel and schedule concerns from BPERNet members, CBEP has decided to move the date of our second meeting to coordinate with the Prince Mahidol Award Conference (PMAC) 2018 in Bangkok, Thailand. We will hold our meeting on Wednesday, 31 January. We have yet to set a time or location, but anticipate that travel planning should support a full day meeting.
>
> Most of PMAC's objectives are focused on zoonoses and some complement BPERNet's ecological focus, this will assist members of the group who plan to attend the conference and use it as an opportunity to advertise our network. I am attaching PMAC information for everyone's situational awareness.
>
> Please consider this email an official a save the date on behalf of CBEP, with more information to follow, which will include travel, agenda, time, and location information. At your earliest convenience, please let me know if you can support attending this meeting.
>
> Thanks!
>
> V/r,
>
> Katie Leahy

From: Lela Urushadze >
Sent: Friday, November 03, 2017 5:54 AM EDT
To: Katie Leahy ; Robert Kityo ; Ian Mendenhall ; Joram Buza ; Vivek Kapur >; Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Kading,Rebekah >; Lela Urushadaze Tamar Kutateladze >; Supaporn Wacharapluesadee >; Abel Wade >; catalino demetria ; Tigga Kingston >; Paul Cryan >; DeeAnn Reeder >; Gavin Smith ; Nisreen Alhmoud >
CC: Stokes, Martha M CIV (US) < >; Lancaster, Mary J CIV (US) ; Flegler, Ayanna J CTR (US)
Subject: Re: BPERNet Update and Meeting Date

Dear Katie
It is will be my pleasure to attend meeting in Thailand
Best regards
Lela

From: Katie Leahy
Sent: Thursday, November 2, 2017 00:53:27
To: Robert Kityo; Ian Mendenhall; Joram Buza; Vivek Kapur; Kevin Olival; Jon Epstein; Rebekah Kading; Lela Urushadaze; Lela Urushadze; Tamar Kutateladze; Supaporn Wacharapluesadee; Abel Wade; Catalino Demetria; Tigga Kingston; Paul Cryan; DeeAnn Reeder; Gavin Smith; Nisreen Alhmoud
Cc: Stokes, Martha M CIV (US); Lancaster, Mary J CIV (US); Flegler, Ayanna J CTR (US)
Subject: BPERNet Update and Meeting Date

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Thanks!

V/r,

Katie Leahy

From: Nesreen Alhmoud >
Sent: Thursday, November 02, 2017 7:16 AM EDT
To: Katie Leahy Robert Kityo < >; Ian Mendenhall Joram Buza ; Vivek Kapur ; Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Kading,Rebekah >; Lela Urushadaze ; Lela Urushadaze ; Tamar Kutateladze ; Supaporn Wacharapluesadee >; Abel Wade ; Catalino Demetria Tigga Kingston ; Paul Cryan >; DeeAnn Reeder ; Gavin Smith
CC: Stokes, Martha M CIV (US) >; Lancaster, Mary J CIV (US) >; Flegler, Ayanna J CTR (US)
Subject: RE: BPERNet Update and Meeting Date

Thank you Katie,

I confirm my interest to attend the meeting.

Nisreen

الجمعية العلمية الملكية
Royal Scientific Society

Dr. Nesreen Alhmoud

Director of Bio-Safety and Bio-Security Center

P.O.Box: 1438 Amman 11941 Jordan

Email: **Website**: www.rss.jo

From: Katie Leahy
Sent: Wednesday, November 1, 2017 11:53 PM
To: Robert Kityo Ian Mendenhall ; Joram Buza Vivek Kapur ; Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Rebekah Kading >; Lela Urushadaze < ; Lela Urushadaze >; Tamar Kutateladze >; Supaporn Wacharapluesadee >; Abel Wade ; Catalino Demetria ; Tigga Kingston ; Paul Cryan >; DeeAnn Reeder Gavin Smith >; Nesreen Alhmoud >
Cc: Stokes, Martha M CIV (US) ; Lancaster, Mary J CIV (US) ; Flegler, Ayanna J CTR (US)
Subject: BPERNet Update and Meeting Date

Dear BPERNet Steering Committee Members,

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Thanks!

V/r,

Katie Leahy

From: catalino demetria >
Sent: Friday, November 03, 2017 2:25 AM EDT
To: Robert Kityo >; Ian Mendenhall Joram Buza ; Vivek Kapur >; Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Kading,Rebekah < >; Lela Urushadaze ; Lela Urushadaze >; Tamar Kutateladze >; Supaporn Wacharapluesadee < >; Abel Wade ; Tigga Kingston >; Paul Cryan >; DeeAnn Reeder < >; Gavin Smith >; Nisreen Alhmoud >; Katie Leahy >
CC: Stokes, Martha M CIV (US) >; Lancaster, Mary J CIV (US) Flegler, Ayanna J CTR (US) >
Subject: Re: BPERNet Update and Meeting Date

Hi Katie,

Thank you for the information, I am attending.

Sincerely,

Catalino S. Demetria, DVM
Section Head
Rabies and Special Pathogens Laboratory

Veterinary Research Department
Research Institute for Tropical Medicine
9002 Research Drive, FCC, Alabang, Muntinlupa City
1771 PHILIPPINES

On Thursday, November 2, 2017, 4:53:34 AM GMT+8, Katie Leahy > wrote:

Dear BPERNet Steering Committee Members,

After careful consideration of the size and scope of PENAPH and increased travel and schedule concerns from BPERNet members, CBEP has decided to move the date of our second meeting to coordinate with the Prince Mahidol Award Conference (PMAC) 2018 in Bangkok, Thailand. We will hold our meeting on Wednesday, 31 January. We have yet to set a time or location, but anticipate that travel planning should support a full day meeting.

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Thanks!

V/r,

Katie Leahy

From: S Wacharapluesadee
Sent: Wednesday, November 01, 2017 6:53 PM EDT
To: Katie Leahy Robert Kityo >; Ian Mendenhall ; Joram Buza ; Vivek Kapur >; Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Kading,Rebekah >; Lela Urushadaze ; Lela Urushadaze ; Tamar Kutateladze >; Abel Wade ; Catalino Demetria >; Tigga Kingston >; Paul Cryan ; DeeAnn Reeder ; Gavin Smith ; Nisreen Alhmoud >
CC: Stokes, Martha M CIV (US) >; Lancaster, Mary J CIV (US) ; Flegler, Ayanna J CTR (US)
Subject: Re: BPERNet Update and Meeting Date

Dear Katie and all,
On January 31, 2018 there will be a PMAC field trip, and one of PREDICT study at site at Chonburi province is selected by Ministry of Public Health for one of 6 visit sites. This is a concurrent site where PREDICT Thailand team has been conducting a longitudinally survrillance on bat and human.
If you are invited by PMAC, please kindly consider to visit this site, it will be posted on the website for selection very soon (site 4) and the number of guests are limited for 40.

I could not attend the steering committee meeting on Jan 31.
Anyway I'm happy to help for organizing the place for the meeting, at Chula hospital! (free of charge).

Best,
Supaporn

TRC-EID, Chulalongkorn Hospital
Bangkok, Thailand

ส่งจากสมาร์ทโฟน Samsung Galaxy ของฉัน

-------- ข้อความดั้งเดิม --------
จาก: Katie Leahy
วันที่: 2/11/17 03:53 (GMT+07:00)
ถึง: Robert Kityo Ian Mendenhall >, Joram Buza < , Vivek Kapur >, Kevin Olival ecohealthalliance.org>, Jon Epstein ecohealthalliance.org>, Rebekah Kading < , Lela Urushadaze Lela Urushadaze >, Tamar Kutateladze >, Supaporn Wacharapluesadee >, Abel Wade < , Catalino Demetria < , Tigga Kingston >, Paul Cryan , DeeAnn Reeder >, Gavin Smith , Nisreen Alhmoud >
Cc: "Stokes, Martha M CIV (US)" >, "Lancaster, Mary J CIV (US)" , "Flegler, Ayanna J CTR (US)" <
เรื่อง: BPERNet Update and Meeting Date

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Thanks!

V/r,

Katie Leahy

From: Robert Kityo
Sent: Wednesday, November 01, 2017 11:51 PM EDT
To: Katie Leahy ; Ian Mendenhall ; Joram Buza ; Vivek Kapur ; Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Kading,Rebekah >; Lela Urushadaze ; Lela Urushadaze >; Tamar Kutateladze ; Supaporn Wacharapluesadee ; Abel Wade Catalino Demetria >; Tigga Kingston ; Paul Cryan >; DeeAnn Reeder ; Gavin Smith ; Nisreen Alhmoud >
CC: Stokes, Martha M CIV (US) < ; Lancaster, Mary J CIV (US) >; Flegler, Ayanna J CTR (US) >
Subject: RE: BPERNet Update and Meeting Date

Thanks Katie
Yours received and date noted.
Best regards
Robert

From: Katie Leahy
Sent: 01/11/2017 23:53
To: Robert Kityo; Ian Mendenhall; Joram Buza; Vivek Kapur; Kevin Olival; Jon Epstein; Rebekah Kading; Lela Urushadaze; Lela Urushadaze; Tamar Kutateladze; Supaporn Wacharapluesadee; Abel Wade; Catalino Demetria; Tigga Kingston; Paul Cryan; DeeAnn Reeder; Gavin Smith; Nisreen Alhmoud
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Thanks!

V/r,

Katie Leahy

From: Flegler, Ayanna J CTR (US) >
Sent: Thursday, February 09, 2017 1:18 PM EST
To: Stokes, Martha M CIV (US) < Lancaster, Mary J CIV (US)
Jon Epstein ecohealthalliance.org>; Gavin James Smith
Ian Mendenhall >; ecohealthalliance.org
>; Kading,Rebekah ; vkapur
>; jkmazet ; joram.buza

Subject: RE: CBEP Global Bat Alliance meeting

We will meet in the open area, by the posters, and move to a different location from there.

Regards,

Ayanna

Ayanna Flegler, Ph.D.
Science Lead, Southeast Asia
Cooperative Biological Engagement Program Toeroek Associates, Inc.\Booz Allen Hamilton CTR A&AS Support Contractor
Office:
Mobile:

-----Original Appointment-----
From: Flegler, Ayanna J CTR (US)
Sent: Tuesday, February 7, 2017 11:23 AM
To: Flegler, Ayanna J CTR (US); Stokes, Martha M CIV (US); Lancaster, Mary J CIV (US); Jon Epstein; Gavin James Smith; Ian Mendenhall; ecohealthalliance.org; Rebekah.Kading vkapur ; jkmazet ; kityrob ; joram.buza

Subject: CBEP Global Bat Alliance meeting
When: Thursday, February 9, 2017 1:30 PM-2:30 PM (UTC-05:00) Eastern Time (US & Canada).
Where: Hilton Alexandria Mark Center; exact location TBD

Update: We will meet in the Foyer area at 1:30PM and move to a different location from there.

CBEP would like to convene researchers from all CBEP-engaged regions to discuss formation of a Global Bat Alliance (GBA). The GBA will aim to build and leverage country and regional capabilities to generate an enhanced understanding of bats and their ecology within the context of pathogens of security concern. This meeting will serve to discuss future collaborative efforts of the Global Bat Alliance.

From: Kendra Phelps ecohealthalliance.org>
Sent: Thursday, June 25, 2020 5:53 PM EDT
To: Kading,Rebekah
Subject: Re: contact

Hi Rebekah,

Great to hear from you, and I hope you are doing well too! I would be happy to chat with Anne about the available positions at EHA, please pass my email to her and we can set up a time to chat. I did a quick search of Anne, and besides being an amazing scientist that I think would be a great fit at EHA, I noticed she completed her undergrad in Iowa (which is also my home state).

In terms of BOHRN initiatives, if I can contribute in any way please feel free to contact me. I often get overlooked with both Jon and Kevin being BOHRN members.

Cheers,
Kendra

Kendra Phelps, PhD
Research Scientist

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200
New York, NY 10018

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

> On Jun 25, 2020, at 1:54 PM, Kading,Rebekah wrote:
>
> Dear Kendra,
>
> I hope this message finds you hanging in there ok during all of this! Thank you also for all your hard work on this North American bat paper! I've been interacting regularly with Tigga through the IUCN Bat Specialist Group and working on another paper; it's been nice keeping up with her outside of BOHRN. With everything going on with the bat research community and SARS-CoV-2 though, lots of BOHRN members are involved in various initiatives and and keeping pretty busy...someday when we are on the other side of this, I hope DTRA revitalizes a BOHRN meeting in person so we can all reconnect, debrief, and move some ideas forward that we had been discussing. I don't think anyone would accept another Zoom meeting at this point though!
>
> Anyway, I'm writing to ask if I can put you in touch with a DVM/PhD student in my lab, Anna Fagre. Anna is outstanding, and interested in applying for one of the open positions at EcoHealth and just wants to do due diligence in finding out more about the position, expectations, etc. I thought of you as being a good person to provide some inside perspective, but wanted to reach out first to make sure that wouldn't put you in an awkward position, like if you're on the hiring committee or something.
>
> Thanks so much!
>
> Best regards,
> Rebekah
>
> **Rebekah C. Kading, PhD**
> Assistant Professor
> Department of Microbiology Immunology and Pathology
> Colorado State University
> Office:

From: Kendra Phelps ecohealthalliance.org>
Sent: Tuesday, June 16, 2020 8:59 AM
To: Raina Plowright
Cc: Paul Cryan >; Wang Linfa >; ecohealthalliance.org< dreedel
Hume Field ecohealthalliance.org>; Charles H Calisher t>; Brian R. Amman ; Ralph S. Baric Blehert, David S
Cara Brook ; Kevin Castle ; Coleman, Jeremy T >; Peter Daszak ;
epstein @ecohealthalliance.org>; wfrick ; Gilbert, Amy T - APHIS < ; David Hayman ; Ip, Hon S
>; William B. Karesh ; Christine Kreuder Johnson Kading,Rebekah >; Tigga Kingston
>; Lorch, Jeffrey M >; Ian Mendenhall ; alisonpee ; Reichard, Jonathan D
>; Sleeman, Jonathan M ; Daniel Streicker < ; Jonathan S. Towner
Subject: Re: [EXTERNAL] SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Agreed, great job Kevin and Paul for the quick turnaround.

The CNN special can be viewed on www.cnn.com/go, click on "Shows" to the left-side of the screen and the special should be an option at the top of the screen (or one scroll to the right). I think you need a cable subscription to log-in to view though.

Cheers,
Kendra

Kendra Phelps, PhD
Research Scientist

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200
New York, NY 10018

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

> On Jun 16, 2020, at 10:48 AM, Raina Plowright wrote:
>
> Thanks for doing the record turn-around! Well done everyone and great leadership Paul and Kevin!
> Does anyone have a link to the full CNN documentary? I heard it was great.
> Raina
>
> > On Jun 16, 2020, at 8:40 AM, Cryan, Paul < wrote:
> >
> > That was one of those unforgettable moments for me watching many of you on the CNN special...in my opinion you all came off very well! Congrats!
> >
> > Paul
> >
> > Paul Cryan
> > Research Biologist
> > USGS Fort Collins Science Center
> >
> > Web Page and Contact Info
> >
> > ---
> >
> > **From:** Wang Linfa >
> > **Sent:** Monday, June 15, 2020 11:22 PM
> > **To:** ecohealthalliance.org ; dreedel Hume Field ecohealthalliance.org>; Charles

H Calisher < Brian R. Amman ; Ralph S. Baric ; Blehert, David S ; Cara Brook >; Kevin Castle Coleman, Jeremy T >; Peter Daszak ; Jon Epstein ecohealthalliance.org>; wfrick Gilbert, Amy T - APHIS ; David Hayman >; Ip, Hon S William Karesh >; Christine Kreuder Johnson Kading,Rebekah >; Tigga Kingstor Lorch, Jeffrey M >; Ian Mendenhall <ian.mendenhall@alisonpee >; Kendra Phelps @ecohealthalliance.org>; Plowright, Raina >; Reichard, Jonathan D >; Sleeman, Jonathan M <; Daniel Streicker < >; Jonathan S. Towner

Cc: Cryan, Paul
Subject: [EXTERNAL] RE: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Thanks Kevin and Paul for doing a great job so quickly.

I guess the CNN documentary yesterday also made this a hot (hotter) topic now and the editor may want to have “a ride on the bat wings” to get it out asap!

Fingers crossed.

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: +65 6516 8397

From: Kevin Olival ecohealthalliance.org>
Sent: Tuesday, 16 June 2020 1:19 PM
To: DeeAnn Reeder ; Hume Field ecohealthalliance.org>; Charles H Calisher < >; Brian R. Amman ; Wang Linfa >; Ralph S. Baric David S Blehert ; Cara Brook >; Kevin Castle < ; Jeremy Coleman < >; Peter Daszak < ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Winifred F Frick, Ph.D. Gilbert, Amy T - APHIS < David Hayman >; Hon S Ip ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson Kading,Rebekah < Tigga Kingston ; Lorch, Jeffrey M ; Ian Mendenhall <ian.mendenhall@alisonpee ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina Jonathan D Reichard ; Jonathan M Sleeman >; Daniel Streicker >; Jonathan S. Towner
Cc: Paul Cryan >
Subject: Re: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Hi Team,

Funny thing, bioRxiv actually rejected us! Apparently they don’t take “reviews”.

In any case we got **very positive reviews back from *PLoS Pathogens*** today, and the revised ms was just resubmitted (<24 hour turnaround). Woohooo! Finger’s crossed that the editors turn it around again quickly and we can see this published soon.

Attached is the cover letter, response to reviewers, and the resubmitted version of ms.

Cheers,
Kevin and Paul

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

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Charlie

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--
DeeAnn M. Reeder, PhD
Professor
Department of Biology
Bucknell University
Lewisburg, PA 17837

http://deeannreeder.scholar.bucknell.edu

Important: This email is confidential and may be privileged. If you are not the intended recipient, please delete it and notify us immediately; you should not copy or use it for any purpose, nor disclose its contents to any other person. Thank you.

From: Kendra Phelps ecohealthalliance.org>
Sent: Thursday, June 25, 2020 6:28 PM EDT
To: Kading,Rebekah
Subject: Re: contact

Hi Rebekah,

I look forward to talking with Anna.

What a small world, I have a lot of family that lives near Adair and I know the exact water tower you are talking about! I typically spend March - October in Western Asia for fieldwork, but find myself stuck in NYC instead this year and have been yearning to travel back to Iowa to visit my family. And honestly to smell fresh air and eat Casey's pizza (only people from the Midwest understand that the best pizza comes from a convenience store….NYC pizza has nothing on Casey's pizza:). Enjoy your time in Iowa, and safe travels.

Cheers,
Kendra

Kendra Phelps, PhD
Research Scientist

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New York, NY 10018

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On Jun 25, 2020, at 6:05 PM, Kading,Rebekah wrote:

Hi Kendra,

Great - thanks so much! I'll send Anna your way. Yes, I agree that EHA may be a great fit for her, and she is thrilled there are open positions! And the Iowa connection. We talk Iowa a lot because my husband's family farms in Iowa....right along I-80 between Omaha and DesMoines, by the yellow smiley face water tower at the Adair/Casey exit...we're headed there next week actually. Small world! I'll definitely loop you in about anything with BOHRN that you could contribute to - I appreciated all your input at the Vienna meeting and it would be great to have you involved. We had a lot of momentum after that meeting but they've been very quiet lately....DTRA seems to be going through some restructuring. But if things calm down by this fall I think they will try to have another meeting and get things going again.

Thanks!
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University
Office:

From: Kendra Phelps ecohealthalliance.org>
Sent: Thursday, June 25, 2020 3:53 PM
To: Kading,Rebekah
Subject: Re: contact

Hi Rebekah,

Great to hear from you, and I hope you are doing well too! I would be happy to chat with Anne about the available positions at EHA, please pass my email to her and we can set up a time to chat. I did a quick search of Anne, and besides being an amazing scientist that I think would be a great fit at EHA, I noticed she completed her undergrad in Iowa (which is also my home state).

In terms of BOHRN initiatives, if I can contribute in any way please feel free to contact me. I often get overlooked with both Jon and Kevin being BOHRN members.

Cheers,
Kendra

Kendra Phelps, PhD
Research Scientist

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On Jun 25, 2020, at 1:54 PM, Kading,Rebekah < wrote:

Dear Kendra,

I hope this message finds you hanging in there ok during all of this! Thank you also for all your hard work on this North American bat paper! I've been interacting regularly with Tigga through the IUCN Bat Specialist Group and working on another paper; it's been nice keeping up with her outside of BOHRN. With everything going on with the bat research community and SARS-CoV-2 though, lots of BOHRN members are involved in various initiatives and and keeping pretty busy...someday when we are on the other side of this, I hope DTRA revitalizes a BOHRN meeting in person so we can all reconnect, debrief, and move some ideas forward that we had been discussing. I don't think anyone would accept another Zoom meeting at this point though!

Anyway, I'm writing to ask if I can put you in touch with a DVM/PhD student in my lab, Anna Fagre. Anna is outstanding, and interested in applying for one of the open positions at EcoHealth and just wants to do due diligence in finding out more about the position, expectations, etc. I thought of you as being a good person to provide some inside perspective, but wanted to reach out first to make sure that wouldn't put you in an awkward position, like if you're on the hiring committee or something.

Thanks so much!

Best regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University
Office:

From: Kendra Phelps ecohealthalliance.org>
Sent: Tuesday, June 16, 2020 8:59 AM
To: Raina Plowright >
Cc: Paul Cryan >; Wang Linfa ; ecohealthalliance.org<c ; dreede
>; Hume Field ecohealthalliance.org>; Charles H Calisher Brian R. Amman Ralph S. Baric
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Subject: Re: [EXTERNAL] SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Agreed, great job Kevin and Paul for the quick turnaround.

The CNN special can be viewed on www.cnn.com/go, click on "Shows" to the left-side of the screen and the special should be an option at the top of the screen (or one scroll to the right). I think you need a cable subscription to log-in to view though.

Cheers,
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On Jun 16, 2020, at 10:48 AM, Raina Plowright < wrote:

Thanks for doing the record turn-around! Well done everyone and great leadership Paul and Kevin!
Does anyone have a link to the full CNN documentary? I heard it was great.
Raina

On Jun 16, 2020, at 8:40 AM, Cryan, Paul < wrote:

That was one of those unforgettable moments for me watching many of you on the CNN special...in my opinion you all came off very well! Congrats!

Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Wang Linfa <
Sent: Monday, June 15, 2020 11:22 PM
To: ecohealthalliance.org < ; dreedel Hume Field @ecohealthalliance.org>; Charles H Calisher ; Brian R. Amman ; Ralph S. Baric ; Blehert, David S >; Cara Brook ; Kevin Castle Coleman, Jeremy T ; Peter Daszak ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; wfrick Gilbert, Amy T - APHIS ; David Hayman massey Ip, Hon S >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah < Tigga Kingston >; Lorch, Jeffrey M ; Ian Mendenhall >; alisonpee Kendra Phelps ecohealthalliance.org>; Plowright, Raina Reichard, Jonathan D Sleeman, Jonathan M >; Daniel Streicker >; Jonathan S. Towner

Cc: Cryan, Paul
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Thanks Kevin and Paul for doing a great job so quickly.

I guess the CNN documentary yesterday also made this a hot (hotter) topic now and the editor may want to have "a ride on the bat wings" to get it out asap!

Fingers crossed.

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857

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- External Email -

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--
DeeAnn M. Reeder, PhD
Professor
Department of Biology
Bucknell University
Lewisburg, PA 17837

http://deeannreeder.scholar.bucknell.edu

From: Batsuli, Nefer
Sent: Wednesday, October 21, 2020 10:31 AM EDT
To: Daniel Park valitutto ecohealthalliance.org>; Tineke CANTAERT Woodson, Sara (NIH/NIAID) [E] < >; Tony Moody, M.D. Dyall, Julie (NIH/NIAID) [E] ; Hilary Bouton-Verville >; Kendra Phelps < ecohealthalliance.org>; tcantaert ; colomaj >; amy.aegypti < ; Morrison, Amy C CIV USN NAMRU SIX LIMA PE (USA) >; Vasilakis, Nikolaos ; Weaver, Scott >; Alex Greninger >; Njenga, M. Kariuki < ; Paredes, Anne

CC: Beaubien, Candice (NIH/NIAID) [E] >; jean.patterson >; Marta Giovanetti ; Van Voorhis, Wes Abdoul Aziz Diallo >; dveasna >; sheahan >; Kading,Rebekah >; samkariuki2 >; Lynn K. Barrett >; Wesley C. Van Voorhis >; Peter Rabinowitz >; Van Vliet, Gretchen ; Macoubray, Aaron Challberg, Mark (NIH/NIAID) [E] >; Linde, Amber (NIH/NIAID) [E]
Subject: RE: CREID Biorepository Oversight and Quality Working Group

Hello Biorepository WG members,

We are looking forward to our **first full working group meeting next Tuesday, October 27th**! In preparation, we have posted a Pre-Survey Information excel document on Teams as an early tool to help brainstorm and guide what information we may need to collect via the surveys for the inventory.

Please have the primary and/or secondary representative populate information for your center. Feel free to use CREATE-NEO's row as an example, and we welcome additional feedback on the document.

Thank you,

Nefer
Project Coordinator, CREID Coordinating Center

-----Original Appointment-----
From: Batsuli, Nefer
Sent: Thursday, September 17, 2020 6:42 PM
To: dpark ecohealthalliance.org; tineke.cantaert ; Batsuli, Nefer; sara.woodson tony.moody ; Dyall, Julie (NIH/NIAID) [E]; Hilary Bouton-Verville; Kendra Phelps; tcantaert ; colomaj ; amy.aegypti ; amy.c.morrison ; nivasila ; sweaver ; agrening mkariuki.njenga anneparedes
Cc: Beaubien, Candice (NIH/NIAID) [E]; Patterson, Jean (NIH/NIAID) [E]; giovanetti.marta ; Van Voorhis, Wes; Abdoulaziz.diallo ; dveasna sheahan rebekah.kading samkariuki2 ; lynnbob wesley ; Peter Rabinowitz; Van Vliet, Gretchen; Macoubray, Aaron; Challberg, Mark (NIH/NIAID) [E]; Linde, Amber (NIH/NIAID) [E]
Subject: CREID Biorepository Oversight and Quality Working Group
When: Tuesday, October 27, 2020 10:00 AM-11:00 AM (UTC-05:00) Eastern Time (US & Canada).
Where: https://rtiorg.zoom.us/j/92113967048?pwd=NXJiOStIZVFTaGRsemNzMGVqMXRlZz09&from=msft

This meeting series invitation is for the CREID Biorepository Oversight and Quality Working Group.

Materials can be found in the Biorepository Oversight and Quality WG Folder in Microsoft Teams.

We appreciate your flexibility in scheduling as we work across various time zones.

Hi there,

Nefer Batsuli is inviting you to a scheduled Zoom meeting.

Join Zoom Meeting

Phone one-tap: US: +13126266799,,92113967048#,,,,,,0#,,531907# or +19292056099,,92113967048#,,,,,,0#,,531907#

Meeting URL: https://rtiorg.zoom.us/j/92113967048?pwd=NXJiOStIZVFTaGRsemNzMGVqMXRlZz09&from=msft

Meeting ID: 921 1396 7048
Passcode: 531907

Join by Telephone

For higher quality, dial a number based on your current location.
Dial:

US: +1 312 626 6799 or +1 929 205 6099 or +1 301 715 8592 or +1 346 248 7799 or +1 669 900 6833 or +1 253 215 8782 or 877 853 5257 (Toll Free) or 888 475 4499 (Toll Free)
Spain: +34 91 787 0058 or +34 917 873 431 or +34 84 368 5025
United Kingdom: +44 203 481 5240 or +44 203 901 7895 or +44 208 080 6591 or +44 208 080 6592 or +44 330 088 5830 or +44 131 460 1196 or +44 203 481 5237
Malaysia: +60 3 3099 2229 or +60 3 7724 4079 or +60 3 7724 4080 or +60 3 9212 1727
El Salvador: +503 2113 9088 or +503 2136 6444

Meeting ID: 921 1396 7048

Passcode: 531907

International numbers

Join from an H.323/SIP room system

H.323: 162.255.37.11 (US West)
162.255.36.11 (US East)
115.114.131.7 (India Mumbai)
115.114.115.7 (India Hyderabad)
213.19.144.110 (Amsterdam Netherlands)
213.244.140.110 (Germany)
103.122.166.55 (Australia)
209.9.211.110 (Hong Kong SAR)
64.211.144.160 (Brazil)
69.174.57.160 (Canada)
207.226.132.110 (Japan)

Meeting ID: 921 1396 7048

Passcode: 531907

SIP: 92113967048@zoomcrc.com

Passcode: 531907

Skype for Business (Lync)

https://rtiorg.zoom.us/skype/92113967048

From: Kingston, Tigga
Sent: Saturday, August 11, 2018 5:28 AM EDT
To: Megan Hudson >; nisreen.hmoud joram.buza cryanp c demetria < >; ecohealthalliance.org ecohealthalliance.org>; Kading,Rebekah >; vkapur >; kityrob ; tamar_kutateladze ; ian.mendenhall ecohealthalliance.org dreeder ksidamonidze >; gavin.smith < >; l.urushadze spwa ; abelwade >; raina.plowright
CC: Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) >; Stokes, Martha M CIV (US) l>; Katie Leahy >; Becker, Stephen M CTR DTRA J3-7 (US)
Subject: RE: Draft Executive Summary and Website Materials

Hi Megan
Just trying to unpack the plans this fall, and have been reading through the Exec summary. Essentially a lot of BOHRN are going to Georgia and you propose an additional meeting in Austria a couple of months later?

I don't want to second guess what you all decided on in Canada, but is there any chance the second meeting (currently scheduled for November) could be when the fall semester is over (i.e. early-mid December through mid January)? As I'm on the WABnet Steering Committee I have committed to the Georgia meeting, but it is challenging to get release for multiple trips during the academic semester, particularly for same entities. I am probably not the only one running into this problem or similar

Thanks for your consideration,
Tigga

From: Megan Hudson >
Sent: Friday, July 13, 2018 11:02 AM
To: nisreen.hmoud ; joram.buza cryanp ; c_demetria ; ecohealthalliance.org; rebekah.kading ; vkapur ; Kingston, Tigga ; kityrob ; tamar_kutateladze ; ian.mendenhall ; ecohealthalliance.org; dreeder ksidamonidze gavin.smith l.urushadze spwa ; abelwade ; raina.plowright
Cc: Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) >; Stokes, Martha M CIV (US) >; Katie Leahy >; Becker, Stephen M CTR DTRA J3-7 (US) >
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All,

Please find the draft report from our BOHRN meeting 20-21 June. This report includes an executive summary, action items, participant list, working group outcomes, and your research quad charts.

We ask that you provide constructive comments (e.g., content changes) no later than 18 July. It is our intent to adjudicate and incorporate any comments to then publish a final report.

In addition, you will find an updated version of the website map here (https://docs.google.com/document/d/1x5GdAKEPpKXTol9utZiYvaGoXNtOQsyTdlub1WvN0tk/edit?usp=sharing). Each page has the title of the website page and the content, make edits, as you see fit, to the language to help us better develop the website.

As a reminder, we will be adding individual bios to the website. If you have not already done so, you may submit your information here: https://www.surveymonkey.com/r/BPMTG2T

You will find the report contains softened language to add a more conservationist view point, please review the language within the report and on the website.

v/r,

Megan

Megan Hudson
Task Lead | Global Systems Engineering
6303 Little River Turnpike #208
Alexandria, VA 22312

http://globalsyseng.com

From: Kingston, Tigga >
Sent: Sunday, July 15, 2018 3:15 AM EDT
To: nisreen.hmoud ; joram.buza
cryanp c demetria ;
ecohealthalliance.org ; Kading,Rebekah
vkapur kityrob >; tamar kutateladze
>; ian.mendenhall ;
ecohealthalliance.org ; dreeder ;
ksidamonidze ; gavin.smith ;
l.urushadze ; spwa >; abelwade
<abelwade >; raina.plowright ; Megan Hudson
>
CC: Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) >; Stokes, Martha M CIV
(US) l>; Katie Leahy ; Becker, Stephen M CTR DTRA J3-7
(US)
Subject: Re: Draft Executive Summary and Website Materials

Hi Meghan
As three of the ecologists could not make it, I think group 3 needs more time to confer remotely than the deadline of the 18th allows. Please give us until at least the end of July. I am I in the field with only intermittent internet as well.

Thanks
Tigga

Get Outlook for Android

From: Megan Hudson >
Sent: Saturday, July 14, 2018 12:01:46 AM
To: nisreen.hmoud joram.buza ; cryanp c_demetria
ecohealthalliance.org; rebekah.kading ; vkapur ; Kingston, Tigga; kityrob ;
tamar_kutateladze ian.mendenhall ecohealthalliance.org; dreeder ;
ksidamonidze ; gavin.smith l.urushadze ; spwa abelwade ;
raina.plowright
Cc: Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US); Stokes, Martha M CIV (US); Katie Leahy; Becker, Stephen M CTR DTRA J3-7 (US)
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v/r,

Megan

Megan Hudson
Task Lead | Global Systems Engineering
6303 Little River Turnpike #208
Alexandria, VA 22312

http://globalsyseng.com

From: Lela Urushadze <
Sent: Thursday, July 19, 2018 7:06 AM EDT
To: Megan Hudson ; nisreen.hmoud
joram.buza cryanp ;
c demetria >; ecohealthalliance.org
; Kading,Rebekah ; vkapur
>; tigga.kingston ; kityrob
tamar kutateladze ; ian.mendenhal
; ecohealthalliance.org >; dreeder
>; Keti Sidamonidze >; gavin.smith
; spwa ; abelwade
>; raina.plowright
CC: Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) >; Stokes, Martha M CIV (US) >; Katie Leahy >; Becker, Stephen M CTR DTRA J3-7 (US)
Subject: Re: Draft Executive Summary and Website Materials

Hi Megan

Please make correction in affiliation of our institution, it should be just
“R. Lugar Center for Public Health Research, National Center for Disease Control & Public Health”

Regards
Lela

From: Megan Hudson >
Sent: Friday, July 13, 2018 20:01:46
To: nisreen.hmoud ; joram.buza ; cryanp c_demetria
ecohealthalliance.org; rebekah.kading vkapur tigga.kingston ; kityrob ;
tamar_kutateladze ; ian.mendenhall ; ecohealthalliance.org; dreeder Keti
Sidamonidze gavin.smith ; Lela Urushadze; spwa ; abelwade
raina.plowright
Cc: Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US); Stokes, Martha M CIV (US); Katie Leahy; Becker, Stephen M CTR DTRA J3-7 (US)
Subject: Draft Executive Summary and Website Materials

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As a reminder, we will be adding individual bios to the website. If you have not already done so, you may submit your information here: https://www.surveymonkey.com/r/BPMTG2T

You will find the report contains softened language to add a more conservationist view point, please review the language within the report and on the website.

v/r,

Megan

Megan Hudson
Task Lead | Global Systems Engineering
6303 Little River Turnpike #208
Alexandria, VA 22312

http://globalsyseng.com

From: calisher
Sent: Monday, June 29, 2020 1:48 PM EDT
To: Kingston, Tigga ; Kading,Rebekah < ; Kevin Olival ecohealthalliance.org>; David Hayman >; epstein ecohealthalliance.org>; DeeAnn Reeder Hume Field ecohealthalliance.org>; Brian R. Amman < Wang Linfa < ; Ralph S. Baric ; David S Blehert < Cara Brook >; Kevin Castle ; Jeremy Coleman < >; Peter Daszak >; Winifred F Frick, Ph.D. >; Gilbert, Amy T - APHIS >; Hon S Ip >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson Lorch, Jeffrey M >; Ian MENDENHALL PhD >; alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina Jonathan D Reichard >; Jonathan M Sleeman Daniel Streicker >; Jonathan S. Towner Paul Cryan
Subject: RE: Editorial Acceptance of "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPATHOGENS-D-20-01...

If Kevin and Paul can get together an eclectic group such as this one, perhaps they should be put in charge of the United Nations or the U.S. Congress (for starters).

Charlie

From: Kingston, Tigga < >
Sent: Monday, June 29, 2020 7:35 AM
To: Kading,Rebekah ; Kevin Olival ecohealthalliance.org>; David Hayman ; epstein < ecohealthalliance.org>; DeeAnn Reeder ; Hume Field ecohealthalliance.org>; Charles H Calisher < >; Brian R. Amman >; Wang Linfa >; Ralph S. Baric ; David S Blehert >; Cara Brook ; Kevin Castle >; Jeremy Coleman >; Peter Daszak Winifred F Frick, Ph.D. ; Gilbert, Amy T - APHIS ; Hon S Ip ; William Karesh ; Christine Kreuder Johnson < >; Lorch, Jeffrey M >; Ian MENDENHALL PhD alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina >; Jonathan D Reichard ; Jonathan M Sleeman >; Daniel Streicker ; Jonathan S. Towner Paul Cryan >
Subject: RE: Editorial Acceptance of "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPATHOGENS-D-20-01...

Great stuff Kevin and Paul
Thanks!
Tigga

From: Kading,Rebekah
Sent: Monday, June 29, 2020 8:23 AM
To: Kevin Olival ecohealthalliance.org>; David Hayman >; epstein ecohealthalliance.org>; DeeAnn Reeder >; Hume Field ecohealthalliance.org>; Charles H Calisher >; Brian R. Amman >; Wang Linfa ; Ralph S. Baric >; David S Blehert >; Cara Brook ; Kevin Castle >; Jeremy Coleman >; Peter Daszak cohealthalliance.org>; Winifred F Frick, Ph.D. >; Gilbert, Amy T - APHIS ; Hon S Ip < >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson >; Kingston, Tigga ; Lorch, Jeffrey M < ; Ian MENDENHALL PhD >; alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina Jonathan D Reichard >; Jonathan M Sleeman >; Daniel Streicker ; Jonathan S. Towner >; Paul Cryan >
Subject: Re: Editorial Acceptance of "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPATHOGENS-D-20-01...

Awesome! □ Thanks for the update Kevin. I'm delighted to be a part of this paper with all of you.
Best,
Rebekah

Rebekah C. Kading, PhD

Assistant Professor

Department of Microbiology Immunology and Pathology

Colorado State University

Office:

From: Kevin Olival ecohealthalliance.org>
Sent: Sunday, June 28, 2020 6:59 AM
To: David Hayman ; epstein ecohealthalliance.org>; DeeAnn Reeder >; Hume Field ecohealthalliance.org>; Charles H Calisher < ; Brian R. Amman < >; Wang Linfa >; Ralph S. Baric ; David S Blehert ; Cara Brook ; Kevin Castle ; Jeremy Coleman >; Peter Daszak ecohealthalliance.org>; Winifred F Frick, Ph.D. >; Gilbert, Amy T - APHIS >; Hon S Ip >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah >; Tigga Kingston >; Lorch, Jeffrey M ; Ian MENDENHALL PhD alisonpeel ; Kendra Phelps < ecohealthalliance.org>; Plowright, Raina ; Jonathan D Reichard >; Jonathan M Sleeman >; Daniel Streicker < >; Jonathan S. Towner Paul Cryan

Subject: Fwd: Editorial Acceptance of "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPATHOGENS-D-20-01...

Paper Accepted!! Thank you all for your patience, perseverance, and invaluable contributions. I haven't received the proofs yet, but will turn them around quickly when I do.

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org
EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

Begin forwarded message:

From: "PLOS Pathogens"
Subject: Editorial Acceptance of "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPATHOGENS-D-20-01177R1) - [EMID:902178ed8cb23641]
Date: June 26, 2020 at 4:39:55 PM EDT
To: "Kevin J. Olival" ecohealthalliance.org>
Reply-To: "PLOS Pathogens" >

CC: "Paul M. Cryan" "Brian R. Amman" "Ralph S. Baric' "David S. Blehert" "Cara E. Brook" , "Charles H. Calisher" , "Kevin T. Castle" "Jeremy T. H. Coleman" , "Peter Daszak" "Jonathan H. Epstein" ecohealthalliance.org, "Hume Field" ecohealthalliance.org, "Winifred F. Frick" , "Amy T. Gilbert' "David T.S. Hayman" , "Hon S. Ip" "William B. Karesh" ecohealthalliance.org, "Christine Kreuder Johnson" "Rebekah C. Kading" "Tigga Kingston" "Jeffrey M. "Ian H. Mendenhall" , "Alison J. Peel" , "Kendra L. Phelps" , "Raina K. Plowright" "DeeAnn M. Reeder" "Jonathan D. Reichard" Jonathan M. Sleeman" , "Daniel G. Streicker' , "Jonathan S. Towner' "Lin-Fa Wang'

Dear Dr. Olival,
We are pleased to inform you that your manuscript 'Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats

Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats' has been provisionally accepted for publication in PLOS Pathogens.
Before your manuscript can be formally accepted you will need to complete some formatting changes, which you will receive in a follow up email. A member of our team will be in touch with a set of requests.
Please note that your manuscript will not be scheduled for publication until you have made the required changes, so a swift response is appreciated.
IMPORTANT: The editorial review process is now complete. PLOS will only permit corrections to spelling, formatting or significant scientific errors from this point onwards. Requests for major changes, or any which affect the scientific understanding of your work, will cause delays to the publication date of your manuscript.
Should you, your institution's press office or the journal office choose to press release your paper, you will automatically be opted out of early publication. We ask that you notify us now if you or your institution is planning to press release the article. All press must be co-ordinated with PLOS.
Thank you again for supporting Open Access publishing; we are looking forward to publishing your work in PLOS Pathogens.
Best regards,

Seema Lakdawala, PhD
Reviews Editor
PLOS Pathogens

Aaron Mitchell
Section Editor
PLOS Pathogens

Kasturi Haldar
Editor-in-Chief
PLOS Pathogens
orcid.org/0000-0001-5065-158X

Michael Malim
Editor-in-Chief
PLOS Pathogens
orcid.org/0000-0002-7699-2064

****

Reviewer Comments (if any, and for reference):

From: Ian Mendenhall
Sent: Monday, June 29, 2020 11:23 PM EDT
To: Kevin Olival ecohealthalliance.org>; David Hayman ; epstein @ecohealthalliance.org>; DeeAnn Reeder Hume Field @ecohealthalliance.org>; Charles H Calisher ; Brian R. Amman Wang Linfa Ralph S. Baric David S Blehert ; Cara Brook < ; Kevin Castle < ; Jeremy Coleman >; Peter Daszak < >; Winifred F Frick, Ph.D. ; Gilbert, Amy T - APHIS >; Hon S Ip >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah ; Tigga Kingston >; Lorch, Jeffrey M >; alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina >; Jonathan D Reichard >; Jonathan M Sleeman Daniel Streicker ; Jonathan S. Towner ; Paul Cryan
Subject: Re: Editorial Acceptance of "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPATHOGENS-D-20-01...

Fantastic work Kevin and Paul. Thanks for including me and hope to see/meet some of you if the Berlin Bat meeting happens in March 2021.

From: Kevin Olival ecohealthalliance.org>
Date: Sunday, 28 June 2020 at 9:00 PM
To: David Hayman , Jon Epstein ecohealthalliance.org>, DeeAnn Reeder >, Hume Field ecohealthalliance.org>, Charles H Calisher , "Brian R. Amman" , Wang Linfa >, "Ralph S. Baric" >, David S Blehert , Cara Brook Kevin Castle Jeremy Coleman >, Peter Daszak ecohealthalliance.org>, "Winifred F Frick, Ph.D." >, "Gilbert, Amy T - APHIS" Hon S Ip , William Karesh ecohealthalliance.org>, Christine Kreuder Johnson , "Kading,Rebekah" , Tigga Kingston , "Lorch, Jeffrey M" , Ian Mendenhall >, "alisonpeel >, Kendra Phelps ecohealthalliance.org>, "Plowright, Raina" >, Jonathan D Reichard >, Jonathan M Sleeman >, Daniel Streicker , "Jonathan S. Towner" Cryan >
Subject: Fwd: Editorial Acceptance of "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPATHOGENS-D-20-01...

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Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org
EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

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From: "PLOS Pathogens"
Subject: Editorial Acceptance of "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPATHOGENS-D-20-01177R1) - [EMID:902178ed8cb23641]

Date: June 26, 2020 at 4:39:55 PM EDT
To: "Kevin J. Olival" ecohealthalliance.org>
Reply-To: "PLOS Pathogens"

CC: "Paul M. Cryan" "Brian R. Amman" , "Ralph S. Baric" r
"David S. Blehert" "Cara E. Brook' , "Charles H. Calisher"
, "Kevin T. Castle" "Jeremy T. H. Coleman" ,
"Peter Daszak" ecohealthalliance.org, "Jonathan H. Epstein" ecohealthalliance.org, "Hume Field"
ecohealthalliance.org, "Winifred F. Frick" , "Amy T. Gilbert" ,
"David T.S. Hayman" , "Hon S. Ip" "William B. Karesh"
ecohealthalliance.org, "Christine Kreuder Johnson" "Rebekah C. Kading"
, "Tigga Kingston" "Jeffrey M. Lorch' , "Ian H.
Mendenhall" | "Alison J. Peel" "Kendra L. Phelps"
, "Raina K. Plowright" , "DeeAnn M. Reeder"
, "Jonathan D. Reichard" "Jonathan M. Sleeman"
, "Daniel G. Streicker" , "Jonathan S. Towner' "Lin-Fa
Wang"

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Should you, your institution's press office or the journal office choose to press release your paper, you will automatically be opted out of early publication. We ask that you notify us now if you or your institution is planning to press release the article. All press must be co-ordinated with PLOS.
Thank you again for supporting Open Access publishing; we are looking forward to publishing your work in PLOS Pathogens.
Best regards,

Seema Lakdawala, PhD
Reviews Editor
PLOS Pathogens

Aaron Mitchell
Section Editor
PLOS Pathogens

Kasturi Haldar
Editor-in-Chief
PLOS Pathogens
orcid.org/0000-0001-5065-158X

Michael Malim
Editor-in-Chief
PLOS Pathogens
orcid.org/0000-0002-7699-2064

****

Reviewer Comments (if any, and for reference):

From: Plowright, Raina >
Sent: Wednesday, April 15, 2020 9:29 PM EDT
To: DeeAnn Reeder ; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)
CC: Coleman, Jeremy T >; Cryan, Paul ; Daniel Streicker >; Gibbs, Samantha ; Gilbert, Amy T - Aphis >; Grant, Evan H ; Hopkins, Maria-Richetta (Camille) C ; epstein ecohealthalliance.org>; Lorch, Jeffrey M >; O'Shea, Thomas >; Kading,Rebekah >; Runge, Michael C ; Sleeman, Jonathan M ; a.peel ; castlekt >; ckjohnson@UCDAVIS.EDU kate.e.jones ; linfa.wang ; ecohealthalliance.org ecohealthalliance.org>; rbaric ; wfrick >
Subject: Re: Expert judgement for SARS-CoV-2 risk assessment for North American bats

Great discussion! Thanks for forwarding the paper Jon, and thanks for summarizing the data Dan.
Receptor binding studies are a great and practical first step, however, susceptibility is far more complex than receptor binding. Many processes must be overcome to infect a new species and experiments are probably the only way to definitively determine susceptibility.
I reached out to Tony S to see if he had insights about Artibeus jamaicensis (susceptible) with respect to the AA considered in the paper – he looked through his transcriptome data and noted it has 13 matched AAs.
I look forward to more discussion tomorrow.
Raina

From: DeeAnn Reeder >
Date: Wednesday, April 15, 2020 at 5:31 PM
To: "Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)"
Cc: "Coleman, Jeremy T" < >, "Cryan, Paul" < , Daniel Streicker >, "Gibbs, Samantha" >, "Gilbert, Amy T - Aphis" >, "Grant, Evan H" "Hopkins, Maria-Richetta (Camille) C" >, Jon Epstein ecohealthalliance.org>, "Lorch, Jeffrey M" "O'Shea, Thomas" , "Rebekah.Kading , "Runge, Michael C" , "Sleeman, Jonathan M" , "a.peel " >, "castlekt " , "ckjohnson " , "kate.e.jones "linfa.wang " , ecohealthalliance.org" >, Raina Plowright , "rbaric " >, "sja " , "wfrick "
Subject: Re: Expert judgement for SARS-CoV-2 risk assessment for North American bats

Thanks Jon!

On Wed, Apr 15, 2020 at 7:15 PM Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) > wrote:

> Some food for thought while considering the effectiveness (or not) of bat workers/researchers putting on some kind of respiratory protection. This data, collected pre-COVID19, basically shows that putting on surgical masks can be effective for minimizing the spread of human coronaviruses, although the total number of patients tested was still pretty low and we don't know the extent to which COVID-19 can be spread in aerosolized form. Note that the masks weren't that effective for rhinoviruses or aerosolized flu.
>
> Jon

From: Daniel Streicker
Sent: Wednesday, April 15, 2020 2:04 PM
To: Jon Epstein ecohealthalliance.org>
Cc: Grant, Evan H ; castlekt ; O'Shea, Thomas raina.plowright ; dreeder ; sja kate.e.jones ckjohnson wfrick ; linfa.wang Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) ; a.peel ; rbaric ; Rebekah.Kading ; Gilbert, Amy T - Aphis >; Lorch, Jeffrey M >; Runge, Michael C ; Cryan, Paul >; ecohealthalliance.org; Sleeman, Jonathan M >; Coleman, Jeremy T ; Gibbs, Samantha ; Hopkins, Maria-Richetta (Camille) C
Subject: Re: Expert judgement for SARS-CoV-2 risk assessment for North American bats

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Best,
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Cheers,
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--
DeeAnn M. Reeder, PhD
Professor
Department of Biology
Bucknell University
Lewisburg, PA 17837

http://deeannreeder.scholar.bucknell.edu

From: Kevin Castle
Sent: Monday, April 20, 2020 9:42 AM EDT
To: Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) >
CC: Plowright, Raina ; DeeAnn Reeder >; Coleman, Jeremy T ; Cryan, Paul ; Daniel Streicker ; Gibbs, Samantha Gilbert, Amy T - Aphis < Grant, Evan H ; Hopkins, Maria-Richetta (Camille) C >; epstein < ecohealthalliance.org>; Lorch, Jeffrey M ; O'Shea, Thomas ; Kading,Rebekah >; Runge, Michael C >; Sleeman, Jonathan M ; a.peel ; ckjohnson ; kate.e.jones >; linfa ; ecohealthalliance.org ecohealthalliance.org>; rbaric ; sja ; wfrick >
Subject: Re: Expert judgement for SARS-CoV-2 risk assessment for North American bats

Thanks Jon!

On Mon, Apr 20, 2020 at 7:18 AM Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) > wrote:

> If you haven't seen it.
>
> Jon

From: Plowright, Raina >
Sent: Wednesday, April 15, 2020 9:29 PM
To: DeeAnn Reeder < ; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)
Cc: Coleman, Jeremy T >; Cryan, Paul ; Daniel Streicker >; Gibbs, Samantha >; Gilbert, Amy T - Aphis >; Grant, Evan H < ; Hopkins, Maria-Richetta (Camille) C >; Jon Epstein ecohealthalliance.org>; Lorch, Jeffrey M >; O'Shea, Thomas >; Rebekah.Kading Runge, Michael C ; Sleeman, Jonathan M >; a.peel ; castlekt ; ckjohnson kate.e.jones ; linfa.wang ecohealthalliance.org; email.unc.edu; sja ; wfrick
Subject: Re: Expert judgement for SARS-CoV-2 risk assessment for North American bats

Great discussion! Thanks for forwarding the paper Jon, and thanks for summarizing the data Dan.

Receptor binding studies are a great and practical first step, however, susceptibility is far more complex than receptor binding. Many processes must be overcome to infect a new species and experiments are probably the only way to definitively determine susceptibility.

I reached out to Tony S to see if he had insights about Artibeus jamaicensis (susceptible) with respect to the AA considered in the paper – he looked through his transcriptome data and noted it has 13 matched AAs.

I look forward to more discussion tomorrow.

Raina

> **From:** DeeAnn Reeder
> **Date:** Wednesday, April 15, 2020 at 5:31 PM
> **To:** "Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)" >
> **Cc:** "Coleman, Jeremy T" >, "Cryan, Paul" , Daniel Streicker , "Gibbs, Samantha" >, "Gilbert, Amy T - Aphis" , "Grant, Evan H" >, "Hopkins, Maria-Richetta (Camille) C" >, Jon Epstein ecohealthalliance.org>, "Lorch, Jeffrey M" "O'Shea, Thomas" < , "Rebekah.Kading " , "Runge, Michael C" , "Sleeman, Jonathan M" >, "a.peel " , "castlekt " , "ckjohnson " <ckjohnson , "kate.e.jones " "linfa.wang " <linfa.wang >, " ecohealthalliance.org"

Raina Plowright >, "rbaric "
, "sja " wfrick "
>
Subject: Re: Expert judgement for SARS-CoV-2 risk assessment for North American bats

Thanks Jon!

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> Some food for thought while considering the effectiveness (or not) of bat workers/researchers putting on some kind of respiratory protection. This data, collected pre-COVID19, basically shows that putting on surgical masks can be effective for minimizing the spread of human coronaviruses, although the total number of patients tested was still pretty low and we don't know the extent to which COVID-19 can be spread in aerosolized form. Note that the masks weren't that effective for rhinoviruses or aerosolized flu.
>
> Jon

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DeeAnn M. Reeder, PhD
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http://deeannreeder.scholar.bucknell.edu

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Kevin T. Castle, DVM, MS
Wildlife Veterinary Consulting, LLC

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Received: 5 March 2020 | Accepted: 30 March 2020

DOI: 10.1002/jmv.25817

SHORT COMMUNICATION

JOURNAL OF MEDICAL VIROLOGY WILEY

SARS-CoV-2 spike protein favors ACE2 from *Bovidae* and *Cricetidae*

Junwen Luan[1] | Xiaolu Jin[1,2] | Yue Lu[1,2] | Leiliang Zhang[1]

[1]Institute of Basic Medicine, Shandong Provincial Hospital Affiliated to Shandong First Medical University, Jinan, Shandong, China

[2]School of Medicine and Life Sciences, Shandong Academy of Medical Sciences, University of Jinan, Jinan, Shandong, China

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Leiliang Zhang, PhD, Institute of Basic Medicine, Shandong Provincial Hospital Affiliated to Shandong First Medical University, Jinan, 250062 Shandong, China.
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Funding information
National Key Plan for Research and Development of China, Grant/Award Number: 2016YFD0500300; Shandong Academy of Medical Sciences Grant, Grant/Award Number: 2017-52; Innovation Project of Shandong Academy of Medical Sciences; Academic promotion programme of Shandong First Medical University, Grant/Award Number: 2019LJ001

Abstract

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) causes the recent COVID-19 public health crisis. Bat is the widely believed original host of SARS-CoV-2. However, its intermediate host before transmitting to humans is not clear. Some studies proposed pangolin, snake, or turtle as the intermediate hosts. Angiotensin-converting enzyme 2 (ACE2) is the receptor for SARS-CoV-2, which determines the potential host range for SARS-CoV-2. On the basis of structural information of the complex of human ACE2 and SARS-CoV-2 receptor-binding domain (RBD), we analyzed the affinity to S protein of the 20 key residues in ACE2 from mammal, bird, turtle, and snake. Several ACE2 proteins from *Primates*, *Bovidae*, *Cricetidae*, and *Cetacea* maintained the majority of key residues in ACE2 for associating with SARS-CoV-2 RBD. The simulated structures indicated that ACE2 proteins from *Bovidae* and *Cricetidae* were able to associate with SARS-CoV-2 RBD. We found that nearly half of the key residues in turtle, snake, and bird were changed. The simulated structures showed several key contacts with SARS-CoV-2 RBD in turtle and snake ACE2 were abolished. This study demonstrated that neither snake nor turtle was the intermediate hosts for SARS-CoV-2, which further reinforced the concept that the reptiles are resistant against infection of coronavirus. This study suggested that *Bovidae* and *Cricetidae* should be included in the screening of intermediate hosts for SARS-CoV-2.

KEYWORDS

ACE2, *Bovidae*, *Cricetidae*, intermediate host, SARS-CoV-2

1 | INTRODUCTION

Coronavirus disease 2019 (COVID-19), which was first reported in Wuhan, Hubei province, China, has caused over 80 422 human infections and more than 2984 deaths (as of 4 March 2020) in China.[1,2] The confirmed cases outside China are increasing, which raised major global concern. Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was identified to be the pathogen of COVID-19. SARS-CoV-2 has joined SARS-CoV and Middle East respiratory syndrome-related coronavirus (MERS-CoV) as another coronavirus that causes severe respiratory disease and human death.[3,4]

The specificity of the interaction between virus and receptor determines its host range for the virus. Spike protein (S) of SARS-CoV-2 has attracted great attention because of its role in receptor binding. Angiotensin-converting enzyme 2 (ACE2) binds to the receptor-binding domain (RBD) of SARS-CoV-2 S protein and functions as a receptor for SARS-CoV-2.[5,6] The origin of SARS-CoV-2 is considered as bat.[6] However, the intermediate host is unknown. Some studies suggest that pangolin is involved in the evolution of SARS-CoV-2.[7,8] Others suggested that snake and turtles are potential intermediate hosts for SARS-CoV-2.[9,10] In this study, we compared the key amino acids (AAs) in ACE2 from different species for the binding ability to RBD. On the basis of

potential interaction between S protein and ACE2, it was speculated that SARS-CoV-2 preserved the ability to infect *Bovidae* and *Cricetidae* but not snake or turtle.

2 | METHODS

2.1 | Sequence analysis of ACE2

A total of 93 ACE2 protein sequences were selected from 85 mammals, 4 birds, 3 turtles, and 1 snake. These ACEs with their corresponding species are listed as follows: hACE2: *Homo sapiens* (BAB40370.1), RhiACE2: *Rhinopithecus roxellana* (XP_010364367.2), MacmACE2: *Macaca mulatta* (NP_001129168.1), MuseACE2: *Mustela erminea* (XP_032187679.1), CamdACE2: *Camelus dromedarius* (XP_031301717.1), PlACE2: *Procyon lotor* (XP_031301717.1), PcACE2: *Paguma larvata* (AAX63775.1), RmACE2: *Rhinolophus macrotis* (ADN93471.1), RfACE2: *Rhinolophus ferrumequinum* (BAH02663.1), RsACE2: *Rhinolophus sinicus* (ADN93472.1), RlACE2: *Rousettus leschenaultii* (BAF50705.1), SsACE2: *Sus scrofa* (NP_001116542.1), MpfACE2: *Mustela putorius furo* (BAE53380.1), RatACE2: *Rattus norvegicus* (Q5EGZ1), MmACE2: *Mus musculus* (Q3URC9), ClfACE2: *Canis lupus familiaris* (J9P7Y2), FcACE2: *Felis catus* (A0A384DV19), MjACE2: *Manis javanica* (XP_017505752.1), RpACE2: *Rhinolophus pearsonii* (ABU54053.1), PvACE2: *Pteropus vampyrus* (XP_011361275.1), PoaACE2: *Pongo abelii* (NP_001124604.1), EcACE2: *Equus caballus* (F6V9L3), BtACE2: *Bos taurus* (Q58DD0), PtACE2: *Pan troglodytes* (A0A2J8KU96), OraACE2: *Ornithorhynchus anatinus* (F7FDA2), OvaACE2: *Ovis aries* (W5PSB6), PanACE2: *Papio Anubis* (A0A096N4X9), LaACE2: *Loxodonta africana* (G3T6Q2), SsdACE2: *Sus scrofa domesticus* (A0A220QT48), EeACE2: *Erinaceus europaeus* (A0A1S3APE5), OcACE2: *Oryctolagus cuniculus* (G1TEF4), NpACE2: *Nyctereutes procyonoides* (B4XEP4), VvACE2: *Vulpes vulpes* (A0A3Q7RAT9), PhcACE2: *Phodopus campbelli* (C7ECU7), MaACE2: *Mesocricetus auratus* (C7ECV1), CjACE2: *Callithrix jacchus* (F7CNJ6), SusACE2: *Suricata suricatta* (XP_029786256.1), HgACE2: *Heterocephalus glaber* (A0A0N8EUX7), DoACE2: *Dipodomys ordii* (A0A1S3GHT7), ItACE2: *Ictidomys tridecemlineatus* (XP_005316051.3), CpACE2: *Cavia porcellus* (XP_023417808.1), CgACE2: *Cricetulus griseus* (A0A061HZ66), ChACE2: *Capra hircus*(A0A452EVJ5); BibtACE2: *Bos indicus x Bos taurus* (A0A4W2H3A1), BmACE2: *Bos mutus* (L8I4I4), NlACE2: *Nomascus leucogenys* (G1RE79); CsACE2: *Chlorocebus sabaeus* (A0A0D9RQZ0); MfACE2: *Macaca fascicularis* (A0A2K5X283); PpACE2: *Pan paniscus* (A0A2R9BKD8); CaACE2: *Cercocebus atys* (A0A2K5KSD8); MnACE2: *Macaca nemestrina* (A0A2K6D1N8); MalACE2: *Mandrillus leucophaeus* (A0A2K5ZV99); TsACE2: *Tarsius syrichta* (A0A1U7TY97); PrcACE2: *Propithecus coquereli* (A0A2K6GHW5); UmACE2: *Ursus maritimus* (A0A452TT30); OgACE2: *Otolemur garnettii* (H0WMI5); SbbACE2: *Saimiri boliviensis boliviensis* (A0A2K6SBD4); CciACE2: *Cebus capucinus imitator* (A0A2K5PYM0); GggACE2: *Gorilla gorillagorilla* (G3QWX4); AnACE2: *Aotus nancymaae* (A0A2K5DQI6); ChaACE2: *Chlorocebus aethiops* (Q1LZX8); AmACE2: *Ailuropoda melanoleuca* (G1MC42); VuACE2: *Vombatus ursinus* (A0A4X2M679); UaACE2: *Ursus americanus* (A0A452R1Z9); UahACE2: *Ursusarctos horribilis* (A0A3Q7TE16); PmACE2: *Physeter macrocephalus* (A0A2Y9S5T9); LvACE2: *Lipotes vexillifer* (A0A340Y3Y6); BasACE2: *Balaenoptera acutorostrata scammoni* (A0A452CBT6); DlACE2: *Delphinapterus leucas* (A0A2Y9M9H3); TtACE2: *Tursiops truncatus* (A0A2U4AJL3); NaaACE2: *Neophocaena asiaeorientalis asiaeorientalis* (A0A341BCI8); CuACE2: *Callorhinus ursinus* (A0A3Q7N3M7); NsACE2: *Neomonachus schauinslandi* (A0A2Y9GEI9); TmlACE2: *Trichechus manatuslatirostris* (A0A2Y9E393); ElkACE2: *Enhydra lutriskenyoni* (A0A2Y9KLV0); ClACE2: *Chinchilla lanigera* (C7ECU0); MdACE2: *Monodelphis domestica* (F6WXR7); LpACE2: *Lynx pardinus* (A0A485NF12); PaACE2: *Pipistrellus abramus* (C7ECT9); MbACE2: *Myotis brandtii* (S7N573); DrACE2: *Desmodus rotundus* (K9INV8); RhpACE2: *Rhinolophus pusillus* (E2DHI9); RaACE2: *Rhinolophus alcyone* (A0A0N7IQX6); RlACE2(2): *Rhinolophus landeri* (A0A0P0IB69); MylACE2: *Myotis lucifugus* (G1PXH7), GgACE2: *Gallus gallus* (F1NHR4), ApACE2: *Anas platyrhynchos* (R0LHX5), MgACE2: *Meleagris gallopavo* (G1NPB8), CaaACE2: *Cathartes aura* (A0A091MDI4), OhACE2: *Ophiophagus hannah* (V8NIH2), CpbACE2: *Chrysemys picta bellii* (XP_023964517.1), CmACE2: *Chelonia mydas* (XP_007070561.1); and PsACE2: *Pelodiscus sinensis* (XP_006122891.1). On the basis of known 20 key sites in human ACE2 interacting with SARS-CoV-2 RBD,[11] we analyzed whether these sites were conserved on other ACE2 proteins. Phylogenetic and molecular evolutionary analysis of ACE2 protein was conducted using molecular evolutionary genetics analysis version X (MEGA-X).[12] Phylogenetic tree was generated with Jones-Taylor-Thornton evolutionary model using a maximum-likelihood method.

2.2 | Structure simulation of ACE2-RBD complex

On the basis of the structure of hACE2 with SARS-CoV-2 S RBD (PDB: 6LZG), the structure of SARS-CoV-2 S and ACE2 from *Bos taurus*, *Cricetulus griseus*, *Pelodiscus sinensis*, and *Ophiophagus hannah* were simulated by SWISS-MODEL online server[13] and analyzed by Chimera software version 1.14.[14]

3 | RESULTS

3.1 | Sequence alignment of ACE2

According to the recently resolved structure of the complex of human ACE2 and SARS-CoV-2 RBD, there are 20 key AAs in hACE2 for interacting with RBM.[11] We analyzed those AAs of ACE2 protein from a list of mammals, birds, turtles, and snake, as shown in Table 1. Next, a phylogenetic tree for mammalian ACE2 proteins was constructed by MEGA-X software. There were 16 *primates* ACE2, 5 *Bovidae* ACE2, 2 *Cricetidae* ACE2, and 3 *Cetacea* ACE2 (Table 1 and Figure 1A), possessing at least 90% (18/20) critical AAs. Pangolin ACE2 preserved only 70% (14/20) AAs. Nearly half of the key residues in turtles (CpbACE2, CmACE2, and PsACE2) and snake (OhACE2) were changed (Table 1). ACE2 from *Aves*, including *Gallus gallus*, *Anas platyrhynchos*, *Meleagris gallopavo*, and *Cathartes aura*, only matched 10 to 11 AAs (Table 1).

TABLE 1 Analysis of the key AAs in ACE2 for SARS-CoV-2 RBD binding

	AA position																			
ACE2	24	27	28	30	31	34	35	37	38	41	42	45	82	83	330	353	354	355	357	393	Matched AA
hACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
RhiACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
MacmACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
PoaACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
PtACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
PanACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
NlACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
CsACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
MfACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
PpACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
CaACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
MnACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
MalACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
GggACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
ChaACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
PrcACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	19
BtACE2	Q	T	F	E	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
OvaACE2	Q	T	F	E	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
MaACE2	Q	T	F	D	K	Q	E	E	D	Y	Q	L	N	Y	N	K	G	D	R	R	18
CgACE2	Q	T	F	D	K	Q	E	E	D	Y	Q	L	N	Y	N	K	G	D	R	R	18
ChACE2	Q	T	F	E	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
BibtACE2	Q	T	F	E	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
BmACE2	Q	T	F	E	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
PmACE2	Q	T	F	Q	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
DlACE2	Q	T	F	Q	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
NaaACE2	Q	T	F	Q	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
PhcACE2	Q	T	F	D	K	Q	E	E	D	Y	Q	L	N	Y	N	K	E	D	R	R	17
HgACE2	Q	T	F	D	K	Q	E	E	D	Y	Q	L	A	Y	N	K	D	D	R	R	17
ItACE2	L	T	F	D	K	Q	E	E	D	Y	Q	L	A	Y	N	K	G	D	R	R	17
BasACE2	Q	T	F	Q	K	H	E	E	D	Y	R	L	T	Y	N	K	G	D	R	R	17
CamdACE2	L	T	F	E	E	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
RlACE2	L	T	F	E	K	T	E	E	D	Y	Q	L	T	Y	K	K	G	D	R	R	16
SsACE2	L	T	F	E	K	L	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
FcACE2	L	T	F	E	K	H	E	E	E	Y	Q	L	T	Y	N	K	G	D	R	R	16
SsdACE2	L	T	F	E	K	L	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
OcACE2	L	T	F	E	K	Q	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
CjACE2	Q	T	F	D	K	H	E	E	D	H	E	L	T	Y	N	K	Q	D	R	R	16
DoACE2	L	T	F	D	N	Q	E	E	D	Y	Q	L	I	Y	N	K	G	D	R	R	16
UmACE2	L	T	F	E	K	Y	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16

(Continues)

TABLE 1 (Continued)

	AA position																				
ACE2	24	27	28	30	31	34	35	37	38	41	42	45	82	83	330	353	354	355	357	393	Matched AA
SbbACE2	Q	T	F	D	K	H	E	E	D	H	E	L	T	Y	N	K	Q	D	R	R	16
CciACE2	Q	T	F	D	K	H	E	E	D	H	E	L	T	Y	N	K	Q	D	R	R	16
AnACE2	Q	T	F	D	K	H	E	E	D	H	E	L	T	Y	N	K	Q	D	R	R	16
AmACE2	L	T	F	E	K	Y	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
UaACE2	L	T	F	E	K	Y	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
UahACE2	L	T	F	E	K	Y	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
LvACE2	R	T	F	Q	K	H	E	E	D	Y	Q	L	T	F	N	K	G	D	R	R	16
TtACE2	R	T	F	Q	K	R	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
LpACE2	L	T	F	E	K	H	E	E	E	Y	Q	L	T	Y	N	K	G	D	R	R	16
MpfACE2	L	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	K	R	D	R	R	15
ClfACE2	L	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	K	G	D	R	R	15
RpACE2	R	T	F	D	K	H	E	E	D	H	E	L	D	Y	N	K	D	D	R	R	15
LaACE2	L	T	F	D	T	Q	E	E	D	Y	Q	L	D	F	N	K	G	D	R	R	15
VvACE2	L	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	K	G	D	R	R	15
CpACE2	Q	T	F	D	E	L	K	E	D	Y	Q	L	A	Y	N	K	N	D	R	R	15
TsACE2	Q	T	F	D	K	Q	E	E	D	H	Q	L	S	Y	N	N	S	D	R	R	15
TmlACE2	L	T	F	D	T	Q	E	E	D	Y	Q	L	N	F	N	K	G	D	R	R	15
ClACE2	Q	T	F	D	N	E	K	E	D	Y	Q	L	A	Y	N	K	D	D	R	R	15
MuseACE2	L	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	K	R	D	R	R	14
PlACE2	L	T	F	E	N	N	E	E	E	Y	Q	L	T	Y	N	K	G	D	R	R	14
MjACE2	E	T	F	E	K	S	E	E	E	Y	Q	L	N	Y	N	K	H	D	R	R	14
PvACE2	L	T	F	E	K	T	E	E	D	Y	Q	L	A	Y	K	K	G	D	R	K	14
EcACE2	L	T	F	E	K	S	E	E	E	H	Q	L	T	Y	N	K	G	D	R	R	14
NpACE2	L	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	R	G	D	R	R	14
OgACE2	Q	T	F	D	N	R	E	E	E	H	Q	L	T	Y	N	K	D	D	R	R	14
VuACE2	R	E	F	E	T	K	E	E	E	Y	Q	L	T	F	N	K	G	D	R	R	14
NsACE2	L	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	K	H	D	R	R	14
ElkACE2	P	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	K	R	D	R	R	14
RhpACE2	L	K	F	N	D	S	E	E	D	Y	Q	L	N	Y	N	K	G	D	R	R	14
RmACE2	E	K	F	D	K	S	K	E	D	Y	E	L	N	Y	K	K	G	D	R	R	13
RsACE2	E	I	F	D	K	T	K	E	D	H	Q	L	N	Y	N	K	G	D	R	R	13
RatACE2	K	S	F	N	K	Q	E	E	D	Y	Q	L	N	F	N	H	G	D	R	R	13
MmACE2	N	T	F	N	N	Q	E	E	D	Y	Q	L	S	F	N	H	G	D	R	R	13
CuACE2	L	T	F	E	K	S	E	E	E	Y	Q	F	T	Y	N	K	H	D	R	R	13
RlACE2(2)	L	T	F	D	D	S	A	E	N	Y	Q	L	N	F	N	K	G	D	R	R	13
PcACE2	L	T	F	E	T	Y	E	Q	E	Y	Q	V	T	Y	N	K	G	D	R	R	12
RfACE2	L	K	F	D	D	S	E	E	N	H	Q	L	N	F	N	K	G	D	R	R	12
SusACE2	L	T	F	E	Q	H	E	Q	E	Y	L	V	A	Y	N	K	G	D	R	R	12

TABLE 1 (Continued)

	AA position																				
ACE2	24	27	28	30	31	34	35	37	38	41	42	45	82	83	330	353	354	355	357	393	Matched AA
MdACE2	D	T	F	D	D	A	K	E	E	H	Q	L	T	Y	N	K	N	D	R	R	12
DrACE2	E	T	F	E	N	T	E	E	E	Y	Q	L	T	Y	N	N	K	D	R	R	12
RaACE2	L	I	F	D	N	S	E	E	N	H	Q	L	N	F	N	K	G	D	R	R	12
OraACE2	E	Q	F	T	Q	K	Q	E	D	Y	Q	L	K	F	N	K	N	D	R	R	11
EeACE2	E	K	F	D	D	R	Q	E	N	Y	E	L	N	Y	N	N	G	D	R	R	11
MbACE2	K	I	F	E	N	S	K	E	D	H	E	L	T	Y	N	K	G	D	R	R	11
MylACE2	K	I	F	E	N	S	A	E	D	H	E	L	T	Y	N	K	G	D	R	R	11
GgACE2	E	T	F	A	E	V	R	E	D	Y	E	L	R	F	N	K	N	D	R	R	11
ApACE2	Q	M	F	A	E	V	R	E	D	Y	E	L	N	F	N	K	N	D	R	R	11
MgACE2	E	T	F	A	E	V	R	E	D	Y	E	L	R	F	N	K	N	D	R	R	11
CpbACE2	E	N	F	S	Q	V	R	E	D	Y	A	L	K	Y	N	K	K	D	R	R	11
CmACE2	E	N	F	S	Q	V	R	E	D	Y	A	L	K	Y	N	K	K	D	R	R	11
PsACE2	E	N	F	S	E	V	Q	E	D	Y	A	L	K	Y	N	K	K	D	R	R	11
PaACE2	E	R	F	V	K	H	E	E	N	H	E	L	G	F	D	K	N	D	R	R	10
CaaACE2	Q	I	F	E	E	P	R	E	N	Y	E	L	S	F	N	K	N	D	R	R	10
OhACE2	…	K	F	E	Q	A	R	T	D	Y	N	I	M	F	N	K	E	D	R	R	9

Note: hACE2, *Homo sapiens* (BAB40370.1), RhiACE2, *Rhinopithecus roxellana* (XP_010364367.2), MacmACE2, *Macaca mulatta* (NP_001129168.1), MuseACE2, *Mustela erminea* (XP_032187679.1), CamdACE2, *Camelus dromedarius* (XP_031301717.1), PlACE2, *Procyon lotor* (XP_031301717.1), PcACE2, *Paguma larvata* (AAX63775.1), RmACE2, *Rhinolophus macrotis* (ADN93471.1), RfACE2, *Rhinolophus ferrumequinum* (BAH02663.1), RsACE2, *Rhinolophus sinicus* (ADN93472.1), RlACE2, *Rousettus leschenaultii* (BAF50705.1), SsACE2, *Sus scrofa* (NP_001116542.1), MpfACE2, *Mustela putorius furo* (BAE53380.1), RatACE2, *Rattus norvegicus* (Q5EGZ1), MmACE2, *Mus musculus* (Q3URC9), ClfACE2, *Canis lupus familiaris* (J9P7Y2), FcACE2, *Felis catus* (A0A384DV19), MjACE2, *Manis javanica* (XP_017505752.1), RpACE2, *Rhinolophus pearsonii* (ABU54053.1), PvACE2, *Pteropus vampyrus* (XP_011361275.1), PoaACE2, *Pongo abelii* (NP_001124604.1), EcACE2, *Equus caballus* (F6V9L3), BtACE2, *Bos taurus* (Q58DD0), PtACE2, *Pan troglodytes* (A0A2J8KU96), OraACE2, *Ornithorhynchus anatinus* (F7FDA2), OvaACE2, *Ovis aries* (W5PSB6), PanACE2, *Papio Anubis* (A0A096N4X9), LaACE2, *Loxodonta africana* (G3T6Q2), SsdACE2, *Sus scrofa domesticus* (A0A220QT48), EeACE2, *Erinaceus europaeus* (A0A1S3APE5), OcACE2, *Oryctolagus cuniculus* (G1TEF4), NpACE2, *Nyctereutes procyonoides* (B4XEP4), VvACE2, *Vulpes vulpes* (A0A3Q7RAT9), PhcACE2, *Phodopus campbelli* (C7ECU7), MaACE2, *Mesocricetus auratus* (C7ECV1), CjACE2, *Callithrix jacchus* (F7CNJ6), SusACE2, *Suricata suricatta* (XP_029786256.1), HgACE2, *Heterocephalus glaber* (A0A0N8EUX7), DoACE2, *Dipodomys ordii* (A0A1S3GHT7), ItACE2, *Ictidomys tridecemlineatus* (XP_005316051.3), CpACE2, *Cavia porcellus* (XP_023417808.1), CgACE2, *Cricetulus griseus* (A0A061HZ66), ChACE2, *Capra hircus*(A0A452EVJ5); BibtACE2, *Bos indicus x Bos taurus* (A0A4W2H3A1), BmACE2, *Bos mutus* (L8I4I4), NlACE2, *Nomascus leucogenys* (G1RE79); CsACE2, *Chlorocebus sabaeus* (A0A0D9RQZ0); MfACE2, *Macaca fascicularis* (A0A2K5X283); PpACE2, *Pan paniscus* (A0A2R9BKD8); CaACE2, *Cercocebus atys* (A0A2K5KSD8); MnACE2, *Macaca nemestrina* (A0A2K6D1N8); MalACE2, *Mandrillus leucophaeus* (A0A2K5ZV99); TsACE2, *Tarsius syrichta* (A0A1U7TY97); PrcACE2, *Propithecus coquereli* (A0A2K6GHW5); UmACE2, *Ursus maritimus* (A0A452TT30); OgACE2, *Otolemur garnettii* (H0WMI5); SbbACE2, *Saimiri boliviensis boliviensis* (A0A2K6SBD4); CciACE2, *Cebus capucinus imitator* (A0A2K5PYM0); GggACE2, *Gorilla gorillagorilla* (G3QWX4); AnACE2, *Aotus nancymaae* (A0A2K5DQI6); ChaACE2, *Chlorocebus aethiops* (Q1LZX8); AmACE2, *Ailuropoda melanoleuca* (G1MC42); VuACE2, *Vombatus ursinus* (A0A4X2M679); UaACE2, *Ursus americanus* (A0A452R1Z9); UahACE2, *Ursusarctos horribilis* (A0A3Q7TE16); PmACE2, *Physeter macrocephalus* (A0A2Y9S5T9); LvACE2, *Lipotes vexillifer* (A0A340Y3Y6); BasACE2, *Balaenoptera acutorostrata scammoni* (A0A452CBT6); DlACE2, *Delphinapterus leucas* (A0A2Y9M9H3); TtACE2, *Tursiops truncatus* (A0A2U4AJL3); NaaACE2, *Neophocaena asiaeorientalis asiaeorientalis* (A0A341BCI8); CuACE2, *Callorhinus ursinus* (A0A3Q7N3M7); NsACE2, *Neomonachus schauinslandi* (A0A2Y9GEI9); TmlACE2, *Trichechus manatuslatirostris* (A0A2Y9E393); ElkACE2, *Enhydra lutriskenyoni* (A0A2Y9KLV0); ClACE2, *Chinchilla lanigera* (C7ECU0); MdACE2, *Monodelphis domestica* (F6WXR7); LpACE2, *Lynx pardinus* (A0A485NF12); PaACE2, *Pipistrellus abramus* (C7ECT9); MbACE2, *Myotis brandtii* (S7N573); DrACE2, *Desmodus rotundus* (K9INV8); RhpACE2, *Rhinolophus pusillus* (E2DHI9); RaACE2, *Rhinolophus alcyone* (A0A0N7IQX6); RlACE2(2), *Rhinolophus landeri* (A0A0P0IB69); MylACE2, *Myotis lucifugus* (G1PXH7), GgACE2, *Gallus gallus* (F1NHR4), ApACE2, *Anas platyrhynchos* (R0LHX5), MgACE2, *Meleagris gallopavo* (G1NPB8), CaaACE2, *Cathartes aura* (A0A091MDI4), OhACE2, *Ophiophagus hannah* (V8NIH2), CpbACE2, *Chrysemys picta bellii* (XP_023964517.1), CmACE2, *Chelonia mydas* (XP_007070561.1); and PsACE2, *Pelodiscus sinensis* (XP_006122891.1).
Abbreviations: AA, amino acid; ACE2, angiotensin-converting enzyme 2; RBD, receptor-binding domain; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

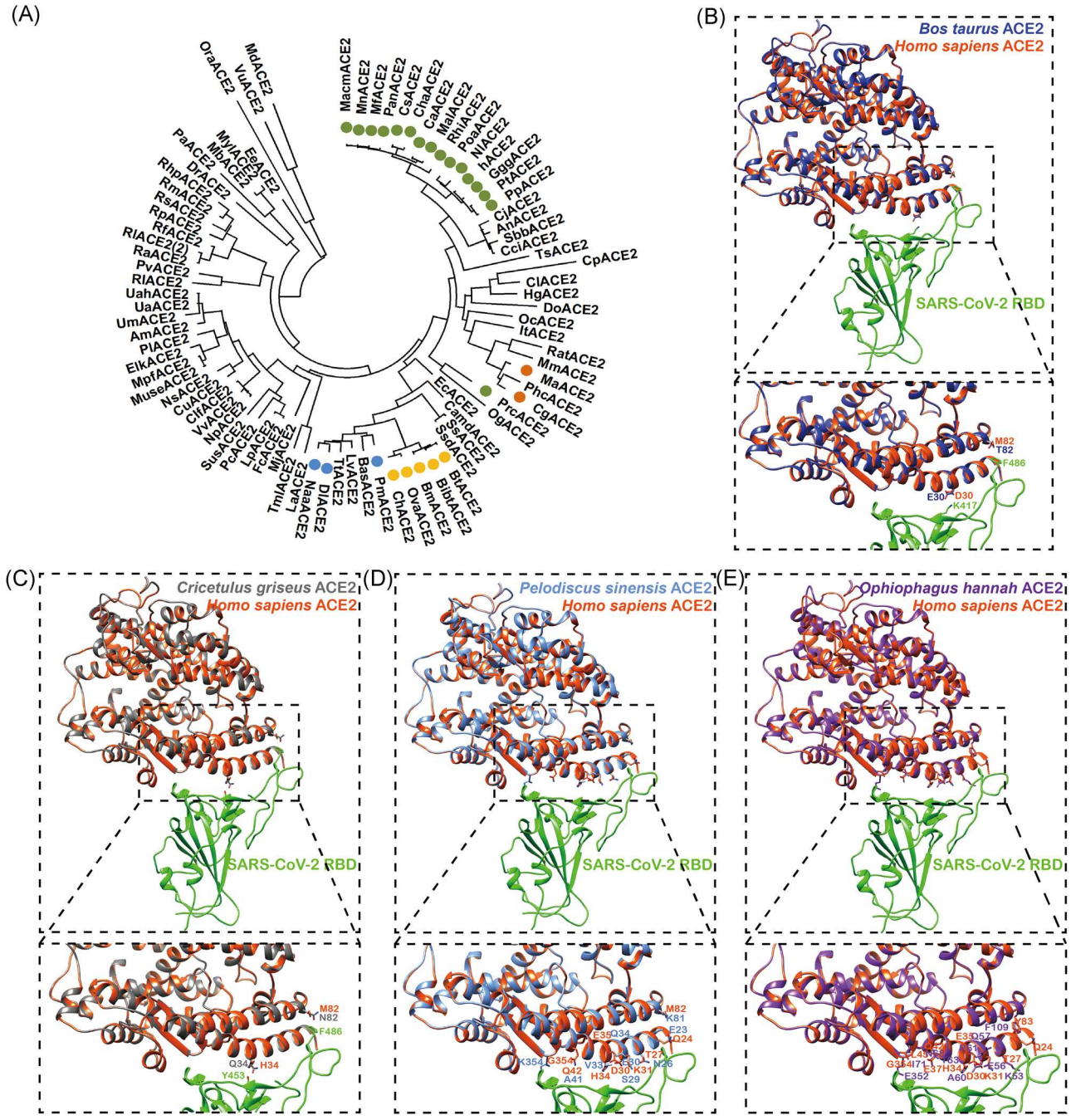

FIGURE 1 Structure simulation of SARS-CoV-2 RBD with ACE2 from different species. A, Phylogenetic tree of mammalian ACE2. ACE2 proteins from a total of 85 mammals were analyzed by MEGA-X and the phylogenetic tree was constructed using a maximum-likelihood method. The green, yellow, orange, and blue represent ACE2 from *Primates*, *Bovidae*, *Cricetidae*, and *Cetacea*, respectively. B, Structural simulation of the protein complex of *Bos taurus* ACE2 and SARS-CoV-2 RBD. *Bos taurus* ACE2, *Homo sapiens* ACE2, and SARS-CoV-2 RBD are in medium blue, orange red, and green, respectively. C, Structural simulation of the protein complex of *Cricetulus griseus* ACE2 and SARS-CoV-2 RBD. *Cricetulus griseus* ACE2, *Homo sapiens* ACE2, and SARS-CoV-2 RBD are in dim gray, orange red, and green, respectively. D, Structural simulation of the protein complex of *Pelodiscus sinensis* ACE2 and SARS-CoV-2 RBD. *Pelodiscus sinensis* ACE2, *Homo sapiens* ACE2, and SARS-CoV-2 RBD are in cornflower blue, orange red, and green, respectively. E, Structural simulation of the protein complex of *Ophiophagus hannah* ACE2 and SARS-CoV-2 RBD. *Ophiophagus hannah* ACE2, *Homo sapiens* ACE2, and SARS-CoV-2 RBD are in purple, orange red, and green, respectively. ACE2, angiotensin-converting enzyme 2; MEGA-X, Molecular Evolutionary Genetics Analysis version X; RBD, receptor-binding domain; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2

3.2 | Structure simulation of the protein complex of SARS-CoV-2 RBD and *Bovidae/Cricetidae*/turtle/snake ACE2

Recently, the structure of SARS-CoV-2 RBD with human ACE2 has been resolved. To investigate whether *Bovidae/Cricetidae* ACE2 maintained the binding affinity with SARS-CoV-2 RBD, we simulated the potential structure of the protein complex. T82 and E30 in *Bos taurus* ACE2 kept the contact to F486 and K417 in SARS-CoV-2 S (Figure 1B). N82 and Q34 in *Cricetulus griseus* ACE2 maintained the contact to F486 and Y453 in SARS-CoV-2 S (Figure 1C). We concluded that *Bovidae/Cricetidae* ACE2 could associate with SARS-CoV-2 S (Figure 1B,C).

To investigate the potential association between SARS-CoV-2 and ACE2 from turtle and snake, we simulated the potential structure of turtle/snake ACE2 with SARS-CoV-2 RBD. The AA correlated to hACE2 Q42 is changed to A (A41) in turtle (Figure 1D). We also noticed that the AA correlated to hACE2 H34 is changed to A (A60) in a snake (Figure 1E). When the contact AA was mutated to smaller AA (A), the contact force for protein-protein interaction will be reduced. Moreover, the corresponding AA of K31 was changed to E (E30) in turtle and Q (Q57) in snake ACE2 (Figure 1D). K31 in hACE2 was critical for SARS-CoV RBD binding and ACE2-K31D mutant abolished its association with SARS-CoV RBD.[15] Taken together, turtle and snake ACE2 are unlikely to bind to S protein of SARS-CoV-2.

4 | DISCUSSION

SARS-CoV, MERS-CoV, and SARS-CoV-2 have caused severe human infectious diseases in the last 2 decades. These three human coronaviruses originated from bats, but the intermediate hosts were different. SARS-CoV came from the *Paguma larvata*,[16] and the intermediate host for MERS-CoV is *Camelus dromedaries*.[17] The new coronavirus SARS-CoV-2 has recently caused a serious pandemic in China and other countries. However, it is not clear which animals are involved in the evolution of SARS-CoV-2 and which animals may be infected by SARS-CoV-2. RBD region in S protein of pangolin coronavirus is similar to that of SARS-CoV-2,[7,8] indicating the involvement of pangolin in the recombination of SARS-CoV-2. By analyzing the codon usage of SARS-CoV-2, people suggested that snake might be a potential host for SARS-CoV-2.[9] Another study indicated that turtle is a potential intermediate host for SARS-CoV-2 based on the key AAs in ACE2 for interacting with SARS-CoV RBD.[10] The late study raised the concerns of SARS-CoV-2 infection in the turtle aquaculture and pet turtle. Most of the coronaviruses hosts are mammals; with a few of exceptions are birds. Considering that all known hosts for coronaviruses are thermostatic animals, it is unlikely that reptiles will be infected with SARS-CoV-2.

There are 20 key AAs in ACE2 critical for binding S protein of SARS-CoV-2.[11] On the basis of these 20 AAs, we analyzed the corresponding AAs in ACE2 from a list of mammal, bird, turtle, and snake. We found that the ACE2 of turtles and snake lost the capability to associate with S protein (Table 1 and Figure 1D,E). These reptiles should be ruled out from the potential host list for SARS-CoV-2. *Aves* ACE2 was unlikely to associate with SARS-CoV-2 RBD because they lost the critical K corresponding to K31 in human ACE2 (Table 1). Pangolin ACE2 was predicted to recognize SARS-CoV-2 RBD less efficiently because it only preserved 14 of 20 critical AAs (Table 1). Interestingly, we found that ACE2 proteins from *Primates*, *Bovidae*, *Cricetidae*, and *Cetacea* were capable to recognize RBD of SARS-CoV-2 by maintaining the majority of key residues in ACE2 for associating with SARS-CoV-2 RBD. Swine ACE2 (CpACE2) with 15 of 20 matched critical AAs was shown to support SARS-CoV-2 entry.[6] *Bovidae/Cricetidae* ACE2 matched more AAs than swine ACE2, thus they should recognize SARS-CoV-2 RBD. It would strengthen our conclusion if we have biochemical evidence for the S-ACE2 interaction analysis for *Bovidae/Cricetidae* ACE2. On the basis of human ACE2 and SARS-CoV-spike complex structure model (PDB ID: 2AJF), we and others recently predicted that hamster ACE2 could associate with SARS-CoV-2 and hamster might be a candidate small animal model for SARS-CoV-2 infection.[18,19] Indeed, golden Syrian hamster (*Mesocricetus auratus*) has been established as a model to study the pathogenesis and transmission of COVID-19.[19] One of *Cetacea*, *Neophocaena asiaeorientalis asiaeorientalis* (Yangtze finless porpoise), lives in the middle and lower reaches of the Yangtze River and its lakes, where Wuhan located nearby.[20] It will be interesting to investigate whether Yangtze finless porpoise could be infected with SARS-CoV-2 or related coronavirus.

In conclusion, we found that *Bovidae/Cricetidae* ACE2 but not turtle/snake ACE2 could recognize SARS-CoV-2 RBD. More attention should be paid to *Bovidae* and *Cricetidae* in hunting the potential intermediate host for SARS-CoV-2.

ACKNOWLEDGMENTS

The authors would like to thank Dr Shan Gao for the discussion. This study is supported by grants from National Key Plan for Research and Development of China (2016YFD0500300), Shandong Academy of Medical Sciences Grant (2017-52), the Innovation Project of Shandong Academy of Medical Sciences, and Academic Promotion Program of Shandong First Medical University (2019LJ001). Molecular graphics and analyses performed with UCSF Chimera, developed by the Resource for Biocomputing, Visualization, and Informatics at the University of California, San Francisco, with support from NIH P41-GM103311.

CONFLICT OF INTERESTS

The authors declare that there are no conflict of interests.

AUTHOR CONTRIBUTIONS

LZ conceived the work. JL and XJ collected and analyzed the data. JL and YL contributed to graphics processing. LZ wrote the manuscript. All authors approved the final version for publication.

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How to cite this article: Luan J, Jin X, Lu Y, Zhang L. SARS-CoV-2 spike protein favors ACE2 from *Bovidae* and *Cricetidae*. *J Med Virol*. 2020;1–8. https://doi.org/10.1002/jmv.25817

From: Winifred F Frick, Ph.D.
Sent: Thursday, April 16, 2020 11:58 AM EDT
To: Plowright, Raina ; DeeAnn Reeder Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)

CC: Coleman, Jeremy T ; Cryan, Paul Daniel Streicker Gibbs, Samantha Gilbert, Amy T - Aphis >; Grant, Evan H < Hopkins, Maria-Richetta (Camille) C epstein < ecohealthalliance.org>; Lorch, Jeffrey M ; O'Shea, Thomas ; Kading,Rebekah >; Runge, Michael C ; Sleeman, Jonathan M ; a.peel ; castlekl ; ckjohnson < >; kate.e.jones ; linfa.wang < ecohealthalliance.org rbaric sja >
Subject: Re: Expert judgement for SARS-CoV-2 risk assessment for North American bats
Attachment(s): "NWRA Position Statement Regarding Covid19 and bat rehabilitation FINAL 15Apr2020 .pdf"

Relevant to conversation this morning regarding rehab practices – attached is position statement from National Wildlife Rehabilitation Association.

Cheers,
fred

From: Raina Plowright >
Date: Wednesday, April 15, 2020 at 6:29 PM
To: DeeAnn Reeder >, "Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)"
Cc: "Coleman, Jeremy T" < >, "Cryan, Paul" , Daniel Streicker < >, "Gibbs, Samantha" >, "Gilbert, Amy T - Aphis" "Grant, Evan H" , "Hopkins, Maria-Richetta (Camille) C" >, Jon Epstein ecohealthalliance.org>, "Lorch, Jeffrey M" >, Thomas O'Shea , "Rebekah.Kading , "Runge, Michael C" >, "Sleeman, Jonathan M" >, "a.peel " >, "castlekl " < >, "ckjohnson >, Kate Jones , "linfa.wang , Kevin Olival ecohealthalliance.org>, "rbaric , "sja " , "Winifred F Frick, Ph.D." >
Subject: Re: Expert judgement for SARS-CoV-2 risk assessment for North American bats

Great discussion! Thanks for forwarding the paper Jon, and thanks for summarizing the data Dan.
Receptor binding studies are a great and practical first step, however, susceptibility is far more complex than receptor binding. Many processes must be overcome to infect a new species and experiments are probably the only way to definitively determine susceptibility.
I reached out to Tony S to see if he had insights about Artibeus jamaicensis (susceptible) with respect to the AA considered in the paper – he looked through his transcriptome data and noted it has 13 matched AAs.
I look forward to more discussion tomorrow.
Raina

From: DeeAnn Reeder >
Date: Wednesday, April 15, 2020 at 5:31 PM
To: "Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)"
Cc: "Coleman, Jeremy T" , "Cryan, Paul" , Daniel Streicker >, "Gibbs, Samantha" "Gilbert, Amy T - Aphis" < "Grant, Evan H" , "Hopkins, Maria-Richetta (Camille) C" >, Jon Epstein ecohealthalliance.org>, "Lorch, Jeffrey M" >, "O'Shea, Thomas" , "Rebekah.Kading , "Runge, Michael C" , "Sleeman, Jonathan M" "a.peel " , "castlekl " "ckjohnson " >, "kate.e.jones " , "linfa.wang " >, " ecohealthalliance.org" , Raina Plowright >, "rbaric < "sja " >, "wfrick "
Subject: Re: Expert judgement for SARS-CoV-2 risk assessment for North American bats

Thanks Jon!

On Wed, Apr 15, 2020 at 7:15 PM Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) < > wrote:

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>
> Jon

From: Daniel Streicker
Sent: Wednesday, April 15, 2020 2:04 PM
To: Jon Epstein ecohealthalliance.org>
Cc: Grant, Evan H ; castlekt O'Shea, Thomas ; raina.plowright ; dreeder sja kate.e.jones ; wfrick ; linfa.wang ; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) >; a.peel rbaric Rebekah.Kading Gilbert, Amy T - Aphis v>; Lorch, Jeffrey M Runge, Michael C >; Cryan, Paul >; ecohealthalliance.org; Sleeman, Jonathan M ; Coleman, Jeremy T >; Gibbs, Samantha < Hopkins, Maria-Richetta (Camille) C >
Subject: Re: Expert judgement for SARS-CoV-2 risk assessment for North American bats

Hi Jon,

Thanks for passing this along. So others don't have to dig through all of the the 2.5 page table full of abbreviations, here are some scores (matching residues of the 20 key AAs considered) for a few selected species which might be relevant to judging the susceptibility of Myotis lucifugus, which had a score of 11/20:

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Desmodus rotundus (12/20), possibly susceptible (same family as Artibeus, which was not included in the study)?

So, Myotis is relatively low on the list, but so are bats which are related to the presumed reservoir and known susceptible species like ferrets are not too much higher up on the list. I'd be curious to know how others with more knowledge than myself interpret these numbers. Is this measure of ACE-2 affinity something we should use and how low is too low for a host to be susceptible?

Best,
Daniel

On 15 Apr 2020, at 17:35, Jon Epstein ecohealthalliance.org> wrote:

Hi All,
Here's the ACE-2 affinity paper.
Cheers,
Jon

On Thu, Apr 9, 2020 at 5:39 PM Grant, Evan H <ehgrant wrote:

Hello experts,

Thank you for volunteering your time and expertise to help estimate the risk of SARS-CoV-2 to North American bats. Mike Runge and I (Evan Grant), with the U.S. Geological Survey Patuxent Wildlife Research Center, are facilitating this effort in collaboration with the USGS National Wildlife Health Center, USGS Fort Collins Science Center, USFWS, and EcoHealth Alliance. We are conducting a rapid assessment of the risks for transmission of SARS-CoV-2 from humans to bats. The goal is to provide scientific information that will guide wildlife management agency response to this potential risk, including development of management recommendations and mitigation strategies.

Attached please find two documents: (1) an introduction to expert elicitation with some background on the issue we are addressing, and (2) a spreadsheet <BatEE Practice Questions v2.xlsx> with calibration questions. There are three tabs (corresponding to the three questions) in the accompanying spreadsheet, and a fourth tab that summarizes the responses and the calculated mean and standard deviation for each question.

We have a very tight timeline to provide guidance to U.S. management agencies, so we thank you for your participation along the following timeline:

i. Respond to ehgrant with your responses to the calibration questions in the attached spreadsheet (due by 12 PM ET 10 Apr)

ii. Review the background information and elicitation questions (we will

send these additional documents to you by 6 pm ET 10 Apr)

iii. Respond with your initial responses to the questions (due by 6 PM ET 13 Apr)

iv. Be available for a 2-hr conference call to discuss initial responses and share insights (4 PM ET 14 Apr – and/or – 4 PM ET 15 Apr)

v. Revise and send your second-round responses to the questions (due 24 hours after the last conference call)

Thank you in advance for your participation. If you have questions – please contact Evan (ehgrant

Kindest regards,
Evan and Mike

--
Jonathan H. Epstein DVM, MPH, PhD
Vice President for Science and Outreach
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New York, NY 10001

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EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

<SARS-CoV 2 spike protein favors ACE2 from Bovidae and Cricetidae_Luan et al 2020.pdf>

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National
WILDLIFE REHABILITATORS
Association

Position Statement:
Rehabilitating North American Bats during the SARS-CoV2/COVID-19 Pandemic

The newly emerging SARS-CoV2, which causes COVID-19 in humans, is currently a worldwide pandemic and has been diagnosed in people from every state and province in the United States[1] and Canada. A summary of the non-human animal SARS-CoV2 positive individuals as of 4/10/2020 is provided as an appendix at the end of this statement. Zoonotic transmission from these animals back to humans has not been reported.

Currently, it is thought that the newly emerging SARS-CoV2 virus originated from wildlife and possibly from East Asian pangolins, and/or East Asian bats[3]. Details about these theories are summarized at the end of this statement. **SARS-CoV2 has not been found naturally in any wild bat**. One preliminary study did show the ability to infect Egyptian fruit bats with SARS-CoV2 in a research setting, however, they did not shed enough virus to infect conspecifics[4]. There are over 1400 different species of bats[5], and it is unknown if this virus acts similarly in other species of bats. Many other coronaviruses use bats as a reservoir[6],[7] and **there is currently no evidence that introduction of SARS-CoV2 to North American bats would or would not cause population declines.**

A certain percentage of humans can be asymptomatic shedders of SARS-CoV2[1]. Current expert understanding is that SARS-CoV2 is primarily transmitted person-to-person, and not a current zoonotic concern in any species[8].

Many species of North American bats are incredibly adaptable and live in and around human dwellings (houses, attics, flashing, backyard foliage and trees, etc.), even in dense human populations. Bats come into close proximity of many people every day.

Wildlife rehabilitators across the continent who are trained to work with bats are a valuable public health resource. Members of the public come into contact with bats regularly, and often are directly exposed to bats before contacting professionals. Wildlife rehabilitators direct these individuals to local public health departments, help walk individuals through learning about rabies risk factors and following all public health recommendations, and ultimately act as an advocate for the health of the finder and the bat.

The NWRA Veterinary Committee supports the continued admittance of bats for rehabilitation to wildlife rehabilitation professionals not only to ensure proper bat care, welfare, and conservation, but foremost as part of the solution to public health concerns surrounding bats. Without wildlife rehabilitators, it is highly likely the public will have more human-bat interactions

that lack the involvement of a professional to guide zoonotic concerns and take necessary biosecurity precautions. Wildlife rehabilitators also represent a valuable resource for sample collection for researchers and are encouraged to collaborate whenever possible.

The NWRA Veterinary Committee supports one-health initiatives to improve human health, animal health and environmental health. Furthermore, the NWRA Veterinary Committee supports evidence-based medicine and subsequent actions.

Restrictions on bat rehabilitation and release have massive implications for the thousands of bats that are rehabilitated in the US and Canada each year, and for the adverse human-bat interactions that will inevitably occur as untrained people continue to find bats in need of care. If SARS-CoV2 is able to be transmitted from humans to bats, it has likely already occurred due to the high number of human cases in the United States and the frequency that people interact with bats at their homes.

Furthermore, due to the COVID-19 outbreak, fewer resources are available at municipalities to handle wildlife cases resulting in additional risk for the public who may take it upon themselves to handle a bat, without appropriate PPE, thus potentially having a negative impact on the health and welfare of the bat and the health of the person who handled it. Wildlife rehabilitators' expertise is needed even more during this crisis to protect human and animal health.

RECOMMENDATIONS

1. We recommend that authorized wildlife rehabilitators should be allowed to accept and rehabilitate bats, following appropriate biosecurity and safety measures to prevent human-bat respiratory virus exposures.
2. New bat admissions should be quarantined for 14 days.
3. There is no need to euthanize captive bats as a method of disease prevention.
4. Limit the number of people who have access to areas where bats are housed and cared for.
5. Rehabilitators showing any clinical signs of Covid-19 such as fever, coughing, or shortness of breath should immediately cease working with bats and consult their doctor for testing and quarantine recommendations. Backup caregivers should be pre-arranged for bats and any other animals undergoing rehabilitation.
6. Working with the local or regional veterinary laboratories and state/provincial public health officials, samples should be collected from rehabilitated bats if feasible, and if/when testing for bats is available, the bats should be tested for Covid-19 prior to release if available. However, bats should not be delayed from appropriate release simply because testing is not available.

Because this is an emerging pathogen, new research may sway directives and this statement will be updated accordingly.

Appendix

Since the outbreak of severe acute respiratory syndrome (SARS) 18 years ago, a large number of SARS-related coronaviruses (SARSr-CoVs) have been discovered in their natural reservoir host, bats, and previous studies have shown that some bat SARSr-CoVs have the potential to infect humans.[6]

The coronaviruses found in the Malayan pangolin (*Manis javanica*) and the *Rhinolophus affinis* bat remain the current closest to SARS-CoV2 across the genome (~96%[6]); some pangolin coronaviruses exhibit strong similarity to SARS-CoV2 in the virus receptor binding domain (RBD), including all six key RBD residues.[3] However, bat coronaviruses are massively understudied[3].

Currently, it is thought that SARS-CoV2 virus originated from wildlife naturally[3], either via natural selection in the species in question before zoonotic transfer or natural selection in humans after zoonotic transfer from the species in question[3]. See the table below for current knowledge regarding positive test results suggestive of human to animal transmission of SARS-CoV2.

Summary below of current non-human animals that have tested positive for SARS-CoV2A[8]:

Species	Location	Antigen test results	Antibody test results	Symptoms	Possible source	Notes
Domestic dog	China	Weak positive	Positive	None	Owner had COVID-19	Elderly, died 3 d after release from unknown causes
Domestic dog[11]	Hong Kong	Positive		None	Owner had COVID-19	German Shepherd
Domestic cat	Belgium	Positive	--	Respiratory, vomiting	Owner had COVID-19	Unknowns around sampling
Domestic cat	China	Positive	--	None	Owner had COVID-19	
Tiger	NY, USA	Positive Confirmed by NVSL		Respiratory	Presumed asymptomatic keeper positive for COVID-19	Several big cats in zoo sick with respiratory signs
Domestic cats[12]	China	Positive (15)	Positive (11)	None? Not clear in report	Owned and stray (community acquired)	Tested 102 cats in Wuhan
Domestic cat	Hong Kong	Positive		None	Owner had COVID-19	

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Sent: Wednesday, April 15, 2020 7:15 PM EDT
To: Daniel Streicker >; epstein ecohealthalliance.org>
CC: Grant, Evan H ; castlekt ; O'Shea, Thomas >; raina.plowright ; dreeder ; sja ; kate.e.jones ; ckjohnson wfrick ; linfa.wang >; a.peel >; rbaric >; Kading,Rebekah >; Gilbert, Amy T - Aphis < >; Lorch, Jeffrey M >; Runge, Michael C ; Cryan, Paul ecohealthalliance.org ; Sleeman, Jonathan M >; Coleman, Jeremy T ; Gibbs, Samantha Hopkins, Maria-Richetta (Camille) C
Subject: RE: Expert judgement for SARS-CoV-2 risk assessment for North American bats
Attachment(s): "Leung NHL et al. 2020 Resp virus shedding in exhaled breath and efficacy of face masks Nature Medicine.pdf"

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Hello experts,

Thank you for volunteering your time and expertise to help estimate the risk of SARS-CoV-2 to North American bats. Mike Runge and I (Evan Grant), with the U.S. Geological Survey Patuxent Wildlife Research Center, are facilitating this effort in collaboration with the USGS National Wildlife Health Center, USGS Fort Collins Science Center, USFWS, and EcoHealth Alliance. We are conducting a rapid assessment of the risks for transmission of SARS-CoV-2 from humans to bats. The goal is to provide scientific information that will guide wildlife management agency response to this potential risk, including development of management recommendations and mitigation strategies.

Attached please find two documents: (1) an introduction to expert elicitation with some background on the issue we are addressing, and (2) a spreadsheet <BatEE Practice Questions v2.xlsx> with calibration questions. There are three tabs (corresponding to the three questions) in the accompanying spreadsheet, and a fourth tab that summarizes the responses and the calculated mean and standard deviation for each question.

We have a very tight timeline to provide guidance to U.S. management agencies, so we thank you for your participation along the following timeline:

i. Respond to ehgrant with your responses to the calibration questions in the attached spreadsheet (due by 12 PM ET 10 Apr)

ii. Review the background information and elicitation questions (we will send these additional documents to you by 6 pm ET 10 Apr)

iii. Respond with your initial responses to the questions (due by 6 PM ET 13 Apr)

iv. Be available for a 2-hr conference call to discuss initial responses and share insights (4 PM ET 14 Apr – and/or – 4 PM ET 15 Apr)

v. Revise and send your second-round responses to the questions (due 24 hours after the last conference call)

Thank you in advance for your participation. If you have questions – please contact Evan (ehgrant .

Kindest regards,
Evan and Mike

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<SARS-CoV 2 spike protein favors ACE2 from Bovidae and Cricetidae_Luan et al 2020.pdf>

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BRIEF COMMUNICATION

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Respiratory virus shedding in exhaled breath and efficacy of face masks

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We identified seasonal human coronaviruses, influenza viruses and rhinoviruses in exhaled breath and coughs of children and adults with acute respiratory illness. Surgical face masks significantly reduced detection of influenza virus RNA in respiratory droplets and coronavirus RNA in aerosols, with a trend toward reduced detection of coronavirus RNA in respiratory droplets. Our results indicate that surgical face masks could prevent transmission of human coronaviruses and influenza viruses from symptomatic individuals.

Respiratory virus infections cause a broad and overlapping spectrum of symptoms collectively referred to as acute respiratory virus illnesses (ARIs) or more commonly the 'common cold'. Although mostly mild, these ARIs can sometimes cause severe disease and death[1]. These viruses spread between humans through direct or indirect contact, respiratory droplets (including larger droplets that fall rapidly near the source as well as coarse aerosols with aerodynamic diameter >5 µm) and fine-particle aerosols (droplets and droplet nuclei with aerodynamic diameter ≤5 µm)[2,3]. Although hand hygiene and use of face masks, primarily targeting contact and respiratory droplet transmission, have been suggested as important mitigation strategies against influenza virus transmission[4], little is known about the relative importance of these modes in the transmission of other common respiratory viruses[2,3,5]. Uncertainties similarly apply to the modes of transmission of COVID-19 (refs. [6,7]).

Some health authorities recommend that masks be worn by ill individuals to prevent onward transmission (source control)[4,8]. Surgical face masks were originally introduced to protect patients from wound infection and contamination from surgeons (the wearer) during surgical procedures, and were later adopted to protect healthcare workers against acquiring infection from their patients. However, most of the existing evidence on the filtering efficacy of face masks and respirators comes from in vitro experiments with nonbiological particles[9,10], which may not be generalizable to infectious respiratory virus droplets. There is little information on the efficacy of face masks in filtering respiratory viruses and reducing viral release from an individual with respiratory infections[8], and most research has focused on influenza[11,12].

Here we aimed to explore the importance of respiratory droplet and aerosol routes of transmission with a particular focus on coronaviruses, influenza viruses and rhinoviruses, by quantifying the amount of respiratory virus in exhaled breath of participants with medically attended ARIs and determining the potential efficacy of surgical face masks to prevent respiratory virus transmission.

Results

We screened 3,363 individuals in two study phases, ultimately enrolling 246 individuals who provided exhaled breath samples (Extended Data Fig. 1). Among these 246 participants, 122 (50%) participants were randomized to not wearing a face mask during the first exhaled breath collection and 124 (50%) participants were randomized to wearing a face mask. Overall, 49 (20%) voluntarily provided a second exhaled breath collection of the alternate type.

Infections by at least one respiratory virus were confirmed by reverse transcription PCR (RT–PCR) in 123 of 246 (50%) participants. Of these 123 participants, 111 (90%) were infected by human (seasonal) coronavirus ($n=17$), influenza virus ($n=43$) or rhinovirus ($n=54$) (Extended Data Figs. 1 and 2), including one participant co-infected by both coronavirus and influenza virus and another two participants co-infected by both rhinovirus and influenza virus. These 111 participants were the focus of our analyses.

There were some minor differences in characteristics of the 111 participants with the different viruses (Table 1a). Overall, 24% of participants had a measured fever ≥37.8 °C, with patients with influenza more than twice as likely than patients infected with coronavirus and rhinovirus to have a measured fever. Coronavirus-infected participants coughed the most with an average of 17 (s.d. = 30) coughs during the 30-min exhaled breath collection. The profiles of the participants randomized to with-mask versus without-mask groups were similar (Supplementary Table 1).

We tested viral shedding (in terms of viral copies per sample) in nasal swabs, throat swabs, respiratory droplet samples and aerosol samples and compared the latter two between samples collected with or without a face mask (Fig. 1). On average, viral shedding was higher in nasal swabs than in throat swabs for each of coronavirus (median 8.1 $\log_{10}$ virus copies per sample versus 3.9), influenza virus (6.7 versus 4.0) and rhinovirus (6.8 versus 3.3), respectively. Viral RNA was identified from respiratory droplets and aerosols for all three viruses, including 30%, 26% and 28% of respiratory droplets and 40%, 35% and 56% of aerosols collected while not wearing a face mask, from coronavirus, influenza virus and rhinovirus-infected participants, respectively (Table 1b). In particular for coronavirus, we identified OC43 and HKU1 from both respiratory

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Table 1a | Characteristics of individuals with symptomatic coronavirus, influenza virus or rhinovirus infection

	All who provided exhaled breath	Coronavirus	Influenza virus	Rhinovirus
	(*n* = 246)	(*n* = 17)	(*n* = 43)	(*n* = 54)
	n (%)	*n* (%)	*n* (%)	*n* (%)
Female	144 (59)	13 (76)	22 (51)	30 (56)
Age group, years				
11–17	12 (5)	0 (0)	8 (19)	4 (7)
18–34	114 (46)	10 (59)	11 (26)	24 (44)
35–50	79 (32)	2 (12)	16 (37)	18 (33)
51–64	35 (14)	4 (24)	8 (19)	5 (9)
≥ 65	6 (2)	1 (6)	0 (0)	3 (6)
Chronic medical conditions				
Any	49 (20)	5 (29)	5 (12)	10 (19)
Respiratory	18 (7)	0 (0)	4 (9)	3 (6)
Influenza vaccination				
Ever	94 (38)	6 (35)	15 (35)	20 (37)
Current season	23 (9)	2 (12)	1 (2)	4 (7)
Previous season only	71 (29)	4 (24)	14 (33)	16 (30)
Ever smoker	31 (13)	1 (6)	6 (14)	6 (11)
Time since illness onset, h				
<24	22 (9)	0 (0)	5 (12)	2 (4)
24–48	100 (41)	9 (53)	13 (30)	25 (46)
48–72	85 (35)	8 (47)	18 (42)	20 (37)
72–96	39 (16)	0 (0)	7 (16)	7 (13)
History of measured fever ≥37.8 °C	58 (24)	3 (18)	17 (40)	8 (15)
Measured fever ≥37.8 °C at presentation	36 (15)	2 (12)	18 (42)	2 (4)
Measured body temperature (˚C) at enrollment (mean, s.d.)	36.8 (0.8)	36.9 (0.8)	37.4 (0.9)	36.6 (0.7)
Symptoms at presentation				
Fever	111 (45)	10 (59)	27 (63)	16 (30)
Cough	198 (80)	15 (88)	40 (93)	44 (81)
Sore throat	211 (86)	15 (88)	31 (72)	49 (91)
Runny nose	200 (81)	17 (100)	36 (84)	48 (89)
Headache	186 (76)	13 (76)	30 (70)	38 (70)
Myalgia	176 (72)	12 (71)	31 (72)	34 (63)
Phlegm	176 (72)	9 (53)	34 (79)	41 (76)
Chest tightness	64 (26)	3 (18)	12 (28)	9 (17)
Shortness of breath	103 (42)	6 (35)	14 (33)	25 (46)
Chills	100 (41)	8 (47)	29 (67)	16 (30)
Sweating	95 (39)	5 (29)	18 (42)	20 (37)
Fatigue	218 (89)	16 (94)	38 (88)	48 (89)
Vomiting	19 (8)	2 (12)	5 (12)	2 (4)
Diarrhea	17 (7)	2 (12)	1 (2)	6 (11)
Number of coughs during exhaled breath collection (mean, s.d.)	8 (14)	17 (30)	8 (11)	5 (9)

Seasonal coronavirus (*n* = 17), seasonal influenza virus (*n* = 43) and rhinovirus (*n* = 54) infections were confirmed in individuals with acute respiratory symptoms by RT–PCR in any samples (nasal swab, throat swab, respiratory droplets and aerosols) collected.

droplets and aerosols, but only identified NL63 from aerosols and not from respiratory droplets (Supplementary Table 2 and Extended Data Fig. 3).

We detected coronavirus in respiratory droplets and aerosols in 3 of 10 (30%) and 4 of 10 (40%) of the samples collected without face masks, respectively, but did not detect any virus in respiratory droplets or aerosols collected from participants wearing face masks, this difference was significant in aerosols and showed a trend toward reduced detection in respiratory droplets (Table 1b). For influenza virus, we detected virus in 6 of 23 (26%) and 8 of 23 (35%) of the

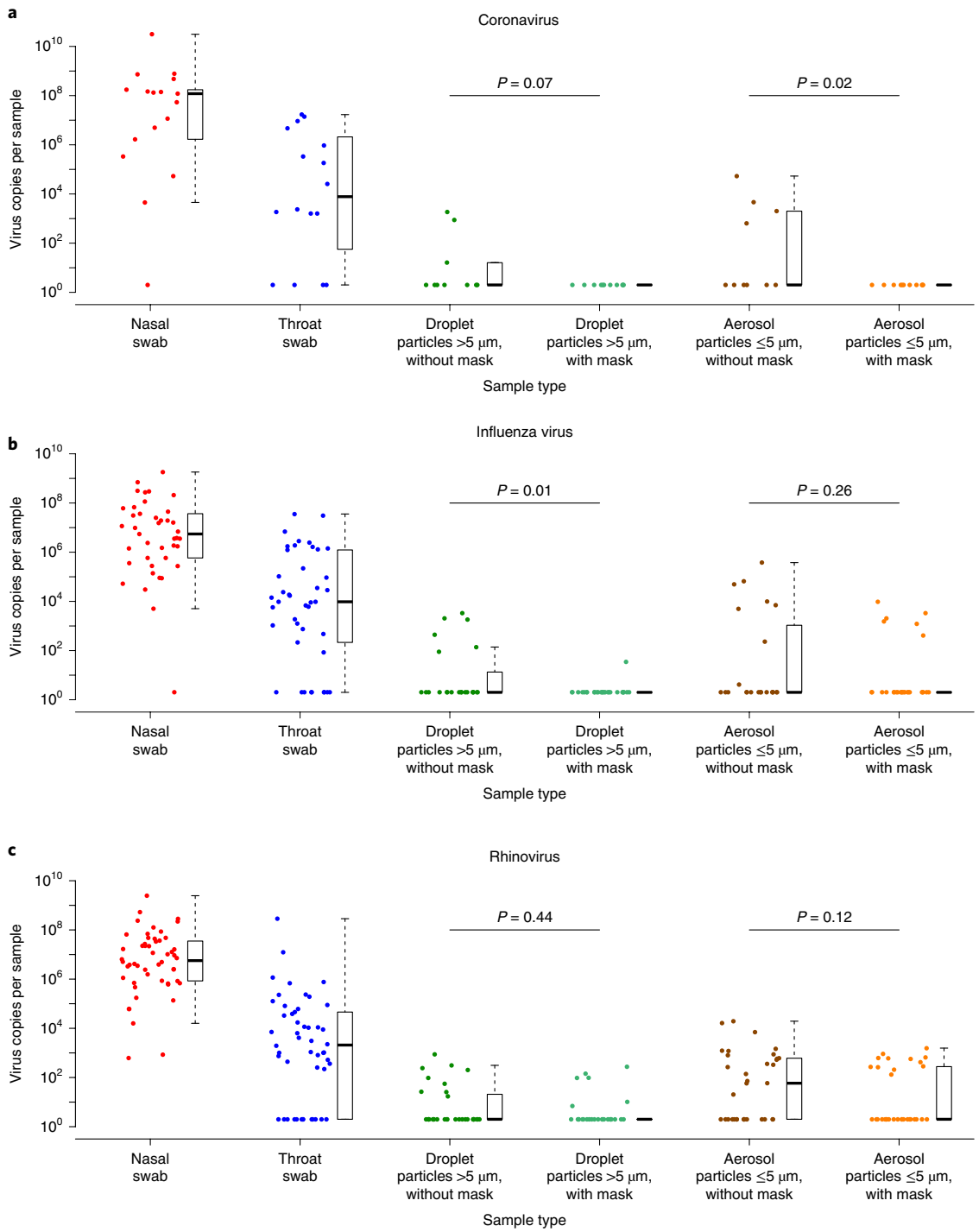

Fig. 1 | Efficacy of surgical face masks in reducing respiratory virus shedding in respiratory droplets and aerosols of symptomatic individuals with coronavirus, influenza virus or rhinovirus infection. a–**c**, Virus copies per sample collected in nasal swab (red), throat swab (blue) and respiratory droplets collected for 30min while not wearing (dark green) or wearing (light green) a surgical face mask, and aerosols collected for 30min while not wearing (brown) or wearing (orange) a face mask, collected from individuals with acute respiratory symptoms who were positive for coronavirus (**a**), influenza virus (**b**) and rhinovirus (**c**), as determined by RT–PCR in any samples. *P* values for mask intervention as predictor of $\log_{10}$ virus copies per sample in an unadjusted univariate Tobit regression model which allowed for censoring at the lower limit of detection of the RT–PCR assay are shown, with significant differences in bold. For nasal swabs and throat swabs, all infected individuals were included (coronavirus, *n*=17; influenza virus, *n*=43; rhinovirus, *n*=54). For respiratory droplets and aerosols, numbers of infected individuals who provided exhaled breath samples while not wearing or wearing a surgical face mask, respectively were: coronavirus (*n*=10 and 11), influenza virus (*n*=23 and 28) and rhinovirus (*n*=36 and 32). A subset of participants provided exhaled breath samples for both mask interventions (coronavirus, *n*=4; influenza virus, *n*=8; rhinovirus, *n*=14). The box plots indicate the median with the interquartile range (lower and upper hinge) and ±1.5×interquartile range from the first and third quartile (lower and upper whiskers).

Table 1b | Efficacy of surgical face masks in reducing respiratory virus frequency of detection and viral shedding in respiratory droplets and aerosols of symptomatic individuals with coronavirus, influenza virus or rhinovirus infection

	Droplet particles >5 µm			Aerosol particles ≤5 µm		
Virus type	**Without surgical face mask**	**With surgical face mask**	***P***	**Without surgical face mask**	**With surgical face mask**	***P***
	Detection of virus					
	No. positive/no. total (%)	**No. positive/no. total (%)**		**No. positive/no. total (%)**	**No. positive/no. total (%)**	
Coronavirus	3 of 10 (30)	0 of 11 (0)	0.09	**4 of 10 (40)**	**0 of 11 (0)**	**0.04**
Influenza virus	**6 of 23 (26)**	**1 of 27 (4)**	**0.04**	8 of 23 (35)	6 of 27 (22)	0.36
Rhinovirus	9 of 32 (28)	6 of 27 (22)	0.77	19 of 34 (56)	12 of 32 (38)	0.15
	Viral load (log_{10} virus copies per sample)					
	Median (IQR)	**Median (IQR)**		**Median (IQR)**	**Median (IQR)**	
Coronavirus	0.3 (0.3, 1.2)	0.3 (0.3, 0.3)	0.07	**0.3 (0.3, 3.3)**	**0.3 (0.3, 0.3)**	**0.02**
Influenza virus	**0.3 (0.3, 1.1)**	**0.3 (0.3, 0.3)**	**0.01**	0.3 (0.3, 3.0)	0.3 (0.3, 0.3)	0.26
Rhinovirus	0.3 (0.3, 1.3)	0.3 (0.3, 0.3)	0.44	1.8 (0.3, 2.8)	0.3 (0.3, 2.4)	0.12

P values for comparing the frequency of respiratory virus detection between the mask intervention were obtained by two-sided Fisher's exact test and (two-sided) *P* values for mask intervention as predictor of log_{10} virus copies per sample were obtained by an unadjusted univariate Tobit regression model, which allowed for censoring at the lower limit of detection of the RT-PCR assay, with significant differences in bold. Undetectable values were imputed as 0.3 log_{10} virus copies per sample. IQR, interquartile range.

respiratory droplet and aerosol samples collected without face masks, respectively. There was a significant reduction by wearing face masks to 1 of 27 (4%) in detection of influenza virus in respiratory droplets, but no significant reduction in detection in aerosols (Table 1b). Moreover, among the eight participants who had influenza virus detected by RT–PCR from without-mask aerosols, five were tested by viral culture and four were culture-positive. Among the six participants who had influenza virus detected by RT–PCR from with-mask aerosols, four were tested by viral culture and two were culture-positive. For rhinovirus, there were no significant differences between detection of virus with or without face masks, both in respiratory droplets and in aerosols (Table 1b). Conclusions were similar in comparisons of viral shedding (Table 1b). In addition, we found a significant reduction in viral shedding (Supplementary Table 2) in respiratory droplets for OC43 (Extended Data Fig. 4) and influenza B virus (Extended Data Fig. 5) and in aerosols for NL63 (Extended Data Fig. 4).

We identified correlations between viral loads in different samples (Extended Data Figs. 6–8) and some evidence of declines in viral shedding by time since onset for influenza virus but not for coronavirus or rhinovirus (Extended Data Fig. 9). In univariable analyses of factors associated with detection of respiratory viruses in various sample types, we did not identify significant association in viral shedding with days since symptom onset (Supplementary Table 3) for respiratory droplets or aerosols (Supplementary Tables 4–6).

A subset of participants (72 of 246, 29%) did not cough at all during at least one exhaled breath collection, including 37 of 147 (25%) during the without-mask and 42 of 148 (28%) during the with-mask breath collection. In the subset for coronavirus ($n=4$), we did not detect any virus in respiratory droplets or aerosols from any participants. In the subset for influenza virus ($n=9$), we detected virus in aerosols but not respiratory droplets from one participant. In the subset for rhinovirus ($n=17$), we detected virus in respiratory droplets from three participants, and we detected virus in aerosols in five participants.

Discussion

Our results indicate that aerosol transmission is a potential mode of transmission for coronaviruses as well as influenza viruses and rhinoviruses. Published studies detected respiratory viruses[13,14] such as influenza[12,15] and rhinovirus[16] from exhaled breath, and the detection of SARS-CoV[17] and MERS-CoV[18] from air samples (without size fractionation) collected from hospitals treating patients with severe acute respiratory syndrome and Middle East respiratory syndrome, but ours demonstrates detection of human seasonal coronaviruses in exhaled breath, including the detection of OC43 and HKU1 from respiratory droplets and NL63, OC43 and HKU1 from aerosols.

Our findings indicate that surgical masks can efficaciously reduce the emission of influenza virus particles into the environment in respiratory droplets, but not in aerosols[12]. Both the previous and current study used a bioaerosol collecting device, the Gesundheit-II (G-II)[12,15,19], to capture exhaled breath particles and differentiated them into two size fractions, where exhaled breath coarse particles >5 µm (respiratory droplets) were collected by impaction with a 5-µm slit inertial Teflon impactor and the remaining fine particles ≤5 µm (aerosols) were collected by condensation in buffer. We also demonstrated the efficacy of surgical masks to reduce coronavirus detection and viral copies in large respiratory droplets and in aerosols (Table 1b). This has important implications for control of COVID-19, suggesting that surgical face masks could be used by ill people to reduce onward transmission.

Among the samples collected without a face mask, we found that the majority of participants with influenza virus and coronavirus infection did not shed detectable virus in respiratory droplets or aerosols, whereas for rhinovirus we detected virus in aerosols in 19 of 34 (56%) participants (compared to 4 of 10 (40%) for influenza and 8 of 23 (35%) for coronavirus). For those who did shed virus in respiratory droplets and aerosols, viral load in both tended to be low (Fig. 1). Given the high collection efficiency of the G-II (ref. [19]) and given that each exhaled breath collection was conducted for 30 min, this might imply that prolonged close contact would be required for transmission to occur, even if transmission was primarily via aerosols, as has been described for rhinovirus colds[20]. Our results also indicate that there could be considerable heterogeneity in contagiousness of individuals with coronavirus and influenza virus infections.

The major limitation of our study was the large proportion of participants with undetectable viral shedding in exhaled breath for each of the viruses studied. We could have increased the sampling duration beyond 30 min to increase the viral shedding being captured, at the cost of acceptability in some participants. An alternative approach would be to invite participants to perform forced coughs during exhaled breath collection[12]. However, it was the aim of our present study to focus on recovering respiratory

virus in exhaled breath in a real-life situation and we expected that some individuals during an acute respiratory illness would not cough much or at all. Indeed, we identified virus RNA in a small number of participants who did not cough at all during the 30-min exhaled breath collection, which would suggest droplet and aerosol routes of transmission are possible from individuals with no obvious signs or symptoms. Another limitation is that we did not confirm the infectivity of coronavirus or rhinovirus detected in exhaled breath. While the G-II was designed to preserve viability of viruses in aerosols, and in the present study we were able to identify infectious influenza virus in aerosols, we did not attempt to culture coronavirus or rhinovirus from the corresponding aerosol samples.

Online content

Any methods, additional references, Nature Research reporting summaries, source data, extended data, supplementary information, acknowledgements, peer review information; details of author contributions and competing interests; and statements of data and code availability are available at https://doi.org/10.1038/s41591-020-0843-2.

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Methods

Study design. Participants were recruited year-round from March 2013 through May 2016 in a general outpatient clinic of a private hospital in Hong Kong. As routine practice, clinic staff screened all individuals attending the clinics for respiratory and any other symptoms regardless of the purpose of the visit at triage. Study staff then approached immediately those who reported at least one of the following symptoms of ARI for further screening: fever ≥37.8 °C, cough, sore throat, runny nose, headache, myalgia and phlegm. Individuals who reported ≥2 ARI symptoms, within 3 d of illness onset and ≥11 years of age were eligible to participate. After explaining the study to and obtaining informed consent from the participants, a rapid influenza diagnostic test, the Sofia Influenza A + B Fluorescent Immunoassay Analyzer (cat. no. 20218, Quidel), was used to identify influenza A or B virus infection as an incentive to participate. All participants provided a nasal swab for the rapid test and an additional nasal swab and a separate throat swab for subsequent virologic confirmation at the laboratory. All participants also completed a questionnaire to record basic information including age, sex, symptom severity, medication, medical conditions and smoking history. In the first phase of the study from March 2013 to February 2014 ('Influenza Study'), the result of the rapid test was used to determine eligibility for further participation in the study and exhaled breath collection, whereas in the second phase of the study from March 2014 to May 2016 ('Respiratory Virus Study'), the rapid test did not affect eligibility. Eligible participants were then invited to provide an exhaled breath sample for 30 min in the same clinic visit.

Before exhaled breath collection, each participant was randomly allocated in a 1:1 ratio to either wearing a surgical face mask (cat. no. 62356, Kimberly-Clark) or not during the collection. To mimic the real-life situation, under observation by the study staff, participants were asked to attach the surgical mask themselves, but instruction on how to wear the mask properly was given when the participant wore the mask incorrectly. Participants were instructed to breathe as normal during the collection, but (natural) coughing was allowed and the number of coughs was recorded by study staff. Participants were then invited to provide a second exhaled breath sample of the alternate type (for example if the participant was first assigned to wearing a mask they would then provide a second sample without a mask), but most participants did not agree to stay for a second measurement because of time constraints. Participants were compensated for each 30-min exhaled breath collection with a supermarket coupon worth approximately US$30 and all participants were gifted a tympanic thermometer worth approximately US$20.

Ethical approval. Written informed consent was obtained from all participants ≥18 years of age and written informed consent was obtained from parents or legal guardians of participants 11–17 years of age in addition to their own written informed consent. The study protocol was approved by the Institutional Review Board of The University of Hong Kong and the Clinical and Research Ethics Committee of Hong Kong Baptist Hospital.

Collection of swabs and exhaled breath particles. Nasal swabs and throat swabs were collected separately, placed in virus transport medium, stored and transported to the laboratory at 2–8 °C and the virus transport medium was aliquoted and stored at −70 °C until further analysis. Exhaled breath particles were captured and differentiated into two size fractions, the coarse fraction containing particles with aerodynamic diameter >5 µm (referred to here as 'respiratory droplets'), which included droplets up to approximately 100 µm in diameter and the fine fraction with particles ≤5 µm (referred to here as 'aerosols') by the G-II bioaerosol collecting device[12,15,19]. In the G-II device, exhaled breath coarse particles >5 µm were collected by a 5-µm slit inertial Teflon impactor and the remaining fine particles ≤5 µm were condensed and collected into approximately 170 ml of 0.1% BSA/PBS. Both the impactor and the condensate were stored and transported to the laboratory at 2–8 °C. The virus on the impactor was recovered into 1 ml and the condensate was concentrated into 2 ml of 0.1% BSA/PBS, aliquoted and stored at −70 °C until further analysis. In a validation study, the G-II was able to recover over 85% of fine particles >0.05 µm in size and had comparable collection efficiency of influenza virus as the SKC BioSampler[19].

Laboratory testing. Samples collected from the two studies were tested at the same time. Nasal swab samples were first tested by a diagnostic-use viral panel, xTAG Respiratory Viral Panel (Abbott Molecular) to qualitatively detect 12 common respiratory viruses and subtypes including coronaviruses (NL63, OC43, 229E and HKU1), influenza A (nonspecific, H1 and H3) and B viruses, respiratory syncytial virus, parainfluenza virus (types 1–4), adenovirus, human metapneumovirus and enterovirus/rhinovirus. After one or more of the candidate respiratory viruses was detected by the viral panel from the nasal swab, all the samples from the same participant (nasal swab, throat swab, respiratory droplets and aerosols) were then tested with RT–PCR specific for the candidate virus(es) for determination of virus concentration in the samples. Infectious influenza virus was identified by viral culture using MDCK cells as described previously[21], whereas viral culture was not performed for coronavirus and rhinovirus.

Statistical analyses. The primary outcome of the study was virus generation rate in tidal breathing of participants infected by different respiratory viruses and the efficacy of face masks in preventing virus dissemination in exhaled breath, separately considering the respiratory droplets and aerosols. The secondary outcomes were correlation between viral shedding in nose swabs, throat swabs, respiratory droplets and aerosols and factors affecting viral shedding in respiratory droplets and aerosols.

We identified three groups of respiratory viruses with the highest frequency of infection as identified by RT–PCR, namely coronavirus (including NL63, OC43, HKU1 and 229E), influenza virus and rhinovirus, for further statistical analyses. We defined viral shedding as $\log_{10}$ virus copies per sample and plotted viral shedding in each sample (nasal swab, throat swab, respiratory droplets and aerosols); the latter two were stratified by mask intervention. As a proxy for the efficacy of face masks in preventing transmission of respiratory viruses via respiratory droplet and aerosol routes, we compared the respiratory virus viral shedding in respiratory droplet and aerosol samples between participants wearing face masks or not, by comparing the frequency of detection with a two-sided Fisher's exact test and by comparing viral load (defined as $\log_{10}$ virus copies per sample) by an unadjusted univariate Tobit regression model, which allowed for censoring at the lower limit of detection of the RT–PCR assay. We also used the unadjusted univariate Tobit regression to investigate factors affecting viral shedding in respiratory droplets and aerosols without mask use, for example age, days since symptom onset, previous influenza vaccination, current medication and number of coughs during exhaled breath collection. We investigated correlations between viral shedding in nasal swab, throat swab, respiratory droplets and aerosols with scatter-plots and calculated the Spearman's rank correlation coefficient between any two types of samples. We imputed 0.3 $\log_{10}$ virus copies ml^{-1} for undetectable values before transformation to $\log_{10}$ virus copies per sample. All analyses were conducted with R v.3.6.0 (ref. [22]) and the VGAM package v.1.1.1 (ref. [23]).

Reporting Summary. Further information on research design is available in the Nature Research Reporting Summary linked to this article.

Data availability

Anonymized raw data and R syntax to reproduce all the analyses, figures, tables and supplementary tables in the published article are available at: https://doi.org/10.5061/dryad.w9ghx3fkt.

References

21. Chan, K. H., Peiris, J. S., Lim, W., Nicholls, J. M. & Chiu, S. S. Comparison of nasopharyngeal flocked swabs and aspirates for rapid diagnosis of respiratory viruses in children. *J. Clin. Virol.* **42**, 65–69 (2008).
22. R: a language and environment for statistical computing (R Foundation for Statistical Computing, Vienna, Austria, 2019).
23. Yee, T. W. *Vector Generalized Linear and Additive Models: with an Implementation in R* (Springer, 2016).

Acknowledgements

This work was supported by the General Research Fund of the University Grants Committee (grant no. 765811), the Health and Medical Research Fund (grant no. 13120592) and a commissioned grant of the Food and Health Bureau and the Theme-based Research Scheme (project no. T11-705/14-N) of the Research Grants Council of the Hong Kong SAR Government. We acknowledge colleagues including R. O. P. Fung, A. K. W. Li, T. W. Y. Ng, T. H. C. So, P. Wu and Y. Xie for technical support in preparing and conducting this study and enrolling participants; J. K. M. Chan, S. Y. Ho, Y. Z. Liu and A. Yu for laboratory support; S. Ferguson, W. K. Leung, J. Pantelic, J. Wei and M. Wolfson for technical support in constructing and maintaining the G-II device; V. J. Fang, L. M. Ho and T. T. K. Lui for setting up the database; and C. W. Y. Cheung, L. F. K. Cheung, P. T. Y. Ching, A. C. H. Lai, D. W. Y. Lam, S. S. Y. Lo, A. S. K. Luk and other colleagues at the Outpatient Center and Infection Control Team of Hong Kong Baptist Hospital for facilitating this study.

Author contributions

All authors meet the International Committee of Medical Journal Editors criteria for authorship. The study protocol was drafted by N.H.L.L. and B.J.C. Data were collected by N.H.L.L., E.Y.C.S. and B.J.P.H. Laboratory testing was performed by D.K.W.C. and K.-H.C. Statistical analyses were conducted by N.H.L.L. N.H.L.L. and B.J.C. wrote the first draft of the manuscript, and all authors provided critical review and revision of the text and approved the final version.

Competing interests

B.J.C. consults for Roche and Sanofi Pasteur. The authors declare no other competing interests.

Additional information

Extended data is available for this paper at https://doi.org/10.1038/s41591-020-0843-2.

Supplementary information is available for this paper at https://doi.org/10.1038/s41591-020-0843-2.

Correspondence and requests for materials should be addressed to B.J.C.

Peer review information Alison Farrell was the primary editor on this article and managed its editorial process and peer review in collaboration with the rest of the editorial team.

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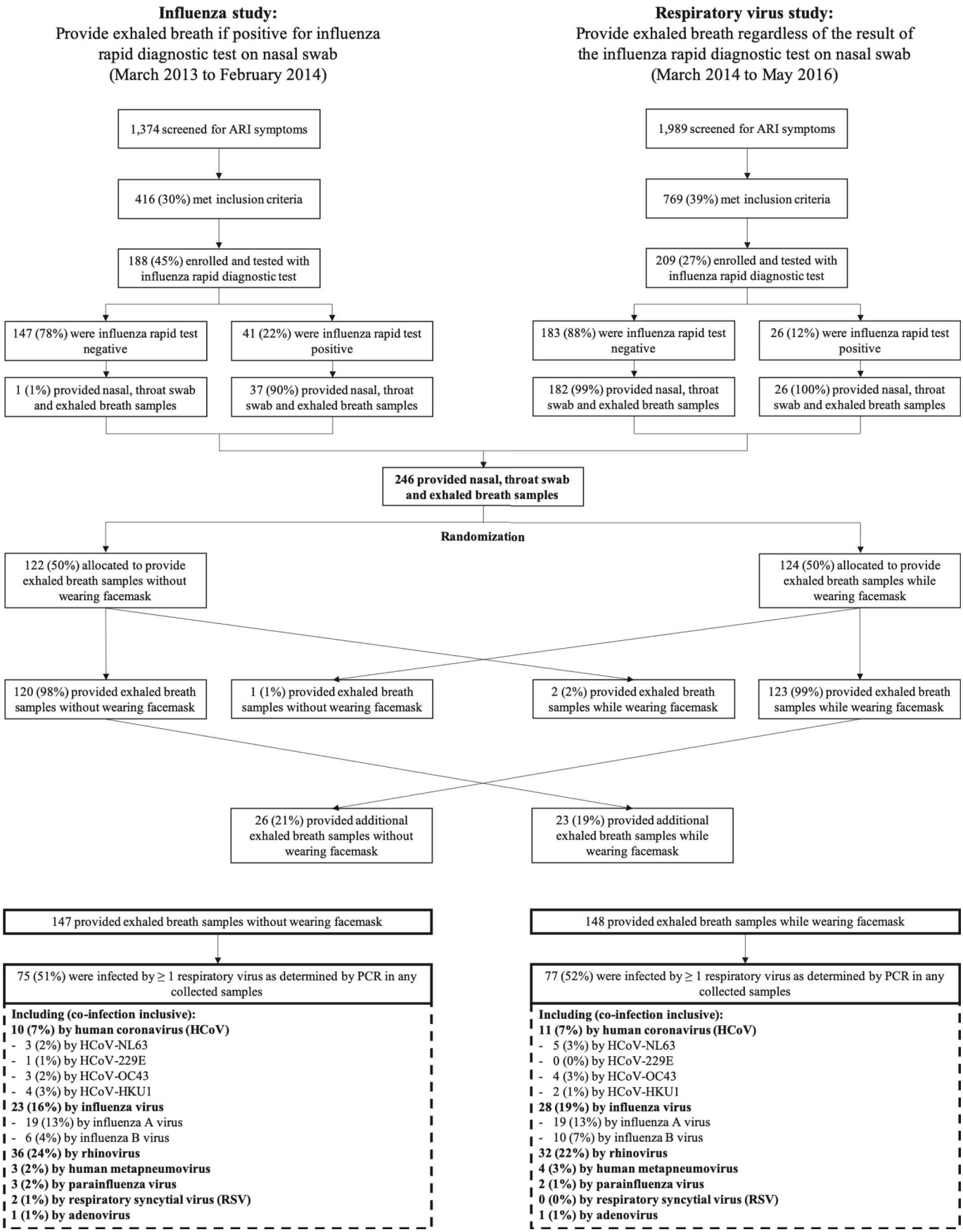
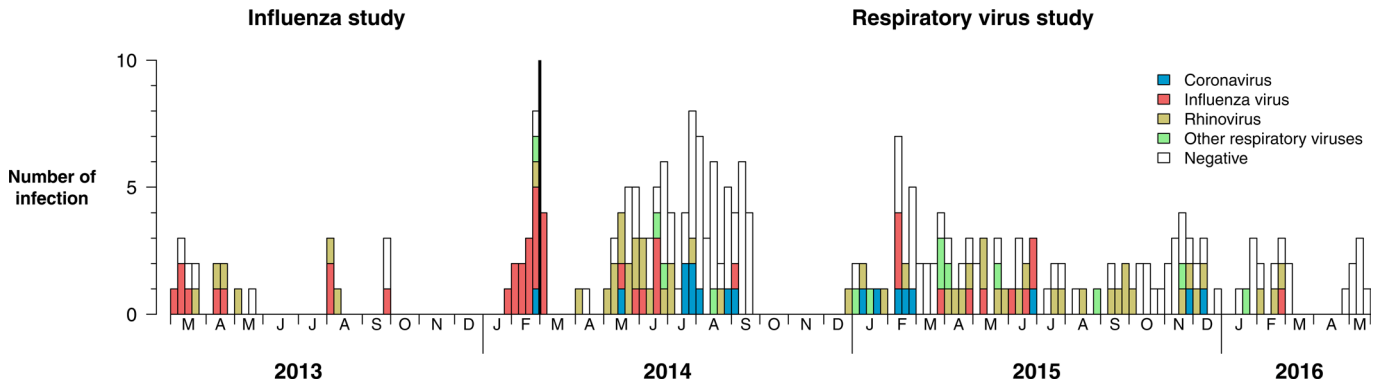
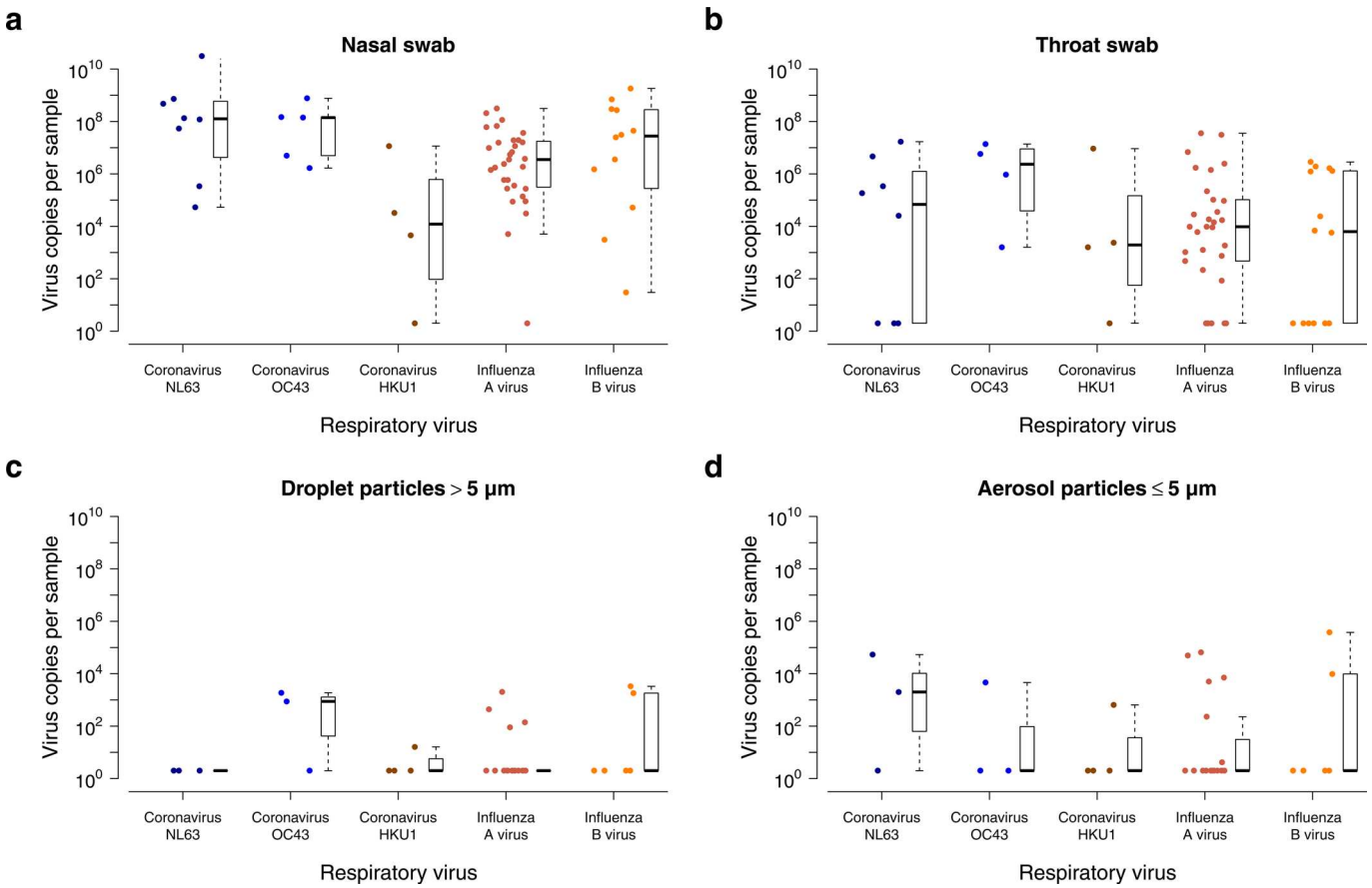


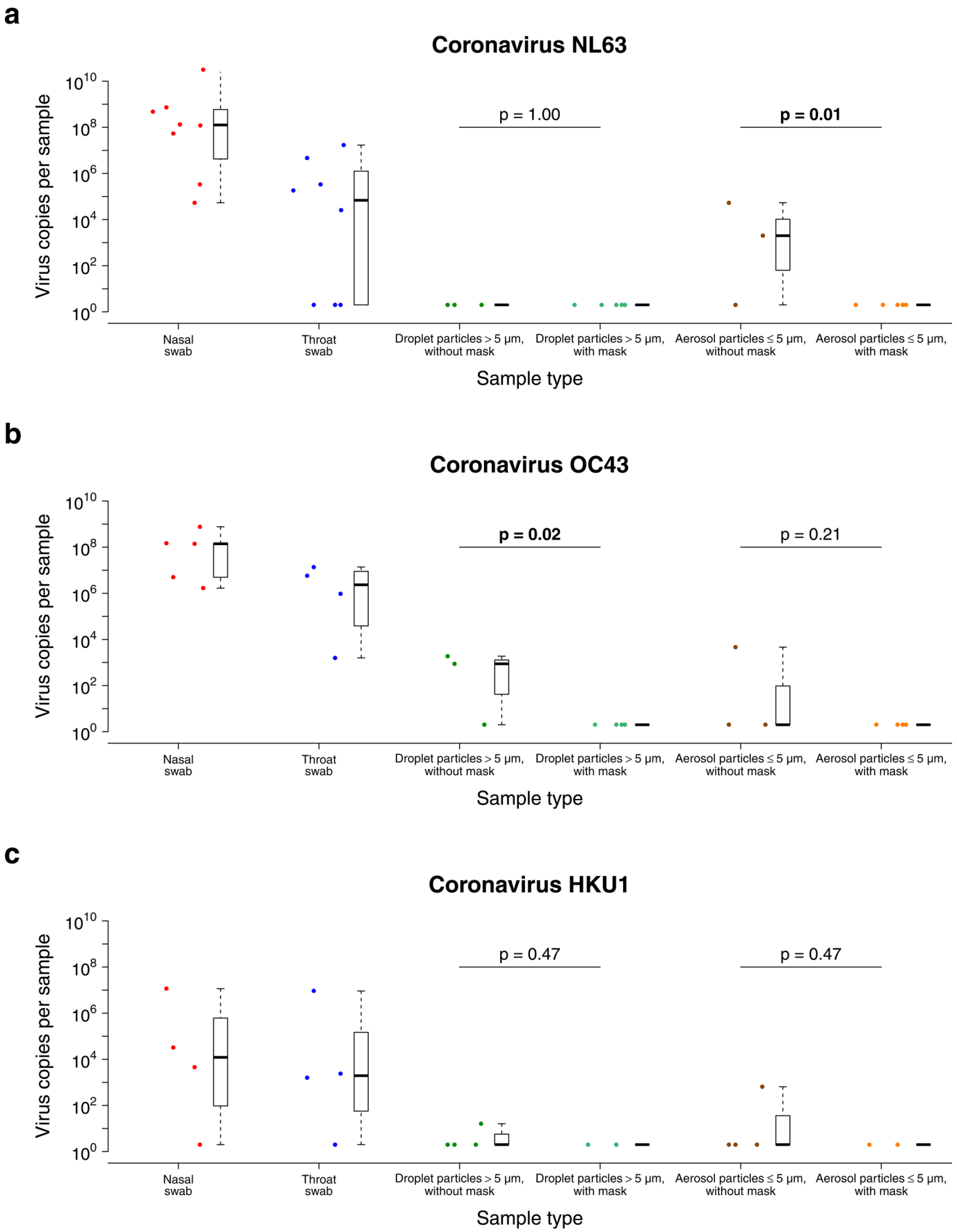
Extended Data Fig. 1 | Participant enrolment, randomization of mask intervention and identification of respiratory virus infection.



Extended Data Fig. 2 | Weekly number of respiratory virus infections identified by RT-PCR in symptomatic individuals who had provided exhaled breath samples (respiratory droplets and aerosols) during the study period. Blue, coronavirus; red, influenza virus; yellow, rhinovirus; green, other respiratory viruses including human metapneumovirus, parainfluenza virus, respiratory syncytial virus and adenovirus; white, no respiratory virus infection identified.

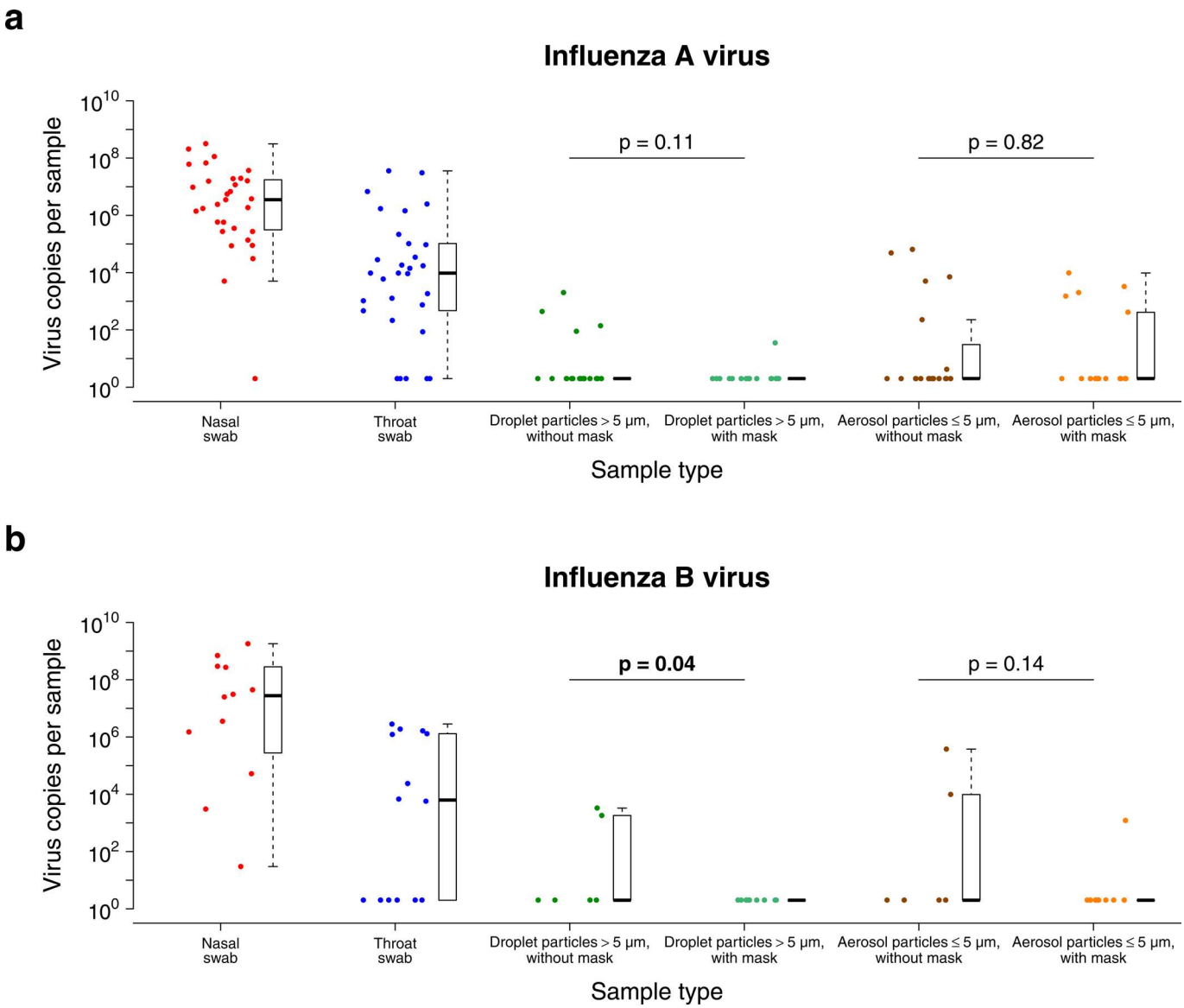


Extended Data Fig. 3 | Respiratory virus shedding in (a) nasal swab, (b) throat swab, (c) respiratory droplets and (d) aerosols in symptomatic individuals with coronavirus NL63, coronavirus OC43, coronavirus HKU1, influenza A and influenza B virus infection. For nasal swabs and throat swabs, all infected individuals identified by RT-PCR in any collected samples were included: coronavirus NL63 (n = 8), coronavirus OC43 (n = 5), coronavirus HKU1 (n = 4), influenza A virus (n = 31) and influenza B virus (n = 14). For respiratory droplets and aerosols, only infected individuals who provided exhaled breath samples while not wearing a surgical face mask were included: coronavirus NL63 (n = 3), coronavirus OC43 (n = 3), coronavirus HKU1 (n = 4), influenza A virus (n = 19) and influenza B virus (n = 6). The box plots indicate the median with the interquartile range (lower and upper hinge) and ±1.5 × interquartile range from the first and third quartile (lower and upper whisker). Dark blue, coronavirus NL63; light blue, coronavirus OC43; brown, coronavirus HKU1; red, influenza A virus; orange, influenza B virus.

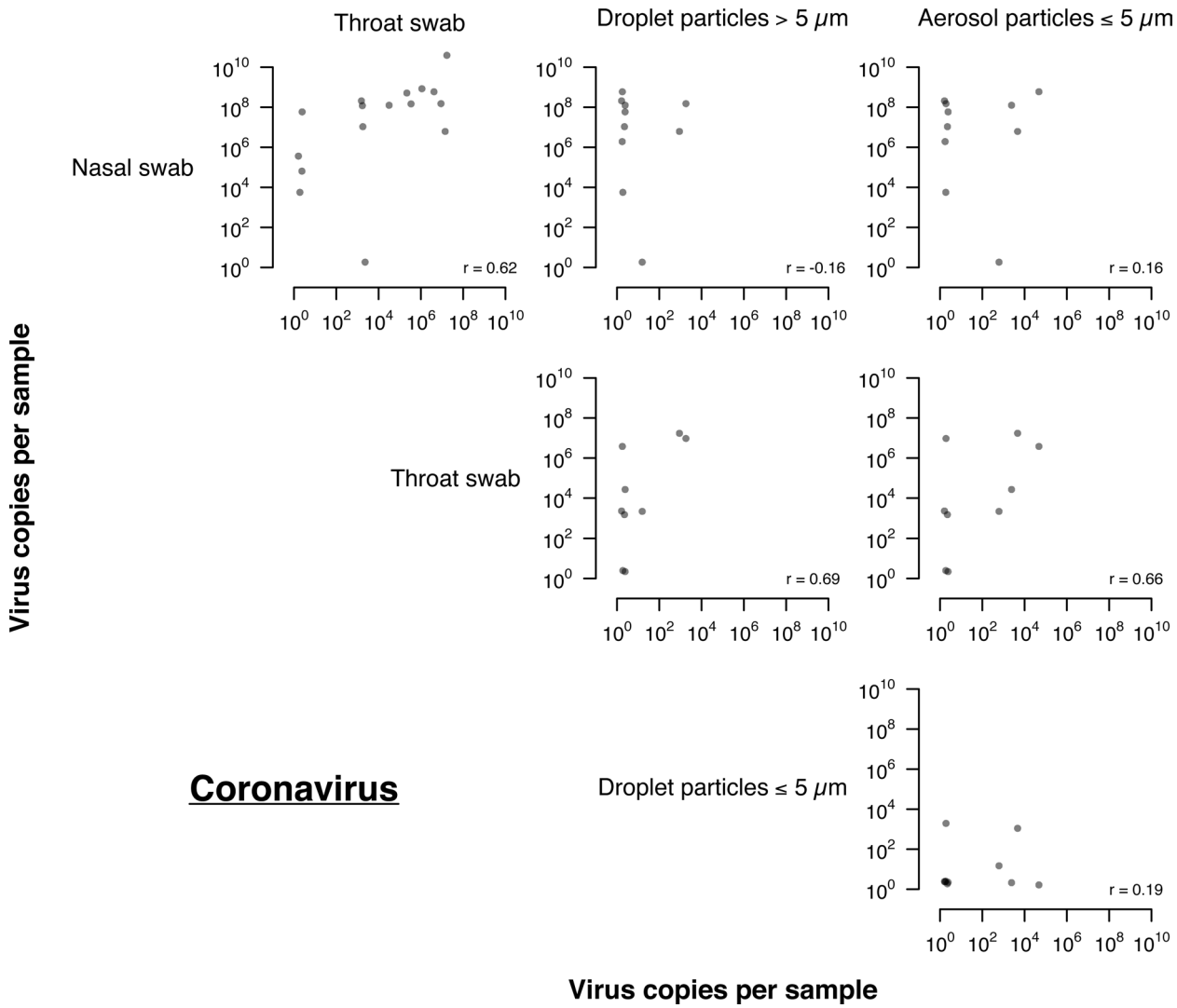


Extended Data Fig. 4 | See next page for caption.

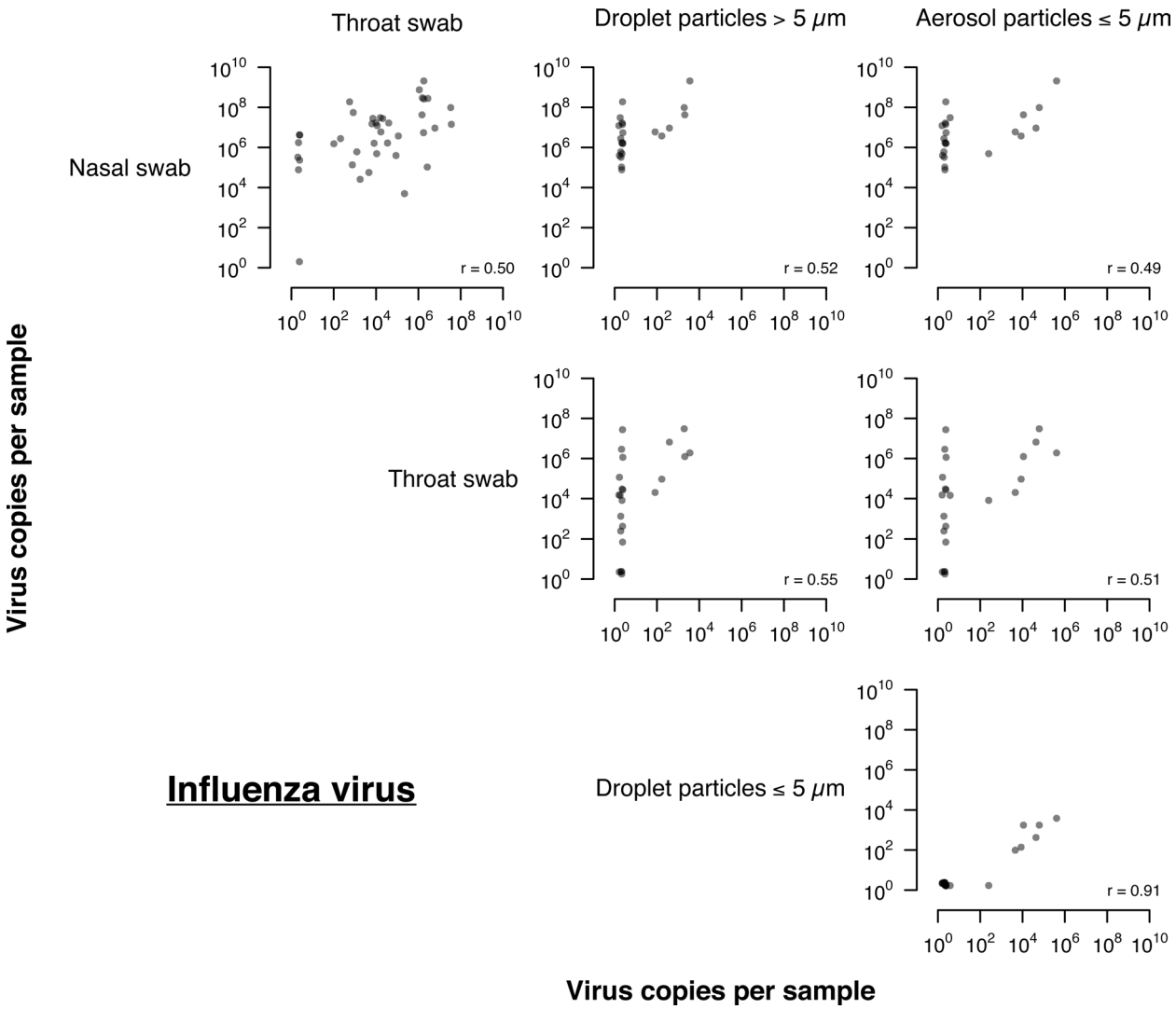
Extended Data Fig. 4 | Efficacy of surgical face masks in reducing respiratory virus shedding in respiratory droplets and aerosols of symptomatic individuals with seasonal coronaviruses including (a) coronavirus NL63, (b) coronavirus OC43 and (c) coronavirus HKU1. The figure shows the virus copies per sample collected in nasal swab (red), throat swab (blue), respiratory droplets collected for 30 min while not wearing (dark green) or wearing (light green) a surgical face mask and aerosols collected for 30 min while not wearing (brown) or wearing (orange) a face mask, collected from individuals with acute respiratory symptoms who were positive for coronavirus NL63, coronavirus OC43 and coronavirus HKU1 as determined by RT-PCR in any samples. *P* values for mask intervention as predictor of $\log_{10}$ virus copies per sample in an unadjusted univariate Tobit regression model which allowed for censoring at the lower limit of detection of the RT-PCR assay are shown, with significant differences in bold. For nasal swabs and throat swabs, all infected individuals were included (coronavirus NL63, n = 8; coronavirus OC43, n = 5; coronavirus HKU1, n = 4). For respiratory droplets and aerosols, numbers of infected individuals who provided exhaled breath samples while not wearing or wearing a surgical face mask, respectively were: coronavirus NL63 (n = 3 and 5), coronavirus OC43 (n = 3 and 4), coronavirus HKU1 (n = 4 and 2). A subset of participants provided exhaled breath samples for both mask interventions (coronavirus NL63, n = 0; coronavirus OC43, n = 2; coronavirus HKU1, n = 2).



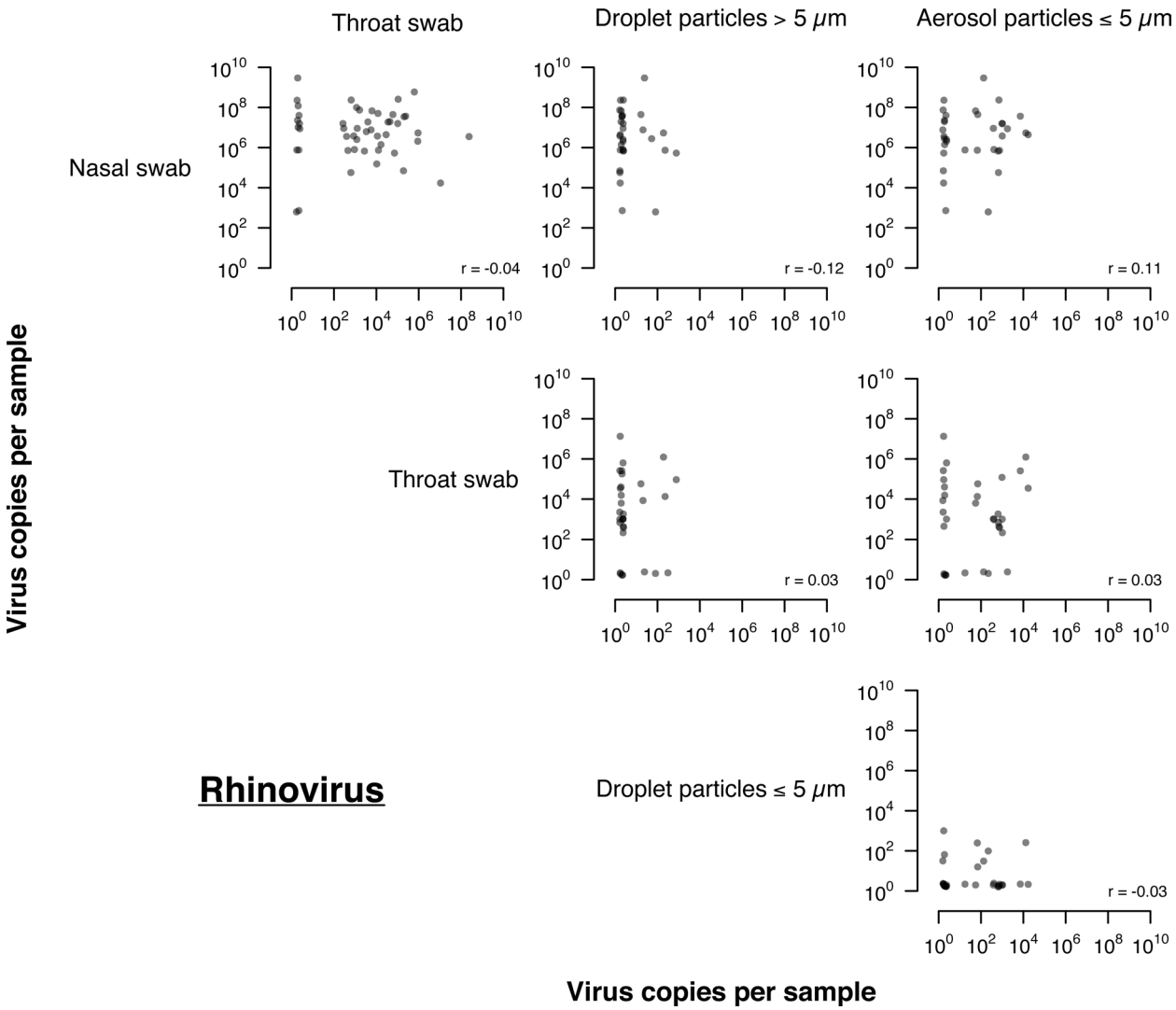
Extended Data Fig. 5 | Efficacy of surgical face masks in reducing respiratory virus shedding in respiratory droplets and aerosols of symptomatic individuals with seasonal influenza viruses including (a) influenza A and (b) influenza B virus. The figure shows the virus copies per sample collected in nasal swab (red), throat swab (blue), respiratory droplets collected for 30 min while not wearing (dark green) or wearing (light green) a surgical face mask and aerosols collected for 30 min while not wearing (brown) or wearing (orange) a face mask, collected from individuals with acute respiratory symptoms who were positive for influenza A and influenza B virus as determined by RT-PCR in any samples. *P* values for mask intervention as predictor of $\log_{10}$ virus copies per sample in an unadjusted univariate Tobit regression model which allowed for censoring at the lower limit of detection of the RT-PCR assay are shown, with significant differences in bold. For nasal swabs and throat swabs, all infected individuals were included (influenza A virus, n = 31; influenza B virus, n = 14). For respiratory droplets and aerosols, numbers of infected individuals who provided exhaled breath samples while not wearing or wearing a surgical face mask, respectively were: influenza A virus (n = 19 and 19), influenza B virus (n = 6 and 10). A subset of participants provided exhaled breath samples for both mask interventions (influenza A virus, n = 7; influenza B virus, n = 2).



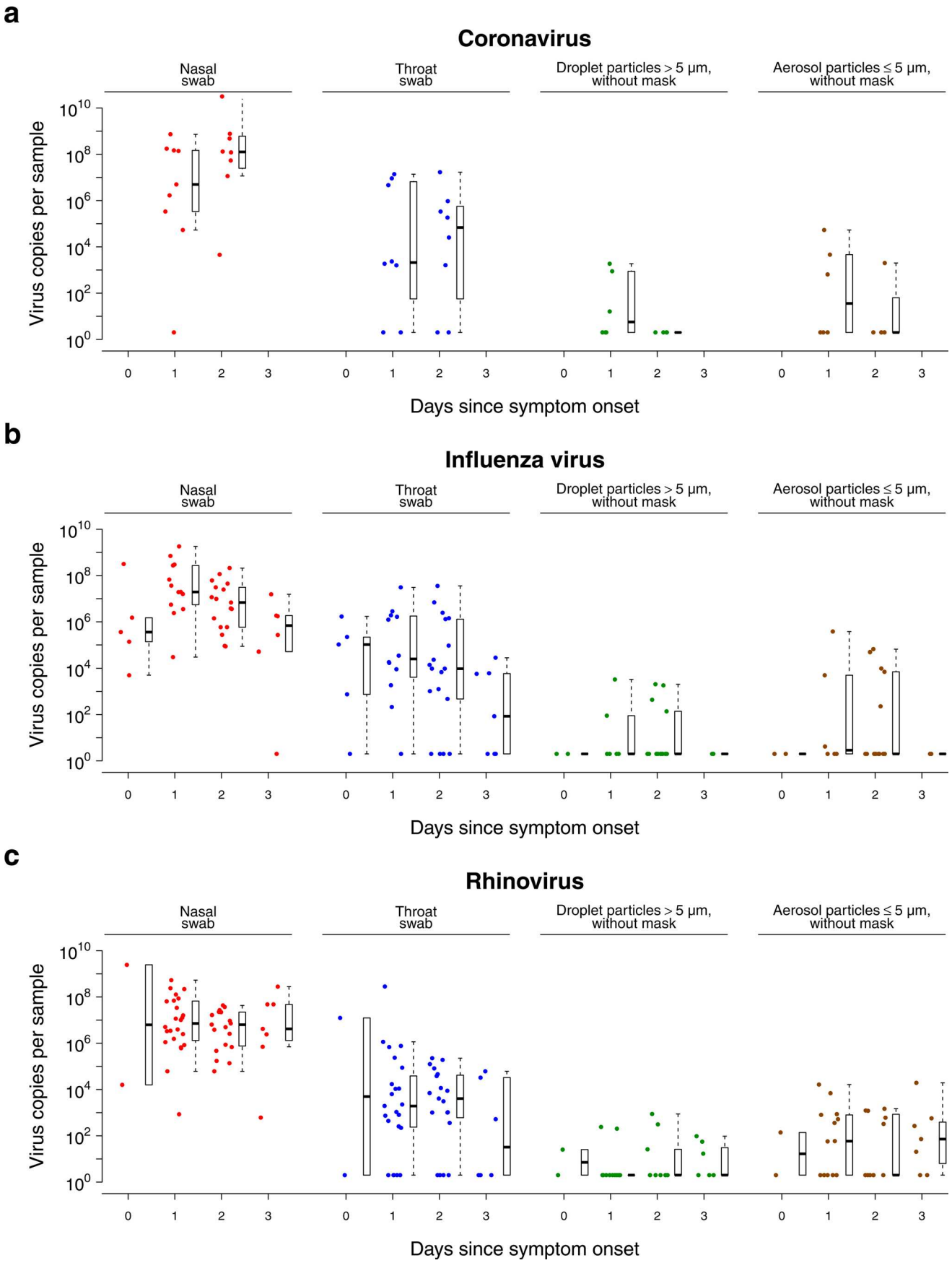
Extended Data Fig. 6 | Correlation of coronavirus viral shedding between different samples (nasal swab, throat swab, respiratory droplets and aerosols) in symptomatic individuals with seasonal coronavirus infection. For nasal swabs and throat swabs, all infected individuals were included (n = 17). For respiratory droplets and aerosols, only infected individuals who provided exhaled breath samples while not wearing a surgical face mask were included (n = 10). r, the Spearman's rank correlation coefficient.



Extended Data Fig. 7 | Correlation of influenza viral shedding between different samples (nasal swab, throat swab, respiratory droplets and aerosols) in symptomatic individuals with seasonal influenza infection. For nasal swabs and throat swabs, all infected individuals were included (n = 43). For respiratory droplets and aerosols, only infected individuals who provided exhaled breath samples while not wearing a surgical face mask were included (n = 23). r, the Spearman's rank correlation coefficient.



Extended Data Fig. 8 | Correlation of rhinovirus viral shedding between different samples (nasal swab, throat swab, respiratory droplets and aerosols) in symptomatic individuals with rhinovirus infection. For nasal swabs and throat swabs, all infected individuals were included (n = 54). For respiratory droplets and aerosols, only infected individuals who provided exhaled breath samples while not wearing a surgical face mask were included (n = 36). r, the Spearman's rank correlation coefficient.



Extended Data Fig. 9 | See next page for caption.

Extended Data Fig. 9 | Respiratory virus shedding in respiratory droplets and aerosols stratified by days from symptom onset for (a) coronavirus, (b) influenza virus or (c) rhinovirus. The figures shows the virus copies per sample collected in nasal swab (red), throat swab (blue), respiratory droplets (dark green) and aerosols (brown) collected for 30 min while not wearing a surgical face mask, stratified by the number of days from symptom onset on which the respiratory droplets and aerosols were collected. For nasal swabs and throat swabs, all infected individuals were included (coronavirus, n = 17; influenza virus, n = 43; rhinovirus, n = 54). For respiratory droplets and aerosols, numbers of infected individuals who provided exhaled breath samples while not wearing or wearing a surgical face mask, respectively were: coronavirus (n = 10 and 11), influenza virus (n = 23 and 28), rhinovirus (n = 36 and 32). A subset of participants provided exhaled breath samples for both mask interventions (coronavirus, n = 4; influenza virus, n = 8; rhinovirus, n = 14). The box plots indicate the median with the interquartile range (lower and upper hinge) and ±1.5 × interquartile range from the first and third quartile (lower and upper whisker).

nature research

Corresponding author(s): Benjamin John Cowling

Last updated by author(s): Mar 4, 2020

Reporting Summary

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Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒	A description of all covariates tested
☐	☒	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	No software was used.
Data analysis	All analyses were conducted with R version 3.6.0 and the VGAM package 1.1.1.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

Anonymized raw data and R syntax to reproduce all the analyses, figures, tables and supplementary tables in the published article are available at: [Dryad link pending].

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	We estimated a priori the sample size to be 300 participants. The primary outcome of the study was the reduction in the exhaled virus concentration of normal tidal breathing by wearing face mask in terms of total virus by RT-PCR as a proxy for infectious virus particle. We expected that a 1-log reduction in exhaled virus particle by face mask intervention would have a clinically relevant effect in reducing the probability of transmission. Except for influenza, there was no quantitative data available from exhaled breath samples from respiratory virus-infected individuals before the present study. If the standard deviation of exhaled virus concentration was 1 log copies/ml (Milton et al., PLoS Pathog 2013), we would detect a difference of >1 log copies/ml in the mask vs control group as long as we have >15 participants with a specific respiratory virus. For example, if our study included 23 participants with rhinovirus detectable in exhaled breath without a mask, we will have 80% power and 0.05 significance level to identify differences in viral shedding in aerosols of 1.28 log10 copies associated with the use of face masks, assuming a standard deviation of 1.54 log10 copies based on data from nasal and throat swab (Lu et al., J Clin Microbiol 2008). We expected from 300 individuals with ARI, at least 150 to have a respiratory virus, and at least 20-30 to have each of rhinovirus, coronavirus, adenovirus and parainfluenza plus small numbers of other respiratory viruses, assuming the Viral Panel would detect respiratory viruses in 60% of participants including 10% by influenza (since we partly recruited during the influenza seasons) and the other 50% made up of rhinovirus, coronavirus, adenovirus and parainfluenza virus.
Data exclusions	As described in the Results section and Supplementary Figure 1, only participants who provided exhaled breath samples and randomized to mask intervention were included; and final analyses were performed only for participants with either coronavirus, influenza virus or rhinovirus infection, which had sufficient sample size for comparison between mask intervention.
Replication	Samples from a subset of participants identified with a coronavirus, influenza or rhinovirus infection were re-tested by RT-PCR with consistent results. R syntax is available to reproduce all the analyses, figures, tables and supplementary tables in the published article.
Randomization	Prior to the exhaled breath collection, each participant was randomly allocated in a 1:1 ratio to either wearing a surgical face mask or not during the exhaled breath collection using a computer-generated sequence. The allocation was concealed to the study stuff performing the exhaled breath collection before allocation of the mask intervention.
Blinding	Blinding to the participant and the study stuff for the mask intervention was not possible. The study staff performing the statistical analyses was also involved in the data collection. We expected there would be minimal bias due to unblinding since data collection for questionnaires was done before randomization to mask intervention, and viral load from a sample measured by RT-PCR is an objective measurement.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☐	☒ Human research participants
☐	☒ Clinical data

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	Madin-Darby Canine Kidney (MDCK) cells
Authentication	European Collection of Authenticated Cell Cultures.
Mycoplasma contamination	We confirm that all cell lines tested negative for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	Nil

Human research participants

Policy information about studies involving human research participants

Population characteristics	As described in the Results section, Table 1a and Supplementary Table 1, there were some differences in characteristics of participants with the different viruses. Overall, most participants were younger adults and 5% were age 11-17 years, but there were more children with influenza virus and no children in the subgroup with coronavirus infection. Overall, 59% were female, but there were more females among the subgroup with coronavirus infection. The majority of participants did not have underlying medical conditions and overall 9% had received influenza vaccination for the current season but only 2% among those with influenza virus infection. The majority of participants were sampled within 24–48 or 48–72 hours of illness onset. 24% of participants had a measured fever ≥37.8ºC, with influenza patients more than twice as likely than coronavirus and rhinovirus-infected patients to have a measured fever. Coronavirus-infected participants coughed the most with an average of 17 (SD 30) coughs during the 30-minute exhaled breath collection. The profile of the participants randomized to with-mask vs without-mask groups were similar.
Recruitment	As described in the Methods section, participants were recruited year-round from March 2013 through May 2016 in a general outpatient clinic of a private hospital in Hong Kong. As routine practice, clinic staff screened all individuals attending the clinics for respiratory and any other symptoms regardless of the purpose of the visit at the triage. Study staff then approached immediately those who reported at least one of the following symptoms of acute respiratory illness (ARI) for further screening: fever≥37.8ºC, cough, sore throat, runny nose, headache, myalgia and phlegm. Individuals who reported ≥2 ARI symptoms, within 3 days of illness onset and ≥11 years of age were eligible to participate.
Ethics oversight	As described in the Methods section, the study protocol was approved by the Institutional Review Board of The University of Hong Kong and the Clinical and Research Ethics Committee of Hong Kong Baptist Hospital.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration	The present study was not registered in clinical trials registries, as it was a laboratory-based study of detection of viruses in exhaled breath and the effect of wearing surgical facemasks on virus detection. It was not a Phase II/III clinical trial.
Study protocol	Not available in clinical trials registries (as above). Study protocol will be made available to editors and peer reviewers if requested.
Data collection	As described in the Methods section, participants were recruited year-round from March 2013 through March 2016 in a general outpatient clinic of a private hospital in Hong Kong. Data collection for questionnaires and exhaled breath sample collection was done face-to-face with the participant by trained study staff at the same clinic on the day of participant enrolment.
Outcomes	As pre-specified in the study protocol, the primary outcomes of the study were the virus generation rate in the tidal breathing of participants infected by different respiratory viruses, and the efficacy of face mask in preventing virus dissemination in exhaled breath especially at the aerosol fraction. As pre-specified in the study protocol, one of the secondary outcomes was to provide indirect evidence for relative importance of different transmission routes of influenza and other respiratory viruses. In this regard, in the present manuscript we examined the correlation between viral shedding in nose swabs, throat swabs, respiratory droplets and aerosols, and factors affecting viral shedding in respiratory droplets and aerosols. As described in the Discussion section in the present manuscript about the limitation of our study, there was large proportion of participants with undetectable viral shedding in exhaled breath for each of the viruses studied, and therefore we were unable to examine the exhaled respiratory virus reduction proportion by chi-squared test, nor the exhaled respiratory virus reduction volume (i.e. viral load) by t-test and linear regression as pre-specified in the study protocol. Instead, we have used Fisher's exact test and Tobit regression for the same purposes respectively.

From: Grant, Evan H [redacted]>
Sent: Monday, April 13, 2020 6:39 PM EDT
To: castlekt [redacted]>; O'Shea, Thomas [redacted]; raina.plowright [redacted]>; dreeder [redacted]; Daniel.Streicker [redacted]>; sja [redacted] epstein ecohealthalliance.org>; kate.e.jones [redacted]; ckjohnson [redacted]; wfrick [redacted]; linfa.wang [redacted] jit [redacted] a.pee [redacted] rbario [redacted]; Kading,Rebekah [redacted]; Amy.T.Gilbert [redacted]; Lorch, Jeffrey M [redacted]
CC: Runge, Michael C [redacted]>; Cryan, Paul [redacted]; oliva [redacted] ecohealthalliance.org>; Sleeman, Jonathan M [redacted] Coleman, Jeremy T [redacted] Gibbs, Samantha [redacted]; Hopkins, Maria-Richetta (Camille) C [redacted]
Subject: RE: Expert judgement for SARS-CoV-2 risk assessment for North American bats
Attachment(s): "SARS-batEE Questions v3p.xlsx"

Hi All,

It has come to my attention that it's impossible to enter a response to Q12. You can send me a response directly to that question, or use the attached spreadsheet if you haven't started the rest of your responses.

All apologies,

Evan

From: Grant, Evan H
Sent: Thursday, April 9, 2020 5:39 PM
To: castlekt [redacted]; O'Shea, Thomas [redacted]; raina. [redacted] dreeder [redacted] Daniel.Streicker [redacted] sja [redacted] ecohealthalliance.org; kate.e.jones [redacted]; ckjohnson [redacted]; wfrick [redacted] linfa.wang [redacted]; jit [redacted] a.pee [redacted]; rbario [redacted]; Rebekah.Kading [redacted]; Amy.T.Gilbert [redacted]; Lorch, Jeffrey M [redacted]
Cc: Runge, Michael C [redacted]; Cryan, Paul [redacted]; [redacted] ecohealthalliance.org; Sleeman, Jonathan M [redacted]; Coleman, Jeremy T [redacted] Gibbs, Samantha [redacted] Hopkins, Maria-Richetta (Camille) C [redacted]
Subject: Expert judgement for SARS-CoV-2 risk assessment for North American bats

Hello experts,

Thank you for volunteering your time and expertise to help estimate the risk of SARS-CoV-2 to North American bats. Mike Runge and I (Evan Grant), with the U.S. Geological Survey Patuxent Wildlife Research Center, are facilitating this effort in collaboration with the USGS National Wildlife Health Center, USGS Fort Collins Science Center, USFWS, and EcoHealth Alliance. We are conducting a rapid assessment of the risks for transmission of SARS-CoV-2 from humans to bats. The goal is to provide scientific information that will guide wildlife management agency response to this potential risk, including development of management recommendations and mitigation strategies.

Attached please find two documents: (1) an introduction to expert elicitation with some background on the issue we are addressing, and (2) a spreadsheet <BatEE Practice Questions v2.xlsx> with calibration questions. There are three tabs (corresponding to the three questions) in the accompanying spreadsheet, and a fourth tab that summarizes the responses and the calculated mean and standard deviation for each question.

We have a very tight timeline to provide guidance to U.S. management agencies, so we thank you for your participation along the following timeline:

i. Respond to ehgrant [redacted] with your responses to the calibration questions in the attached spreadsheet (due by 12 PM ET 10 Apr)
ii. Review the background information and elicitation questions (we will send these additional documents to you by 6 pm ET 10 Apr)
iii. Respond with your initial responses to the questions (due by 6 PM ET 13 Apr)
iv. Be available for a 2-hr conference call to discuss initial responses and share insights (4 PM ET 14 Apr – and/or – 4 PM ET 15 Apr)
v. Revise and send your second-round responses to the questions (due 24 hours after the last conference call)

Thank you in advance for your participation. If you have questions – please contact Evan (ehgrant [redacted].

Kindest regards,
Evan and Mike

	A	B	C	D	E
1		Consider a wildlife biologist engaged in research, survey, monitoring, or management (RSM) who is actively shedding SARS-CoV-2 virus (CoV+), performing their routine activities in the absence of any new restrictions, regulations, or protocols.			
2	Q1	1. If that biologist **directly handles** 100 average little brown bats, how many of those bats do you estimate will be exposed to a sufficient viral dose of SARS-CoV-2 that they could become infected?			
3					
4				logit(x)	
5		What is the lowest reasonable estimate?		Error: must be between 0 and 100	
6		What is the highest reasonable estimate?		Error: must be between 0 and 100	
7		What is your central estimate?		Error: must be between 0 and 100	
8		How confidence are you that the true mean is between your low and high estimates?		Error: Confidence should be >50	
9		(Confidence should be a number between 50 and 100)			
10					x
11					#N/A
12					#N/A
13					#N/A
14					#N/A
15					#N/A
16					#N/A
17					#N/A
18					#N/A
19					#N/A
20					#N/A
21					#N/A
22					#N/A
23					#N/A
24					#N/A
25					#N/A
26					#N/A
27					#N/A
28					#N/A
29					#N/A
30					#N/A
31					#N/A
32					#N/A
33					#N/A
34					#N/A
35					#N/A
36					#N/A

	F	G	H	I	J
1					
2					
3	Assume: logit-normal uncertainty distribution				
4	Quantile	IPDF			
5	0.5	0	#N/A	mean	#N/A
6	0.5	0	#N/A	sd	#N/A
7	0.5	0		min	#N/A
8				max	#N/A
9				delta	#N/A
10	logit(x)	Npdf	pdf		
11	#N/A	#N/A	#N/A		
12	#N/A	#N/A	#N/A		
13	#N/A	#N/A	#N/A		
14	#N/A	#N/A	#N/A		
15	#N/A	#N/A	#N/A		
16	#N/A	#N/A	#N/A		
17	#N/A	#N/A	#N/A		
18	#N/A	#N/A	#N/A		
19	#N/A	#N/A	#N/A		
20	#N/A	#N/A	#N/A		
21	#N/A	#N/A	#N/A		
22	#N/A	#N/A	#N/A		
23	#N/A	#N/A	#N/A		
24	#N/A	#N/A	#N/A		
25	#N/A	#N/A	#N/A		
26	#N/A	#N/A	#N/A		
27	#N/A	#N/A	#N/A		
28	#N/A	#N/A	#N/A		
29	#N/A	#N/A	#N/A		
30	#N/A	#N/A	#N/A		
31	#N/A	#N/A	#N/A		
32	#N/A	#N/A	#N/A		
33	#N/A	#N/A	#N/A		
34	#N/A	#N/A	#N/A		
35	#N/A	#N/A	#N/A		
36	#N/A	#N/A	#N/A		

	A	B	C	D	E	F
1		Consider a wildlife biologist engaged in research, survey, monitoring, or management (RSM) who is actively shedding SARS-CoV-2 virus (CoV+), performing their routine activities in the absence of any new restrictions, regulations, or protocols.				
2	Q2	2. If that biologist is **in an enclosed space and within 6 feet** of 100 average little brown bats (but does not handle them), how many of those bats will be exposed to a sufficient viral dose that they could become infected?				
3						Assume: logi
4				logit(x)		Quantile
5		What is the lowest reasonable estimate?		Error: must be between 0 and 100		0.5
6		What is the highest reasonable estimate?		Error: must be between 0 and 100		0.5
7		What is your central estimate?		Error: must be between 0 and 100		0.5
8		How confidence are you that the true mean is between your low and high estimates?		Error: Confidence should be >50		
9		(Confidence should be a number between 50 and 100)				
10					x	logit(x)
11					#N/A	#N/A
12					#N/A	#N/A
13					#N/A	#N/A
14					#N/A	#N/A
15					#N/A	#N/A
16					#N/A	#N/A
17					#N/A	#N/A
18					#N/A	#N/A
19					#N/A	#N/A
20					#N/A	#N/A
21					#N/A	#N/A
22					#N/A	#N/A
23					#N/A	#N/A
24					#N/A	#N/A
25					#N/A	#N/A
26					#N/A	#N/A
27					#N/A	#N/A
28					#N/A	#N/A
29					#N/A	#N/A
30					#N/A	#N/A
31					#N/A	#N/A
32					#N/A	#N/A
33					#N/A	#N/A
34					#N/A	#N/A
35					#N/A	#N/A
36					#N/A	#N/A

	G	H	I	J
1				
2				
3	it-normal uncertainty distribution			
4	IPDF			
5	0	#N/A	mean	#N/A
6	0	#N/A	sd	#N/A
7	0		min	#N/A
8			max	#N/A
9			delta	#N/A
10	Npdf	pdf		
11	#N/A	#N/A		
12	#N/A	#N/A		
13	#N/A	#N/A		
14	#N/A	#N/A		
15	#N/A	#N/A		
16	#N/A	#N/A		
17	#N/A	#N/A		
18	#N/A	#N/A		
19	#N/A	#N/A		
20	#N/A	#N/A		
21	#N/A	#N/A		
22	#N/A	#N/A		
23	#N/A	#N/A		
24	#N/A	#N/A		
25	#N/A	#N/A		
26	#N/A	#N/A		
27	#N/A	#N/A		
28	#N/A	#N/A		
29	#N/A	#N/A		
30	#N/A	#N/A		
31	#N/A	#N/A		
32	#N/A	#N/A		
33	#N/A	#N/A		
34	#N/A	#N/A		
35	#N/A	#N/A		
36	#N/A	#N/A		

	A	B	C	D	E	F
1		Consider a wildlife biologist engaged in research, survey, monitoring, or management (RSM) who is actively shedding SARS-CoV-2 virus (CoV+), performing their routine activities in the absence of any new restrictions, regulations, or protocols.				
2	Q3	3. If the RSM biologist is **not in an enclosed space but is within a 6-foot proximity** of 100 little brown bats (and does not handle them), how many of those bats will be exposed to a sufficient viral dose that they could become infected?				
3						Assume: logi
4				logit(x)		Quantile
5		What is the lowest reasonable estimate?		Error: must be between 0 and 100		0.5
6		What is the highest reasonable estimate?		Error: must be between 0 and 100		0.5
7		What is your central estimate?		Error: must be between 0 and 100		0.5
8		How confidence are you that the true mean is between your low and high estimates?		Error: Confidence should be >50		
9		(Confidence should be a number between 50 and 100)				
10					x	logit(x)
11					#N/A	#N/A
12					#N/A	#N/A
13					#N/A	#N/A
14					#N/A	#N/A
15					#N/A	#N/A
16					#N/A	#N/A
17					#N/A	#N/A
18					#N/A	#N/A
19					#N/A	#N/A
20					#N/A	#N/A
21					#N/A	#N/A
22					#N/A	#N/A
23					#N/A	#N/A
24					#N/A	#N/A
25					#N/A	#N/A
26					#N/A	#N/A
27					#N/A	#N/A
28					#N/A	#N/A
29					#N/A	#N/A
30					#N/A	#N/A
31					#N/A	#N/A
32					#N/A	#N/A
33					#N/A	#N/A
34					#N/A	#N/A
35					#N/A	#N/A
36					#N/A	#N/A

	G	H	I	J
1				
2				
3	it-normal uncertainty distribution			
4	IPDF			
5	0	#N/A	mean	#N/A
6	0	#N/A	sd	#N/A
7	0		min	#N/A
8			max	#N/A
9			delta	#N/A
10	Npdf	pdf		
11	#N/A	#N/A		
12	#N/A	#N/A		
13	#N/A	#N/A		
14	#N/A	#N/A		
15	#N/A	#N/A		
16	#N/A	#N/A		
17	#N/A	#N/A		
18	#N/A	#N/A		
19	#N/A	#N/A		
20	#N/A	#N/A		
21	#N/A	#N/A		
22	#N/A	#N/A		
23	#N/A	#N/A		
24	#N/A	#N/A		
25	#N/A	#N/A		
26	#N/A	#N/A		
27	#N/A	#N/A		
28	#N/A	#N/A		
29	#N/A	#N/A		
30	#N/A	#N/A		
31	#N/A	#N/A		
32	#N/A	#N/A		
33	#N/A	#N/A		
34	#N/A	#N/A		
35	#N/A	#N/A		
36	#N/A	#N/A		

	A	B	C	D	E	F
1		Now consider a wildlife rehabilitator (WR) who is actively shedding SARS-CoV-2 virus, performing their routine activities in the absence of any new restrictions, regulations, or protocols.				
2	Q4	4. If that rehabilitator directly handles 100 average little brown bats, how many of those bats do you estimate will be exposed to a sufficient viral dose of SARS-CoV-2 that they could become infected?				
3						Assume: logi
4				logit(x)		Quantile
5		What is the lowest reasonable estimate?		Error: must be between 0 and 100		0.5
6		What is the highest reasonable estimate?		Error: must be between 0 and 100		0.5
7		What is your central estimate?		Error: must be between 0 and 100		0.5
8		How confidence are you that the true mean is between your low and high estimates?		Error: Confidence should be >50		
9		(Confidence should be a number between 50 and 100)				
10					x	logit(x)
11					#N/A	#N/A
12					#N/A	#N/A
13					#N/A	#N/A
14					#N/A	#N/A
15					#N/A	#N/A
16					#N/A	#N/A
17					#N/A	#N/A
18					#N/A	#N/A
19					#N/A	#N/A
20					#N/A	#N/A
21					#N/A	#N/A
22					#N/A	#N/A
23					#N/A	#N/A
24					#N/A	#N/A
25					#N/A	#N/A
26					#N/A	#N/A
27					#N/A	#N/A
28					#N/A	#N/A
29					#N/A	#N/A
30					#N/A	#N/A
31					#N/A	#N/A
32					#N/A	#N/A
33					#N/A	#N/A
34					#N/A	#N/A
35					#N/A	#N/A
36					#N/A	#N/A

	G	H	I	J
1				
2				
3	it-normal uncertainty distribution			
4	IPDF			
5	0	#N/A	mean	#N/A
6	0	#N/A	sd	#N/A
7	0		min	#N/A
8			max	#N/A
9			delta	#N/A
10	Npdf	pdf		
11	#N/A	#N/A		
12	#N/A	#N/A		
13	#N/A	#N/A		
14	#N/A	#N/A		
15	#N/A	#N/A		
16	#N/A	#N/A		
17	#N/A	#N/A		
18	#N/A	#N/A		
19	#N/A	#N/A		
20	#N/A	#N/A		
21	#N/A	#N/A		
22	#N/A	#N/A		
23	#N/A	#N/A		
24	#N/A	#N/A		
25	#N/A	#N/A		
26	#N/A	#N/A		
27	#N/A	#N/A		
28	#N/A	#N/A		
29	#N/A	#N/A		
30	#N/A	#N/A		
31	#N/A	#N/A		
32	#N/A	#N/A		
33	#N/A	#N/A		
34	#N/A	#N/A		
35	#N/A	#N/A		
36	#N/A	#N/A		

	A	B	C	D	E	F
1		Now consider a wildlife rehabilitator (WR) who is actively shedding SARS-CoV-2 virus, performing their routine activities in the absence of any new restrictions, regulations, or protocols.				
2	Q5	5. If that rehabilitator is **within a 6-foot proximity (whether enclosed or unenclosed)** of 100 average little brown bats but does not handle them, how many of those bats will be exposed to a sufficient viral dose that they could become infected?				
3						Assume: logi
4				logit(x)		Quantile
5		What is the lowest reasonable estimate?		Error: must be between 0 and 100		0.5
6		What is the highest reasonable estimate?		Error: must be between 0 and 100		0.5
7		What is your central estimate?		Error: must be between 0 and 100		0.5
8		How confidence are you that the true mean is between your low and high estimates?		Error: Confidence should be >50		
9		(Confidence should be a number between 50 and 100)				
10					x	logit(x)
11					#N/A	#N/A
12					#N/A	#N/A
13					#N/A	#N/A
14					#N/A	#N/A
15					#N/A	#N/A
16					#N/A	#N/A
17					#N/A	#N/A
18					#N/A	#N/A
19					#N/A	#N/A
20					#N/A	#N/A
21					#N/A	#N/A
22					#N/A	#N/A
23					#N/A	#N/A
24					#N/A	#N/A
25					#N/A	#N/A
26					#N/A	#N/A
27					#N/A	#N/A
28					#N/A	#N/A
29					#N/A	#N/A
30					#N/A	#N/A
31					#N/A	#N/A
32					#N/A	#N/A
33					#N/A	#N/A
34					#N/A	#N/A
35					#N/A	#N/A
36					#N/A	#N/A

	G	H	I	J
1				
2				
3	it-normal uncertainty distribution			
4	IPDF			
5	0	#N/A	mean	#N/A
6	0	#N/A	sd	#N/A
7	0		min	#N/A
8			max	#N/A
9			delta	#N/A
10	Npdf	pdf		
11	#N/A	#N/A		
12	#N/A	#N/A		
13	#N/A	#N/A		
14	#N/A	#N/A		
15	#N/A	#N/A		
16	#N/A	#N/A		
17	#N/A	#N/A		
18	#N/A	#N/A		
19	#N/A	#N/A		
20	#N/A	#N/A		
21	#N/A	#N/A		
22	#N/A	#N/A		
23	#N/A	#N/A		
24	#N/A	#N/A		
25	#N/A	#N/A		
26	#N/A	#N/A		
27	#N/A	#N/A		
28	#N/A	#N/A		
29	#N/A	#N/A		
30	#N/A	#N/A		
31	#N/A	#N/A		
32	#N/A	#N/A		
33	#N/A	#N/A		
34	#N/A	#N/A		
35	#N/A	#N/A		
36	#N/A	#N/A		

	A	B	C	D	E	F
1		Now consider a wildlife control operator (WC) who is actively shedding SARS-CoV-2 virus, performing their routine activities that involve handling bats, in the absence of any new restrictions, regulations, or protocols. For example, a typical activity might involve capturing bats in a home or trapping and transporting bats from an attic.				
2	Q6	6. If that WC operator **directly handles** 100 average little brown bats, how many of those bats do you estimate will be exposed to a sufficient viral dose of SARS-CoV-2 that they could become infected?				
3						Assume: logi
4				logit(x)		Quantile
5		What is the lowest reasonable estimate?		Error: must be between 0 and 100		0.5
6		What is the highest reasonable estimate?		Error: must be between 0 and 100		0.5
7		What is your central estimate?		Error: must be between 0 and 100		0.5
8		How confidence are you that the true mean is between your low and high estimates?		Error: Confidence should be >50		
9		(Confidence should be a number between 50 and 100)				
10					x	logit(x)
11					#N/A	#N/A
12					#N/A	#N/A
13					#N/A	#N/A
14					#N/A	#N/A
15					#N/A	#N/A
16					#N/A	#N/A
17					#N/A	#N/A
18					#N/A	#N/A
19					#N/A	#N/A
20					#N/A	#N/A
21					#N/A	#N/A
22					#N/A	#N/A
23					#N/A	#N/A
24					#N/A	#N/A
25					#N/A	#N/A
26					#N/A	#N/A
27					#N/A	#N/A
28					#N/A	#N/A
29					#N/A	#N/A
30					#N/A	#N/A
31					#N/A	#N/A
32					#N/A	#N/A
33					#N/A	#N/A
34					#N/A	#N/A
35					#N/A	#N/A
36					#N/A	#N/A

	G	H	I	J
1				
2				
3	it-normal uncertainty distribution			
4	IPDF			
5	0	#N/A	mean	#N/A
6	0	#N/A	sd	#N/A
7	0		min	#N/A
8			max	#N/A
9			delta	#N/A
10	Npdf	pdf		
11	#N/A	#N/A		
12	#N/A	#N/A		
13	#N/A	#N/A		
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15	#N/A	#N/A		
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18	#N/A	#N/A		
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20	#N/A	#N/A		
21	#N/A	#N/A		
22	#N/A	#N/A		
23	#N/A	#N/A		
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25	#N/A	#N/A		
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33	#N/A	#N/A		
34	#N/A	#N/A		
35	#N/A	#N/A		
36	#N/A	#N/A		

	A	B	C	D	E	F
1		Now consider a wildlife control operator (WC) who is actively shedding SARS-CoV-2 virus, performing their routine activities that involve handling bats, in the absence of any new restrictions, regulations, or protocols. For example, a typical activity might involve capturing bats in a home or trapping and transporting bats from an attic.				
2	Q7	7. If that WC operator is **within a 6-foot proximity (whether enclosed or unenclosed)** of 100 average little brown bats but does not handle them, how many of those bats will be exposed to a sufficient viral dose that they could become infected?				
3						Assume: logi
4				logit(x)		Quantile
5		What is the lowest reasonable estimate?		Error: must be between 0 and 100		0.5
6		What is the highest reasonable estimate?		Error: must be between 0 and 100		0.5
7		What is your central estimate?		Error: must be between 0 and 100		0.5
8		How confidence are you that the true mean is between your low and high estimates?		Error: Confidence should be >50		
9		(Confidence should be a number between 50 and 100)				
10					x	logit(x)
11					#N/A	#N/A
12					#N/A	#N/A
13					#N/A	#N/A
14					#N/A	#N/A
15					#N/A	#N/A
16					#N/A	#N/A
17					#N/A	#N/A
18					#N/A	#N/A
19					#N/A	#N/A
20					#N/A	#N/A
21					#N/A	#N/A
22					#N/A	#N/A
23					#N/A	#N/A
24					#N/A	#N/A
25					#N/A	#N/A
26					#N/A	#N/A
27					#N/A	#N/A
28					#N/A	#N/A
29					#N/A	#N/A
30					#N/A	#N/A
31					#N/A	#N/A
32					#N/A	#N/A
33					#N/A	#N/A
34					#N/A	#N/A
35					#N/A	#N/A
36					#N/A	#N/A

	G	H	I	J
1				
2				
3	it-normal uncertainty distribution			
4	IPDF			
5	0	#N/A	mean	#N/A
6	0	#N/A	sd	#N/A
7	0		min	#N/A
8			max	#N/A
9			delta	#N/A
10	Npdf	pdf		
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12	#N/A	#N/A		
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15	#N/A	#N/A		
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18	#N/A	#N/A		
19	#N/A	#N/A		
20	#N/A	#N/A		
21	#N/A	#N/A		
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33	#N/A	#N/A		
34	#N/A	#N/A		
35	#N/A	#N/A		
36	#N/A	#N/A		

	A	B	C	D	E	F
1						
2	Q8	8. What is the probability that a little brown bat exposed to a sufficient viral dose of SARS-CoV-2 would actually become infected by the virus (that is, sustained viral replication would occur in their tissue)?				
3						Assume: log
4				logit(x)		Quantile
5		What is the lowest reasonable estimate?		Error: must be between 0 and 1		0.5
6		What is the highest reasonable estimate?		Error: must be between 0 and 1		0.5
7		What is your central estimate?		Error: must be between 0 and 1		0.5
8		How confidence are you that the true mean is between your low and high estimates?		Error: Confidence should be >50		
9		(Confidence should be a number between 50 and 100)				
10					x	logit(x)
11					#N/A	#N/A
12					#N/A	#N/A
13					#N/A	#N/A
14					#N/A	#N/A
15					#N/A	#N/A
16					#N/A	#N/A
17					#N/A	#N/A
18					#N/A	#N/A
19					#N/A	#N/A
20					#N/A	#N/A
21					#N/A	#N/A
22					#N/A	#N/A
23					#N/A	#N/A
24					#N/A	#N/A
25					#N/A	#N/A
26					#N/A	#N/A
27					#N/A	#N/A
28					#N/A	#N/A
29					#N/A	#N/A
30					#N/A	#N/A
31					#N/A	#N/A
32					#N/A	#N/A
33					#N/A	#N/A
34					#N/A	#N/A
35					#N/A	#N/A
36					#N/A	#N/A

	G	H	I	J
1				
2				
3	it-normal uncertainty distribution			
4	IPDF			
5	0	#N/A	mean	#N/A
6	0	#N/A	sd	#N/A
7	0		min	#N/A
8			max	#N/A
9			delta	#N/A
10	Npdf	pdf		
11	#N/A	#N/A		
12	#N/A	#N/A		
13	#N/A	#N/A		
14	#N/A	#N/A		
15	#N/A	#N/A		
16	#N/A	#N/A		
17	#N/A	#N/A		
18	#N/A	#N/A		
19	#N/A	#N/A		
20	#N/A	#N/A		
21	#N/A	#N/A		
22	#N/A	#N/A		
23	#N/A	#N/A		
24	#N/A	#N/A		
25	#N/A	#N/A		
26	#N/A	#N/A		
27	#N/A	#N/A		
28	#N/A	#N/A		
29	#N/A	#N/A		
30	#N/A	#N/A		
31	#N/A	#N/A		
32	#N/A	#N/A		
33	#N/A	#N/A		
34	#N/A	#N/A		
35	#N/A	#N/A		
36	#N/A	#N/A		

	A	B	C	D	E	F
1		Consider your response to question 1, regarding exposure through handling by RSM scientists. The new guidance and protocols consist of: restriction of fieldwork to people without symptoms and without contact with someone who had symptoms of COVID-19 in the last 14 days; proper training and compliance protocols for the use of PPE; proper use of Tyvek or other dedicated clothing; proper use of an N95 respirator; and proper use of gloves for handling bats. In these questions, please assume that the biologists have proper training, have access to PPE, and are using it appropriately.				
2	Q9	9. By what proportion should this exposure probability be multiplied if the new guidance and protocols are put into place? (Note that a proportion of 1 means there would be no change in exposure probability; a proportion of less than 1 would indicate a reduction in exposure probability; and a proportion of greater than 1 would indicate an increase in exposure probability as a result of such guidance.)				
3						Assume: log
4				ln(x)		Quantile
5		What is the lowest reasonable estimate?		Error: proportion must be >0		0.5
6		What is the highest reasonable estimate?		Error: proportion must be >0		0.5
7		What is your central estimate?		Error: proportion must be >0		0.5
8		How confidence are you that the true mean is between your low and high estimates?		Error: Confidence should be >50		
9		(Confidence should be a number greater than 50 and less than 100)				
10					x	ln(x)
11					#N/A	#N/A
12					#N/A	#N/A
13					#N/A	#N/A
14					#N/A	#N/A
15					#N/A	#N/A
16					#N/A	#N/A
17					#N/A	#N/A
18					#N/A	#N/A
19					#N/A	#N/A
20					#N/A	#N/A
21					#N/A	#N/A
22					#N/A	#N/A
23					#N/A	#N/A
24					#N/A	#N/A
25					#N/A	#N/A
26					#N/A	#N/A
27					#N/A	#N/A
28					#N/A	#N/A
29					#N/A	#N/A
30					#N/A	#N/A
31					#N/A	#N/A
32					#N/A	#N/A
33					#N/A	#N/A
34					#N/A	#N/A
35					#N/A	#N/A
36					#N/A	#N/A

	G	H	I	J
1				
2				
3	-normal uncertainty distribution			
4	IPDF			
5	0	#N/A	mean	#N/A
6	0	#N/A	sd	#N/A
7	0		min	#N/A
8			max	#N/A
9			delta	#N/A
10	Npdf	pdf		
11	#N/A	#N/A		
12	#N/A	#N/A		
13	#N/A	#N/A		
14	#N/A	#N/A		
15	#N/A	#N/A		
16	#N/A	#N/A		
17	#N/A	#N/A		
18	#N/A	#N/A		
19	#N/A	#N/A		
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21	#N/A	#N/A		
22	#N/A	#N/A		
23	#N/A	#N/A		
24	#N/A	#N/A		
25	#N/A	#N/A		
26	#N/A	#N/A		
27	#N/A	#N/A		
28	#N/A	#N/A		
29	#N/A	#N/A		
30	#N/A	#N/A		
31	#N/A	#N/A		
32	#N/A	#N/A		
33	#N/A	#N/A		
34	#N/A	#N/A		
35	#N/A	#N/A		
36	#N/A	#N/A		

	A	B	C	D	E	F
1		Consider your response to question 2, regarding exposure through proximity in an enclosed space by RSM scientists. The new guidance and protocols consist of: restriction of fieldwork to people without symptoms and without contact with someone who had symptoms of COVID-19 in the last 14 days; proper training and compliance protocols for the use of PPE; proper use of Tyvek or other dedicated clothing; proper use of an N95 respirator; and proper use of gloves for handling bats. In these questions, please assume that the biologists have proper training, have access to PPE, and are using it appropriately.				
2	Q10	10. By what proportion should this exposure probability be multiplied if the new guidance and protocols are put into place?				
3						Assume: log
4				ln(x)		Quantile
5		What is the lowest reasonable estimate?		Error: proportion must be >0		0.5
6		What is the highest reasonable estimate?		Error: proportion must be >0		0.5
7		What is your central estimate?		Error: proportion must be >0		0.5
8		How confidence are you that the true mean is between your low and high estimates?		Error: Confidence should be >50		
9		(Confidence should be a number greater than 50 and less than 100)				
10					x	ln(x)
11					#N/A	#N/A
12					#N/A	#N/A
13					#N/A	#N/A
14					#N/A	#N/A
15					#N/A	#N/A
16					#N/A	#N/A
17					#N/A	#N/A
18					#N/A	#N/A
19					#N/A	#N/A
20					#N/A	#N/A
21					#N/A	#N/A
22					#N/A	#N/A
23					#N/A	#N/A
24					#N/A	#N/A
25					#N/A	#N/A
26					#N/A	#N/A
27					#N/A	#N/A
28					#N/A	#N/A
29					#N/A	#N/A
30					#N/A	#N/A
31					#N/A	#N/A
32					#N/A	#N/A
33					#N/A	#N/A
34					#N/A	#N/A
35					#N/A	#N/A
36					#N/A	#N/A

	G	H	I	J
1				
2				
3	-normal uncertainty distribution			
4	IPDF			
5	0	#N/A	mean	#N/A
6	0	#N/A	sd	#N/A
7	0		min	#N/A
8			max	#N/A
9			delta	#N/A
10	Npdf	pdf		
11	#N/A	#N/A		
12	#N/A	#N/A		
13	#N/A	#N/A		
14	#N/A	#N/A		
15	#N/A	#N/A		
16	#N/A	#N/A		
17	#N/A	#N/A		
18	#N/A	#N/A		
19	#N/A	#N/A		
20	#N/A	#N/A		
21	#N/A	#N/A		
22	#N/A	#N/A		
23	#N/A	#N/A		
24	#N/A	#N/A		
25	#N/A	#N/A		
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28	#N/A	#N/A		
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30	#N/A	#N/A		
31	#N/A	#N/A		
32	#N/A	#N/A		
33	#N/A	#N/A		
34	#N/A	#N/A		
35	#N/A	#N/A		
36	#N/A	#N/A		

	A	B	C	D	E	F
1		Consider your response to question 3, regarding exposure through proximity in an *un*enclosed space by RSM scientists. The new guidance and protocols consist of: restriction of fieldwork to people without symptoms and without contact with someone who had symptoms of COVID-19 in the last 14 days; proper training and compliance protocols for the use of PPE; proper use of Tyvek or other dedicated clothing; proper use of an N95 respirator; and proper use of gloves for handling bats. In these questions, please assume that the biologists have proper training, have access to PPE, and are using it appropriately.				
2	Q11	11. By what proportion should this exposure probability be multiplied if the new guidance and protocols are put into place?				
3						Assume: log
4				ln(x)		Quantile
5		What is the lowest reasonable estimate?		Error: proportion must be >0		0.5
6		What is the highest reasonable estimate?		Error: proportion must be >0		0.5
7		What is your central estimate?		Error: proportion must be >0		0.5
8		How confidence are you that the true mean is between your low and high estimates?		Error: Confidence should be >50		
9		(Confidence should be a number greater than 50 and less than 100)				
10					x	ln(x)
11					#N/A	#N/A
12					#N/A	#N/A
13					#N/A	#N/A
14					#N/A	#N/A
15					#N/A	#N/A
16					#N/A	#N/A
17					#N/A	#N/A
18					#N/A	#N/A
19					#N/A	#N/A
20					#N/A	#N/A
21					#N/A	#N/A
22					#N/A	#N/A
23					#N/A	#N/A
24					#N/A	#N/A
25					#N/A	#N/A
26					#N/A	#N/A
27					#N/A	#N/A
28					#N/A	#N/A
29					#N/A	#N/A
30					#N/A	#N/A
31					#N/A	#N/A
32					#N/A	#N/A
33					#N/A	#N/A
34					#N/A	#N/A
35					#N/A	#N/A
36					#N/A	#N/A

	G	H	I	J
1				
2				
3	-normal uncertainty distribution			
4	IPDF			
5	0	#N/A	mean	#N/A
6	0	#N/A	sd	#N/A
7	0		min	#N/A
8			max	#N/A
9			delta	#N/A
10	Npdf	pdf		
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33	#N/A	#N/A		
34	#N/A	#N/A		
35	#N/A	#N/A		
36	#N/A	#N/A		

	A	B	C	D	E	F	G	H	I	J	K	L
1	**Open-ended response**. Are there reasons to believe that the proportional change in the handling and proximity exposure probabilities for wildlife rehabilitators (WR) and wildlife control operators (WC), owing to the same protocol guidance, would be different than for scientists involved in research, survey, and management (RSM)? Explain.											
2												
3												
4												
5												
6												
7												
8												
9												
10												
11												
12												
13												
14												
15												

	A	B	C	D	E	F
1						
2	Q13	13. What is R_0 for SARS-CoV-2 in little brown bats during the active season? That is, for each infected little brown bat, how many other little brown bats would become infected with the virus? Note that R_0 can be less than 1, in which case you can think of it as the probability that an infected bat will infect one other bat, or it can be greater than 1, in which case each infected bat infects more than one other bat. Note that the spreadsheet calculates from your responses (in cell D13) the probability that R_0 is greater than 1.				
3						Assume: log
4				ln(x)		Quantile
5		What is the lowest reasonable estimate?		Error: R0 must be >0		0.5
6		What is the highest reasonable estimate?		Error: R0 must be >0		0.5
7		What is your central estimate?		Error: R0 must be >0		0.5
8		How confidence are you that the true mean is between your low and high estimates?		Error: Confidence should be >50		
9		(Confidence should be a number between 50 and 100)				
10					x	ln(x)
11					#N/A	#N/A
12			Based on your responses:		#N/A	#N/A
13			$p(R_0>1)$	#N/A	#N/A	#N/A
14					#N/A	#N/A
15					#N/A	#N/A
16					#N/A	#N/A
17					#N/A	#N/A
18					#N/A	#N/A
19					#N/A	#N/A
20					#N/A	#N/A
21					#N/A	#N/A
22					#N/A	#N/A
23					#N/A	#N/A
24					#N/A	#N/A
25					#N/A	#N/A
26					#N/A	#N/A
27					#N/A	#N/A
28					#N/A	#N/A
29					#N/A	#N/A
30					#N/A	#N/A
31					#N/A	#N/A
32					#N/A	#N/A
33					#N/A	#N/A
34					#N/A	#N/A
35					#N/A	#N/A
36					#N/A	#N/A

	G	H	I	J
1				
2				
3	-normal uncertainty distribution			
4	IPDF			
5	0	#N/A	mean	#N/A
6	0	#N/A	sd	#N/A
7	0		min	#N/A
8			max	#N/A
9			delta	#N/A
10	Npdf	pdf		
11	#N/A	#N/A		
12	#N/A	#N/A		
13	#N/A	#N/A		
14	#N/A	#N/A		
15	#N/A	#N/A		
16	#N/A	#N/A		
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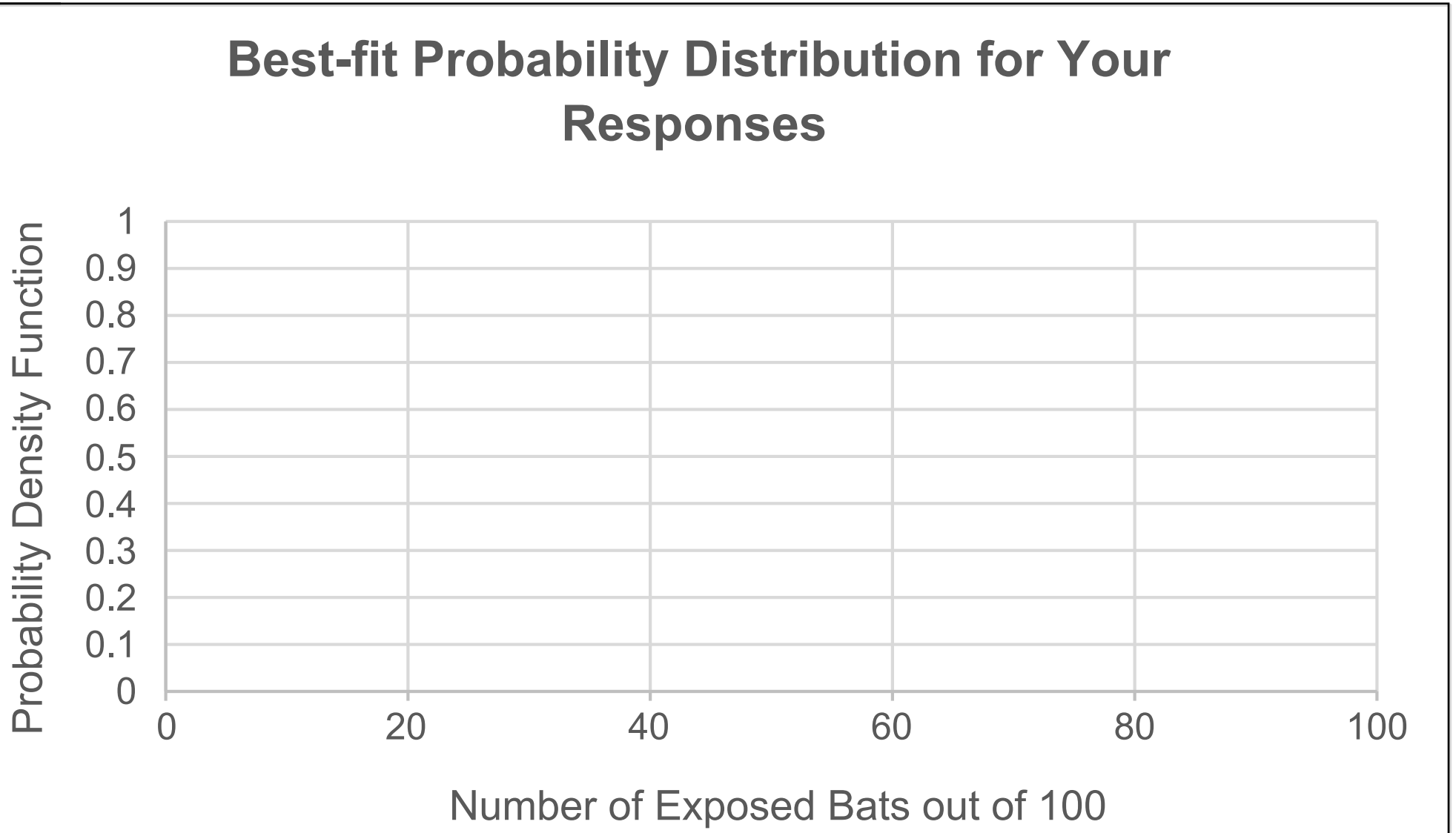
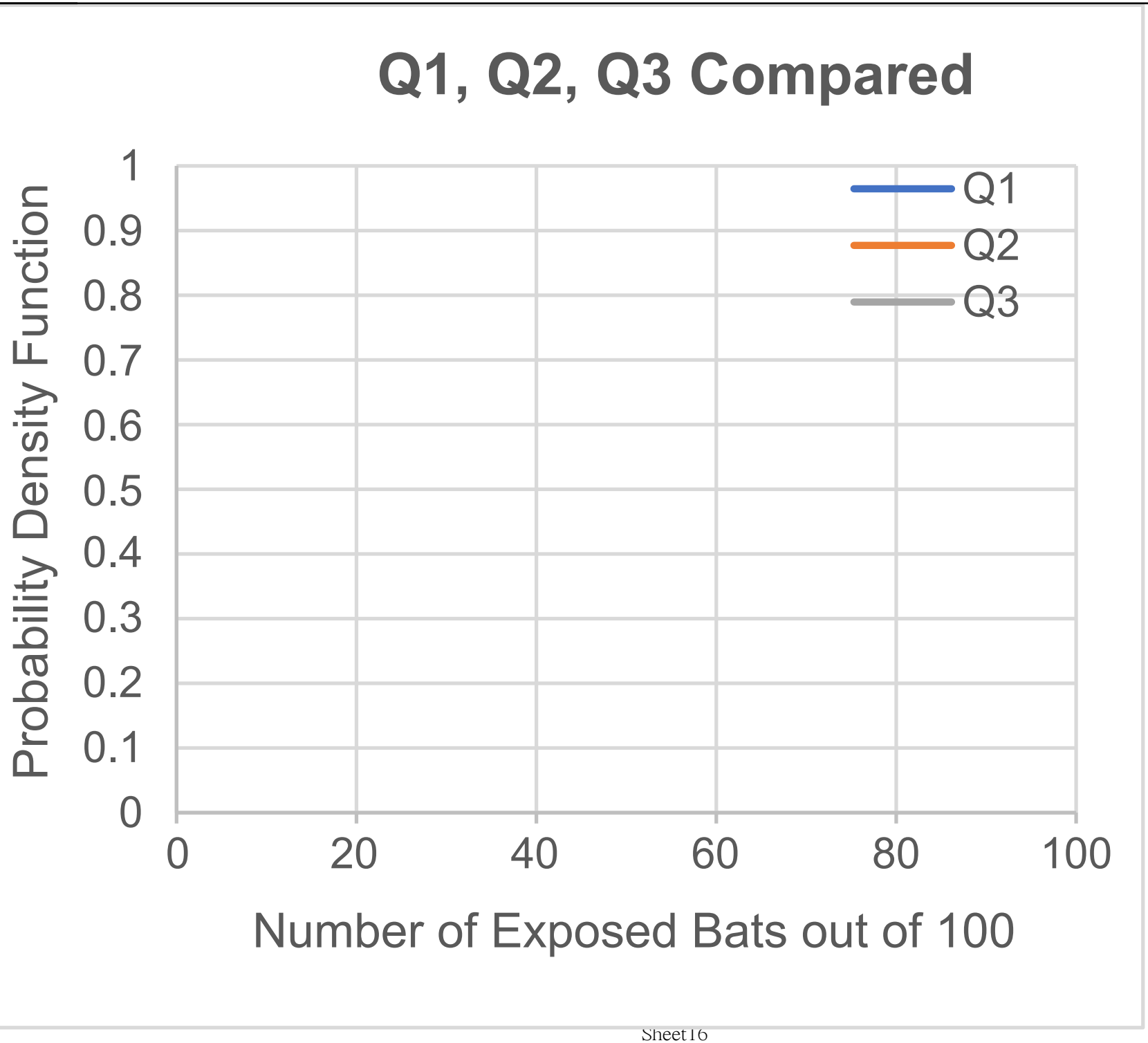
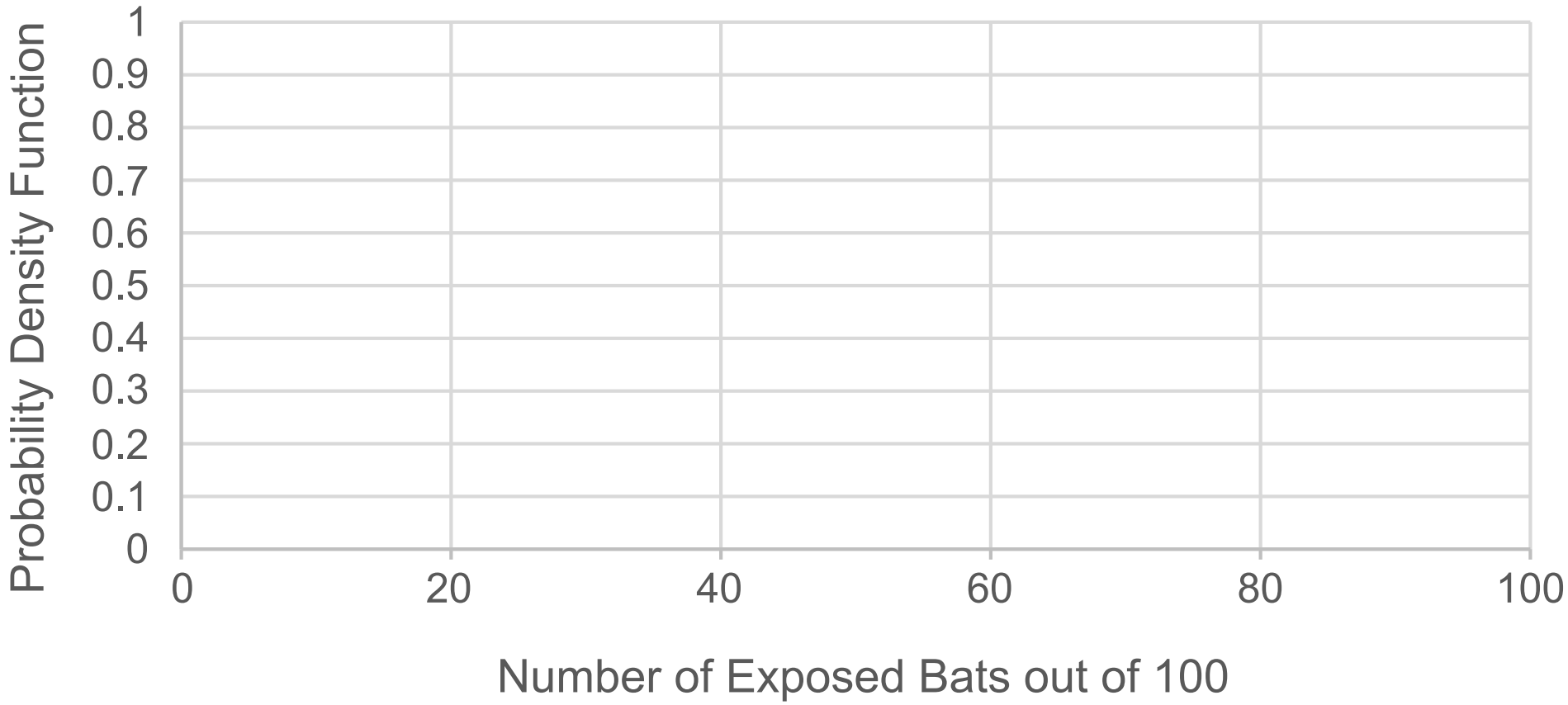
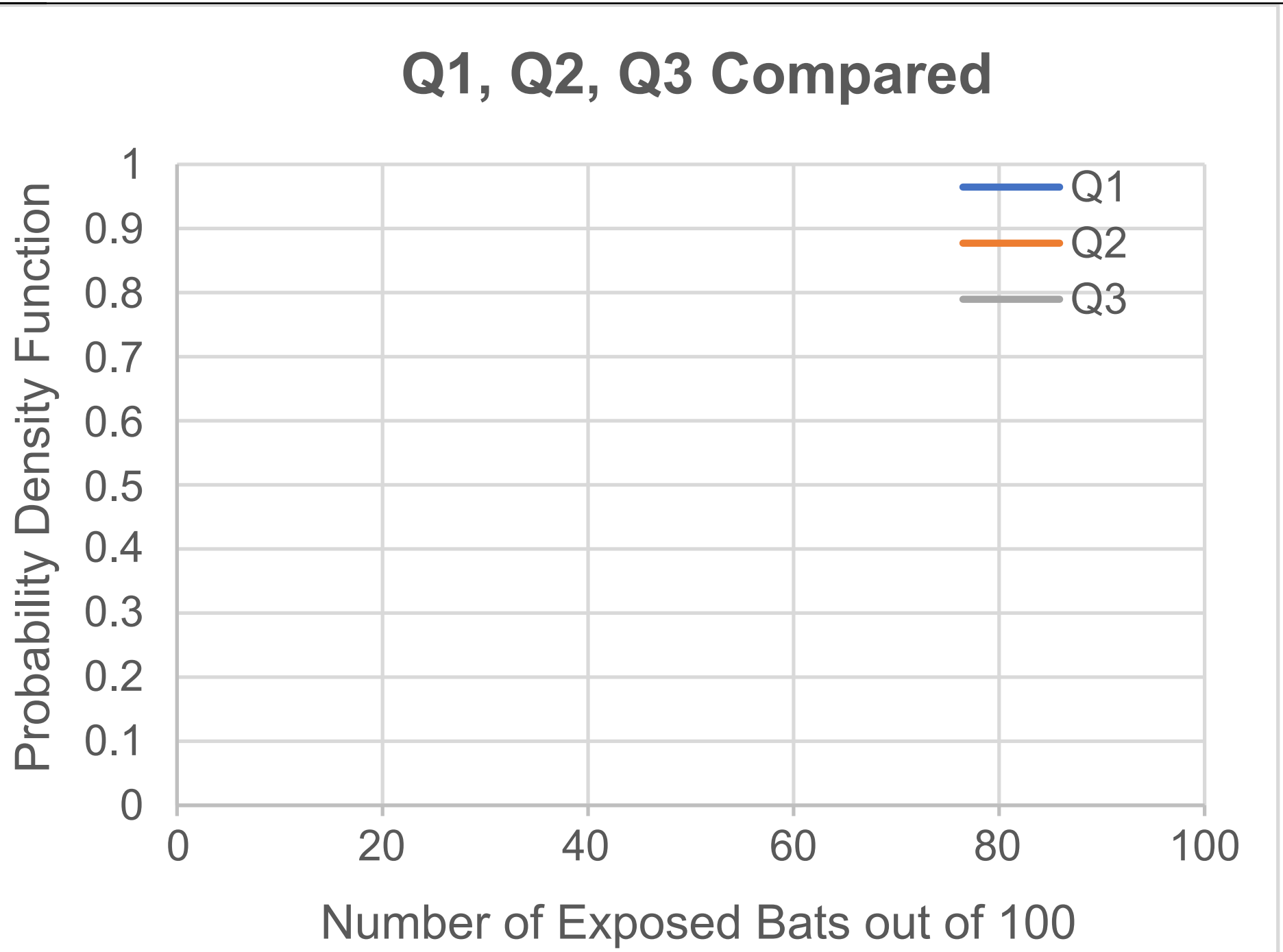
19	#N/A	#N/A		
20	#N/A	#N/A		
21	#N/A	#N/A		
22	#N/A	#N/A		
23	#N/A	#N/A		
24	#N/A	#N/A		
25	#N/A	#N/A		
26	#N/A	#N/A		
27	#N/A	#N/A		
28	#N/A	#N/A		
29	#N/A	#N/A		
30	#N/A	#N/A		
31	#N/A	#N/A		
32	#N/A	#N/A		
33	#N/A	#N/A		
34	#N/A	#N/A		
35	#N/A	#N/A		
36	#N/A	#N/A		

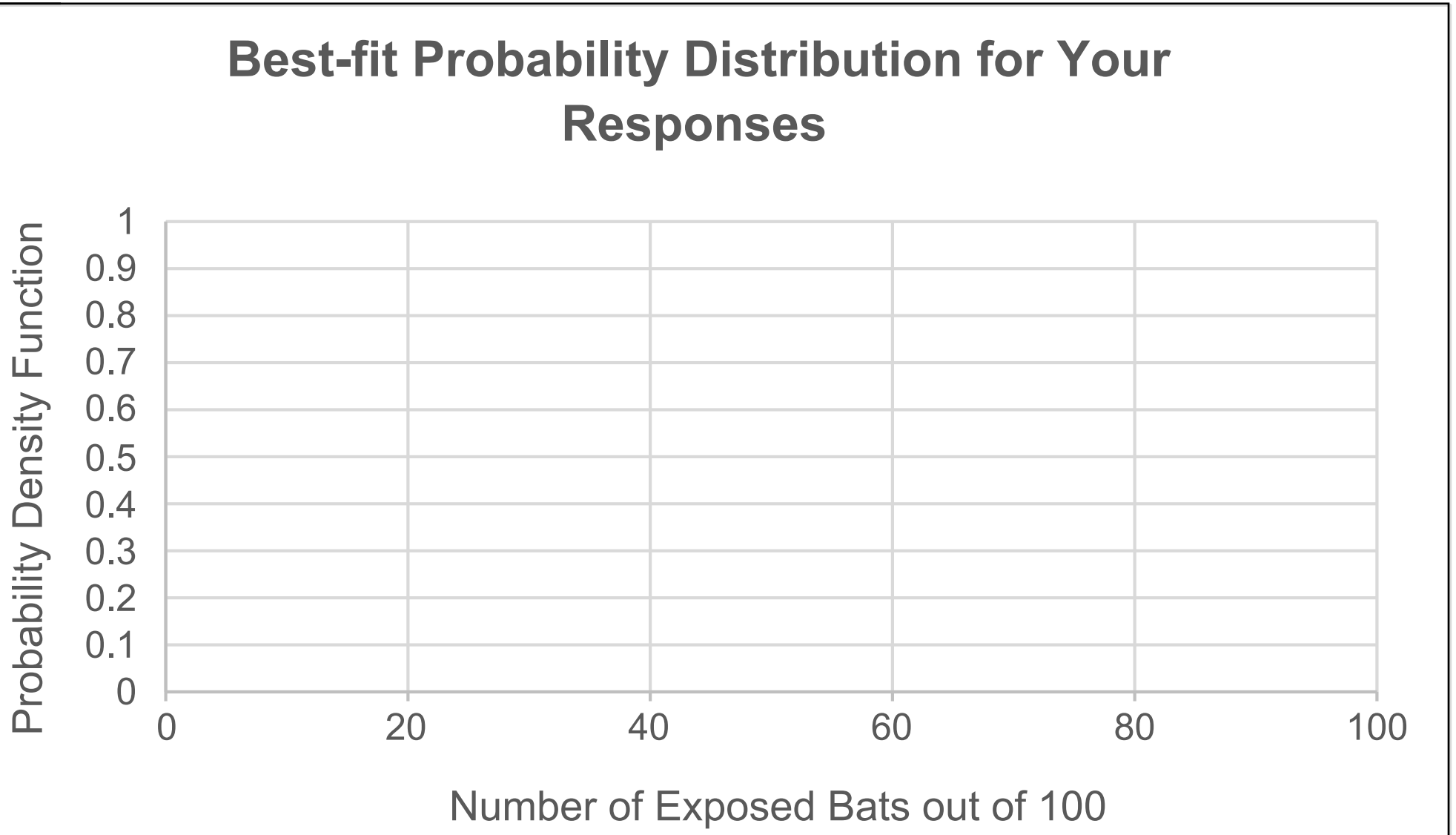
	A	B	C	D	E	F	G	H	I
1									
2									
3			lo	hi	best	CI	distn	mean	sd
4		Question 1	0	0	0	0	logit-normal	#N/A	#N/A
5		Question 2	0	0	0	0	logit-normal	#N/A	#N/A
6		Question 3	0	0	0	0	logit-normal	#N/A	#N/A
7		Question 4	0	0	0	0	logit-normal	#N/A	#N/A
8		Question 5	0	0	0	0	logit-normal	#N/A	#N/A
9		Question 6	0	0	0	0	logit-normal	#N/A	#N/A
10		Question 7	0	0	0	0	logit-normal	#N/A	#N/A
11		Question 8	0	0	0	0	logit-normal	#N/A	#N/A
12		Question 9	0	0	0	0	lognormal	#N/A	#N/A
13		Question 10	0	0	0	0	lognormal	#N/A	#N/A
14		Question 11	0	0	0	0	lognormal	#N/A	#N/A
15		Question 13	0	0	0	0	lognormal	#N/A	#N/A

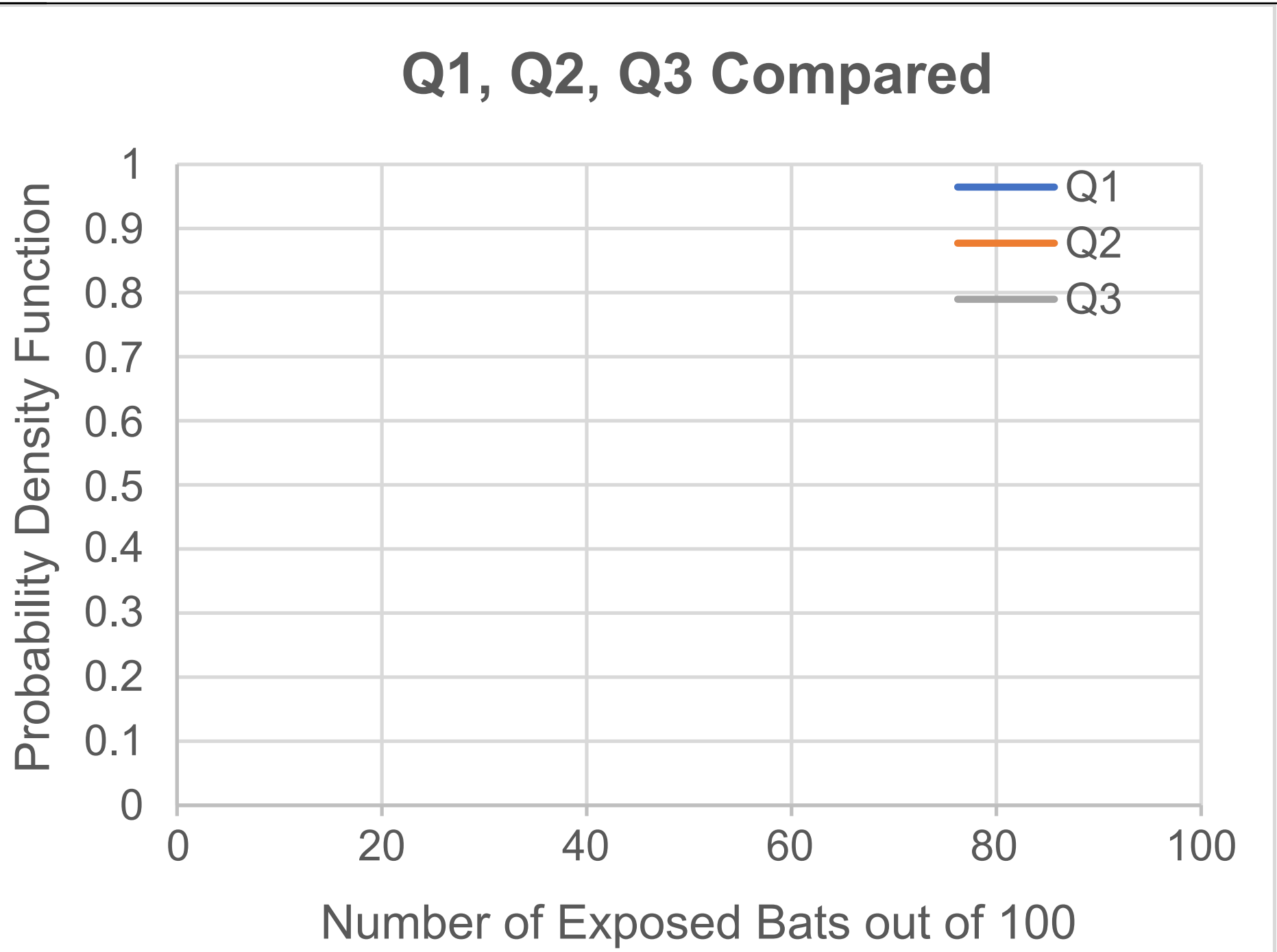

Best-fit Probability Distribution for Your Responses
Probability Density Function
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
20
40
60
80
100
Number of Exposed Bats out of 100

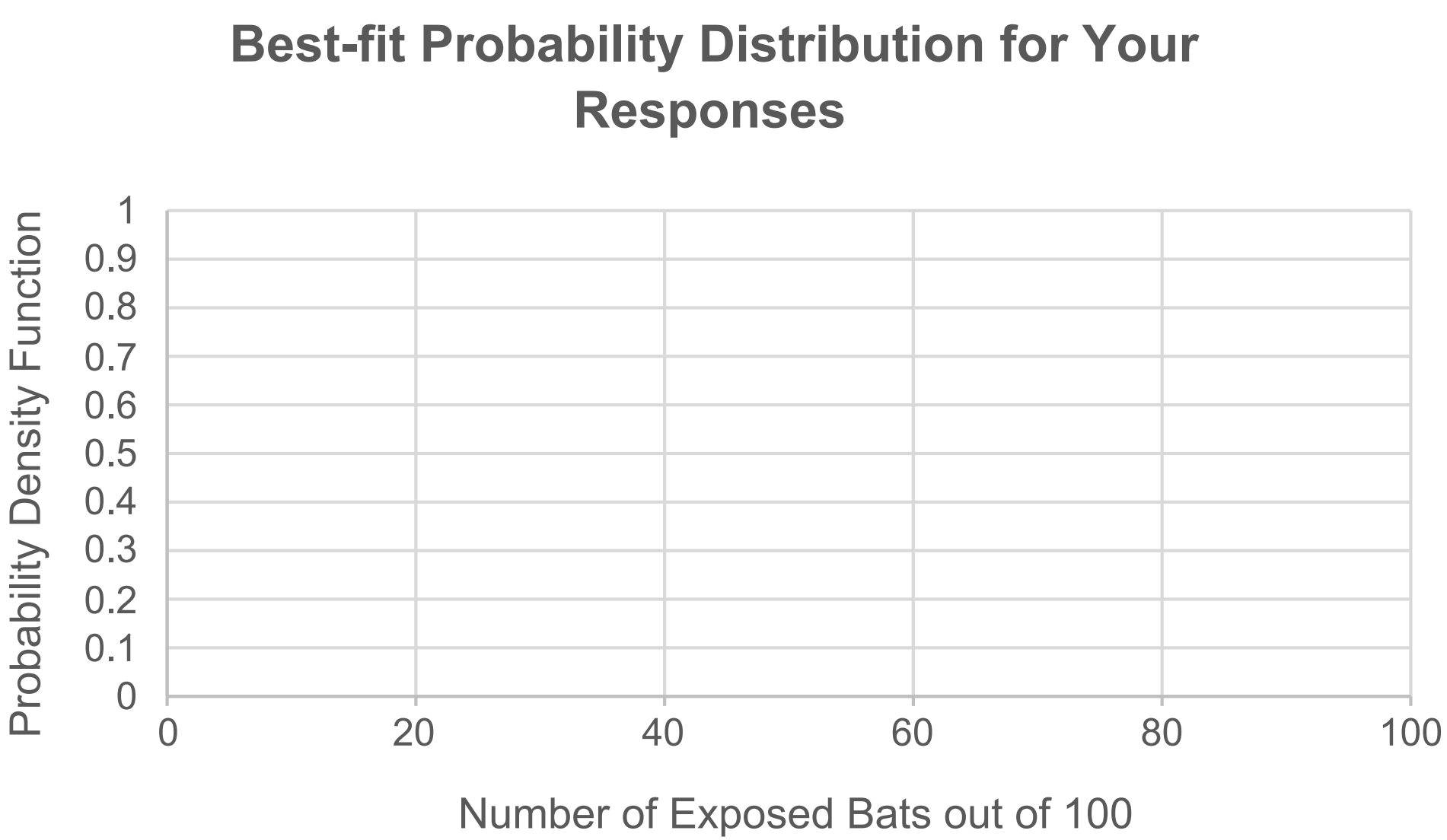

Q1, Q2, Q3 Compared
Probability Density Function
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
20
40
60
80
100
Number of Exposed Bats out of 100
Q1
Q2
Q3

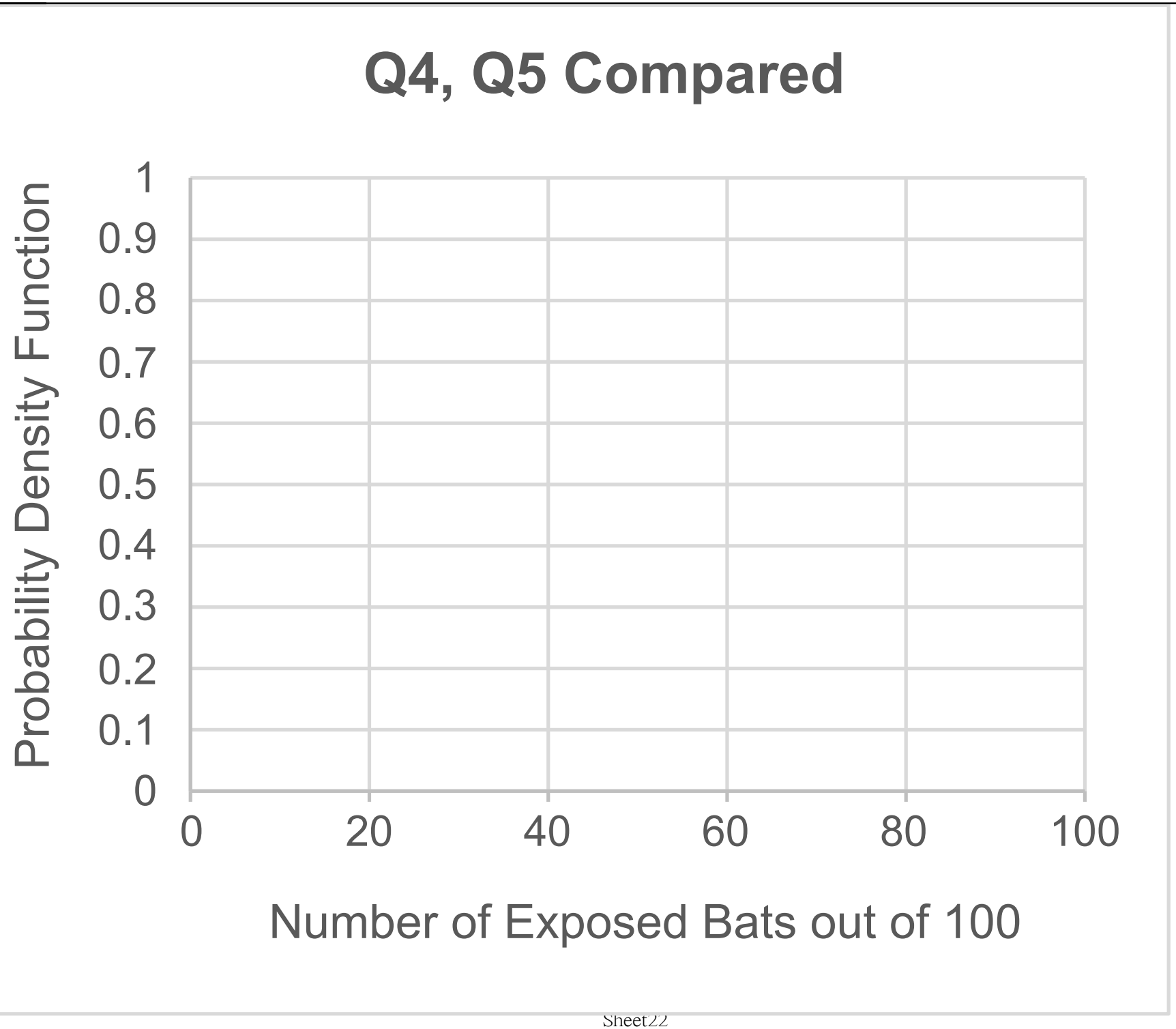

Best-fit Probability Distribution for Your Responses
Probability Density Function
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
20
40
60
80
100
Number of Exposed Bats out of 100


Q1, Q2, Q3 Compared
Probability Density Function
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
20
40
60
80
100
Number of Exposed Bats out of 100
Q1
Q2
Q3


Best-fit Probability Distribution for Your Responses
Probability Density Function
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
20
40
60
80
100
Number of Exposed Bats out of 100


Q1, Q2, Q3 Compared
Probability Density Function
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
20
40
60
80
100
Number of Exposed Bats out of 100
Q1
Q2
Q3


Best-fit Probability Distribution for Your Responses
Probability Density Function
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
20
40
60
80
100
Number of Exposed Bats out of 100


Q4, Q5 Compared
Probability Density Function
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
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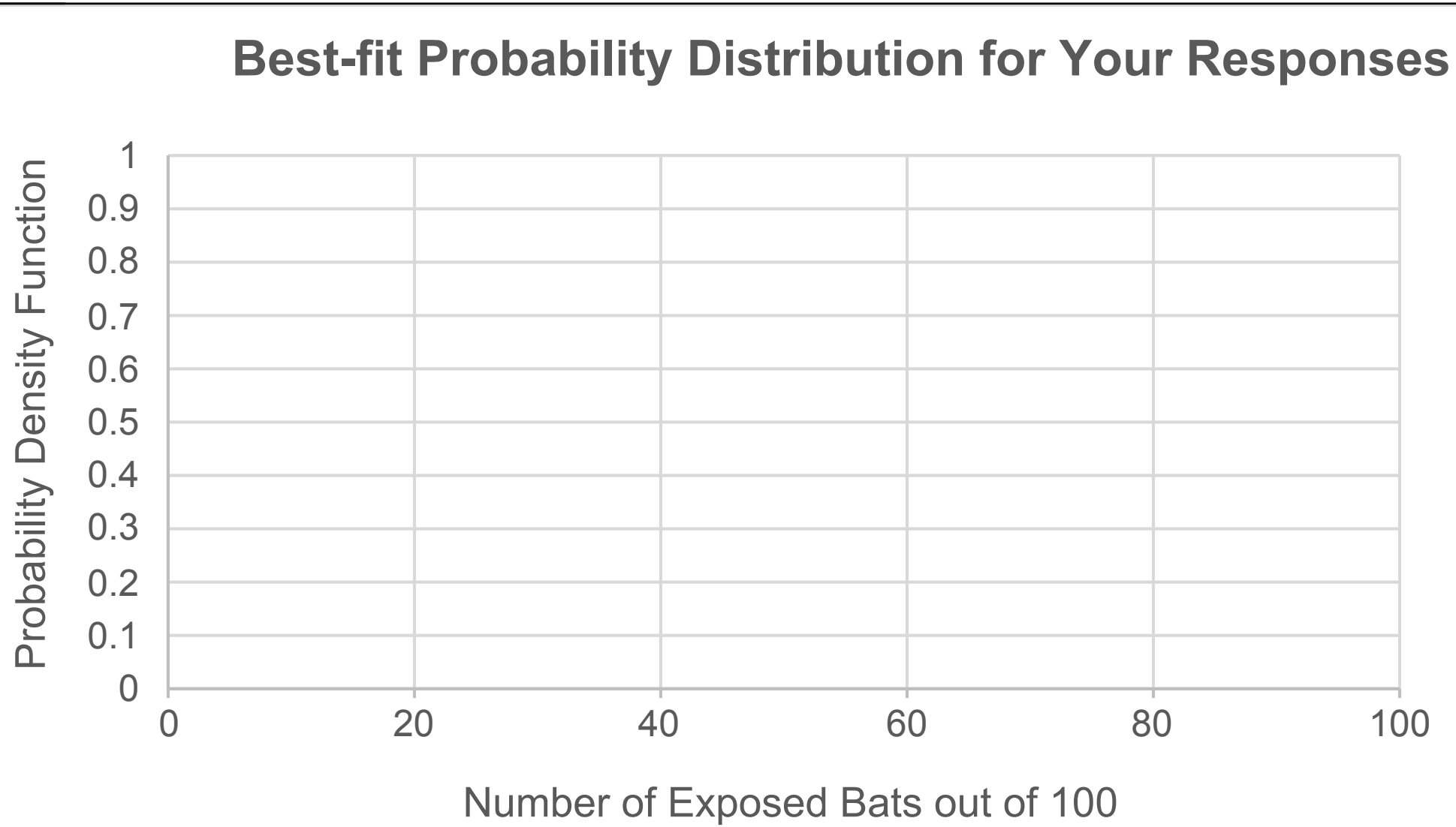
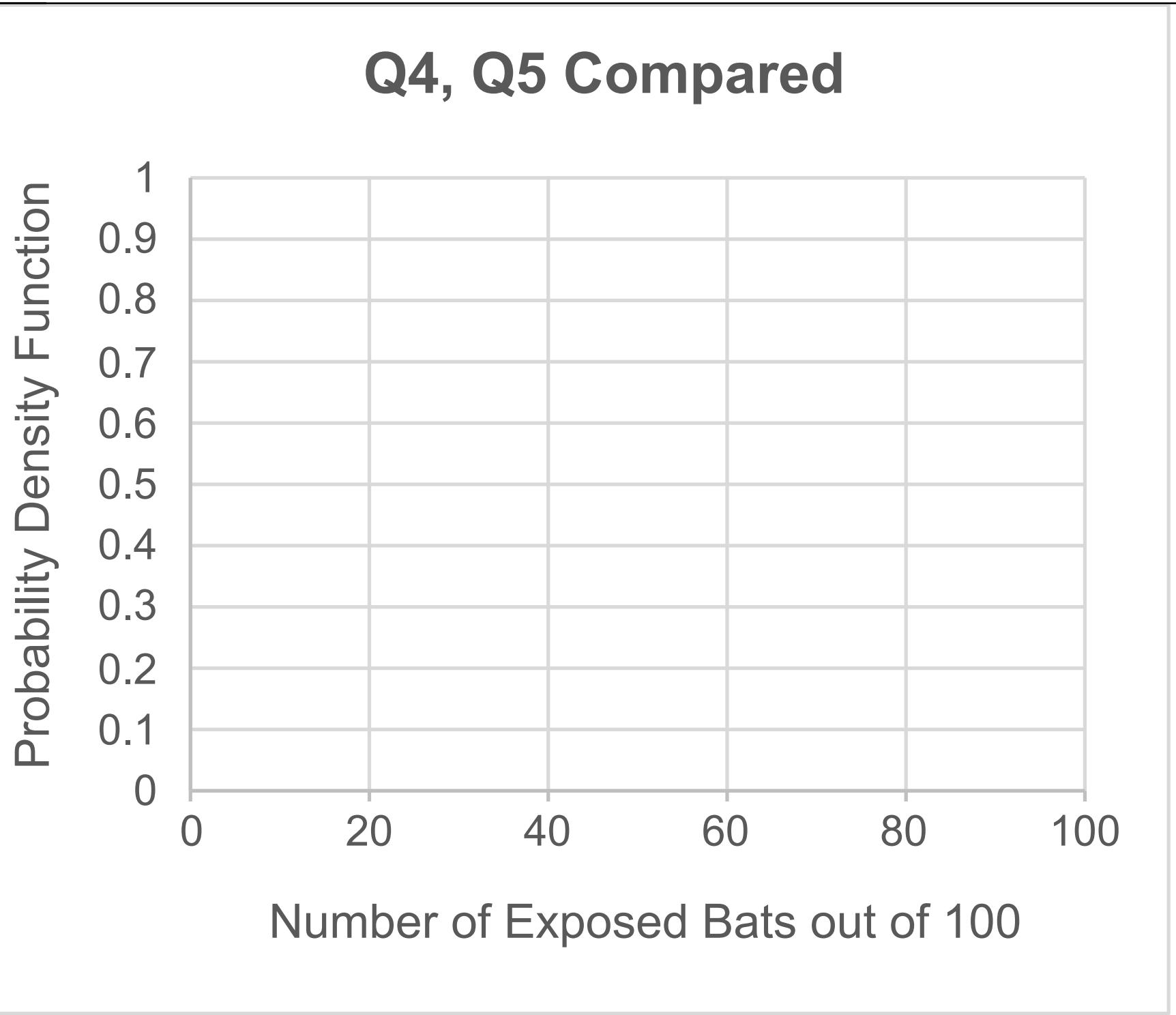
20
40
60
80
100
Number of Exposed Bats out of 100


Best-fit Probability Distribution for Your Responses
Probability Density Function
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
20
40
60
80
100
Number of Exposed Bats out of 100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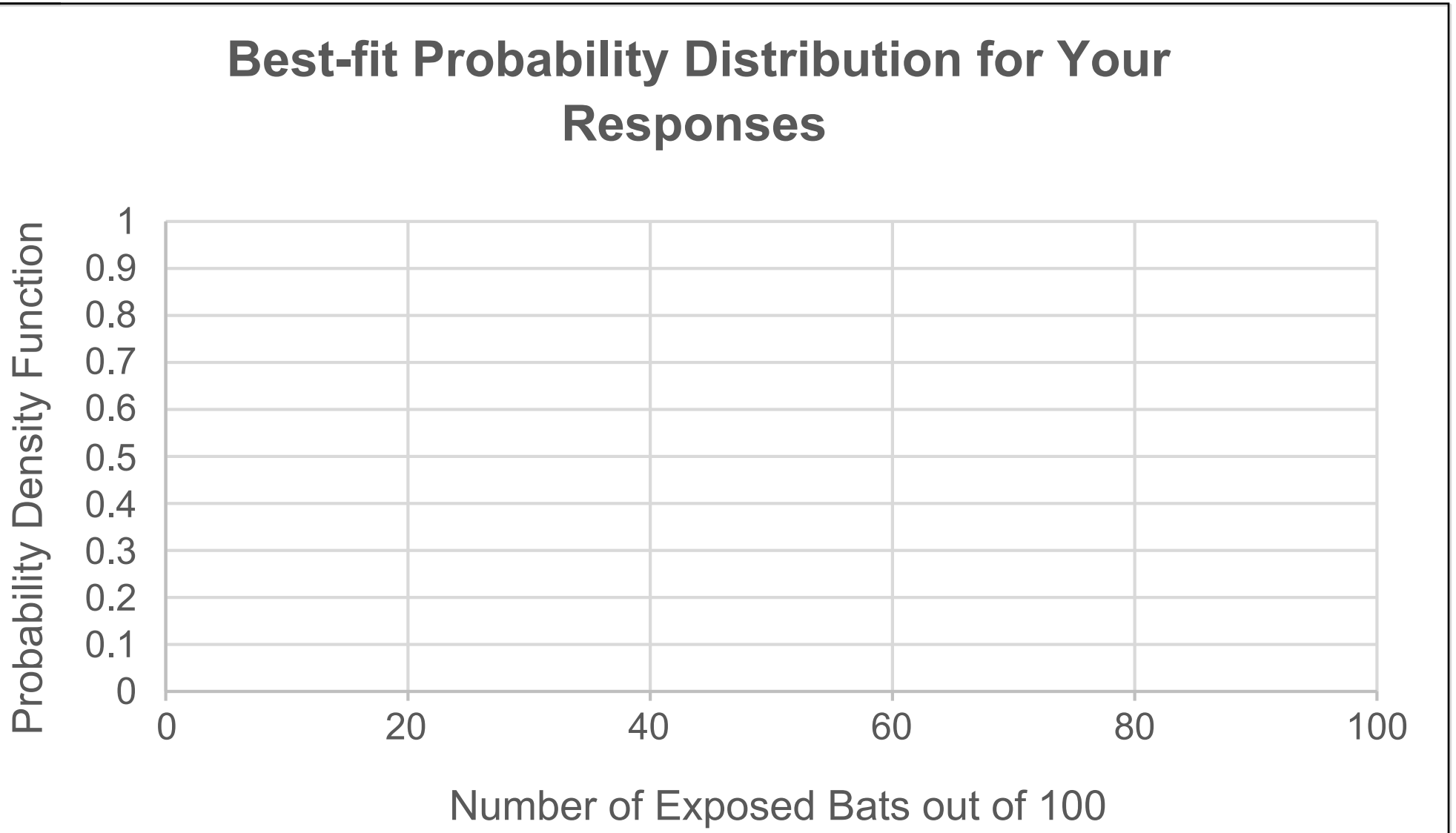
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
20
40
60
80
100
Number of Exposed Bats out of 100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0.8
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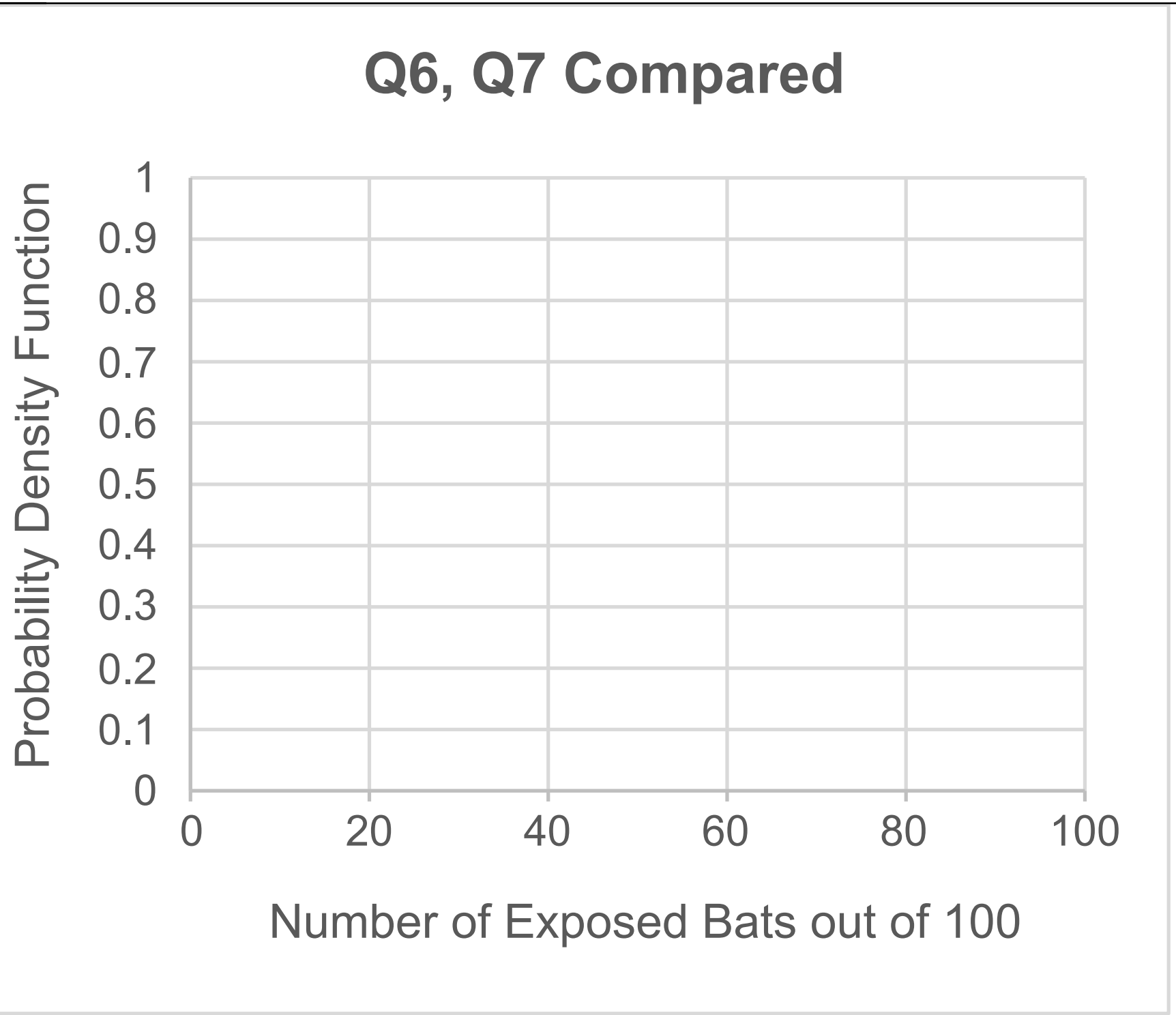
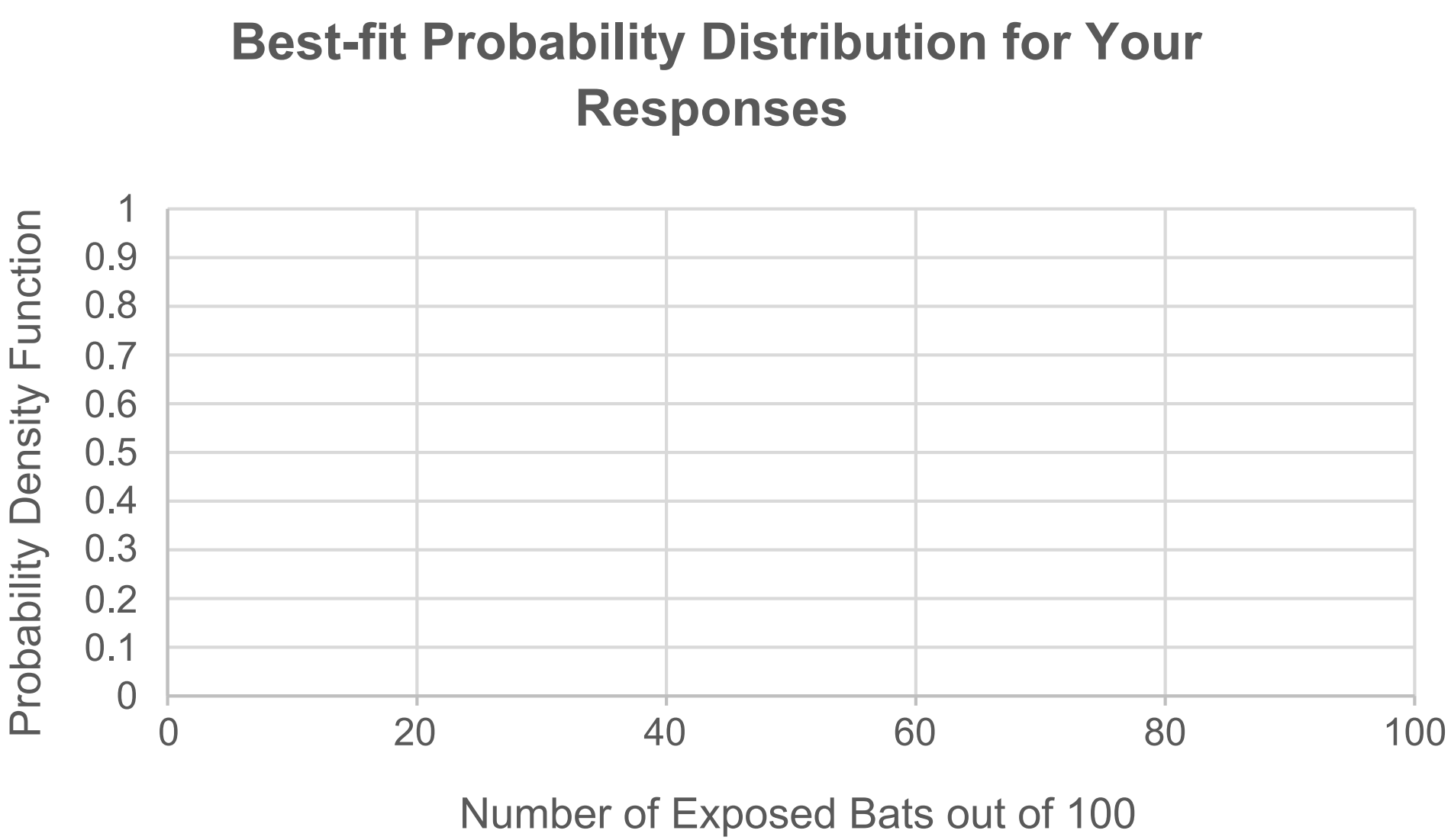
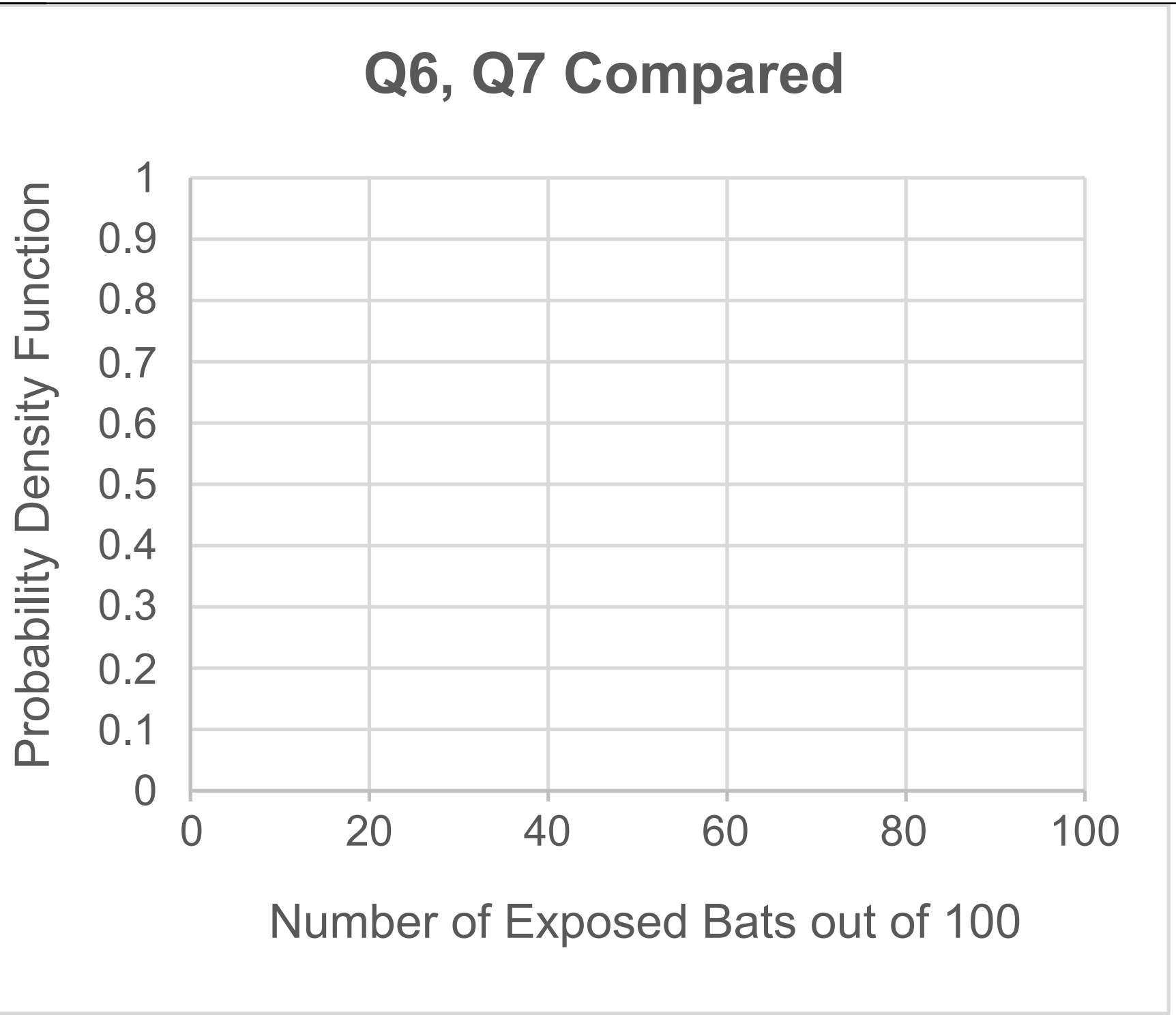
0.6
0.5
0.4
0.3
0.2
0.1
0
0
20
40
60
80
100
Number of Exposed Bats out of 100


Q6, Q7 Compared
Probability Density Function
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
20
40
60
80
100
Number of Exposed Bats out of 100


Best-fit Probability Distribution for Your Responses
Probability Density Function
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
20
40
60
80
100
Number of Exposed Bats out of 100


Q6, Q7 Compared
Probability Density Function
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
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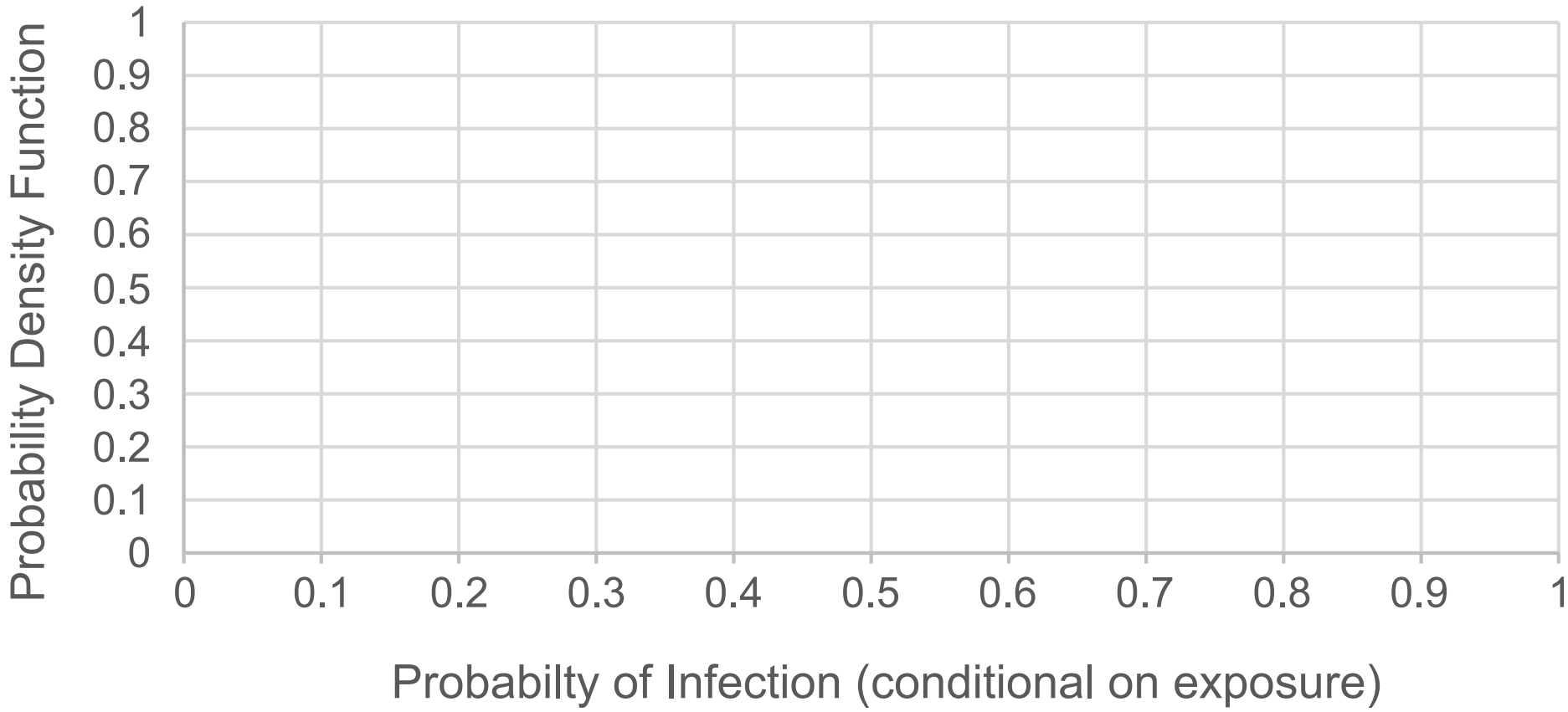
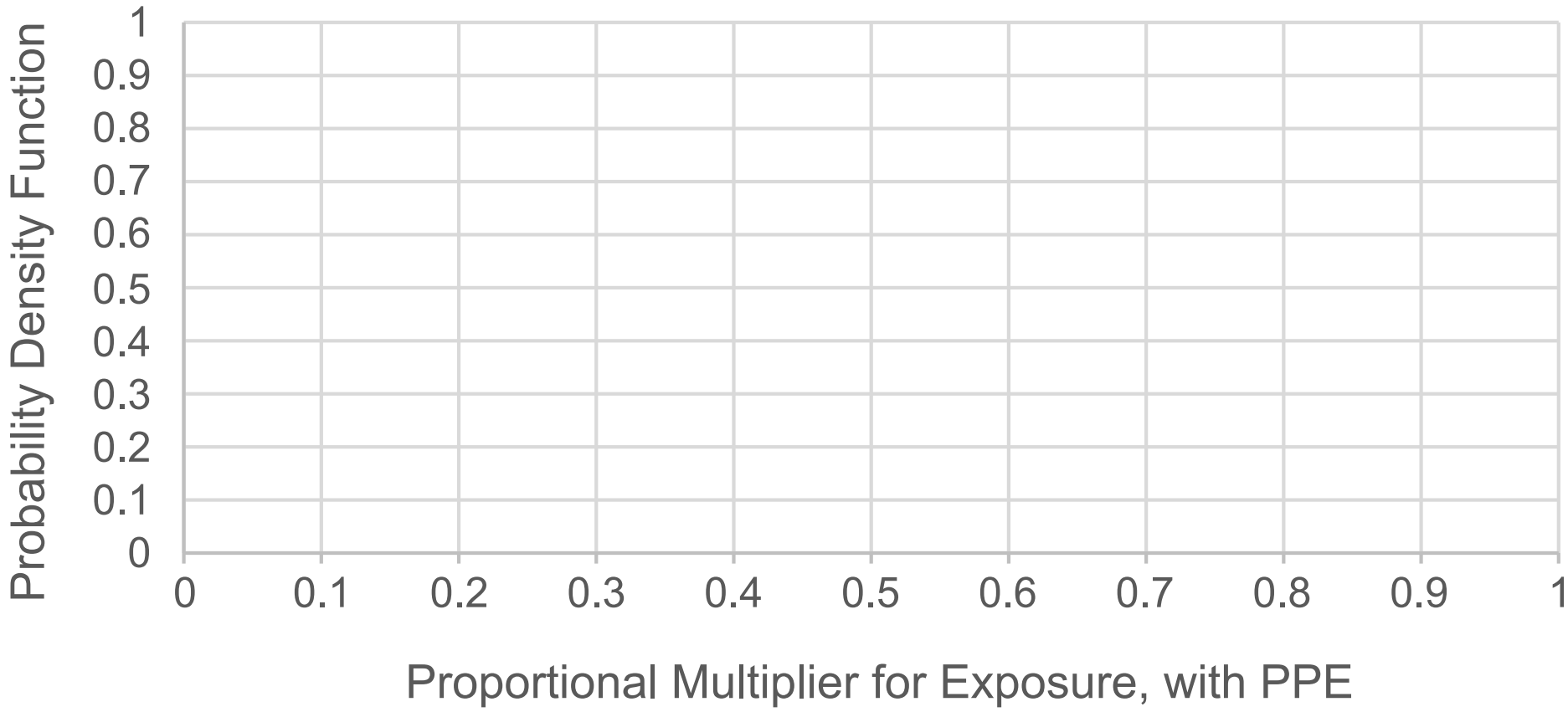
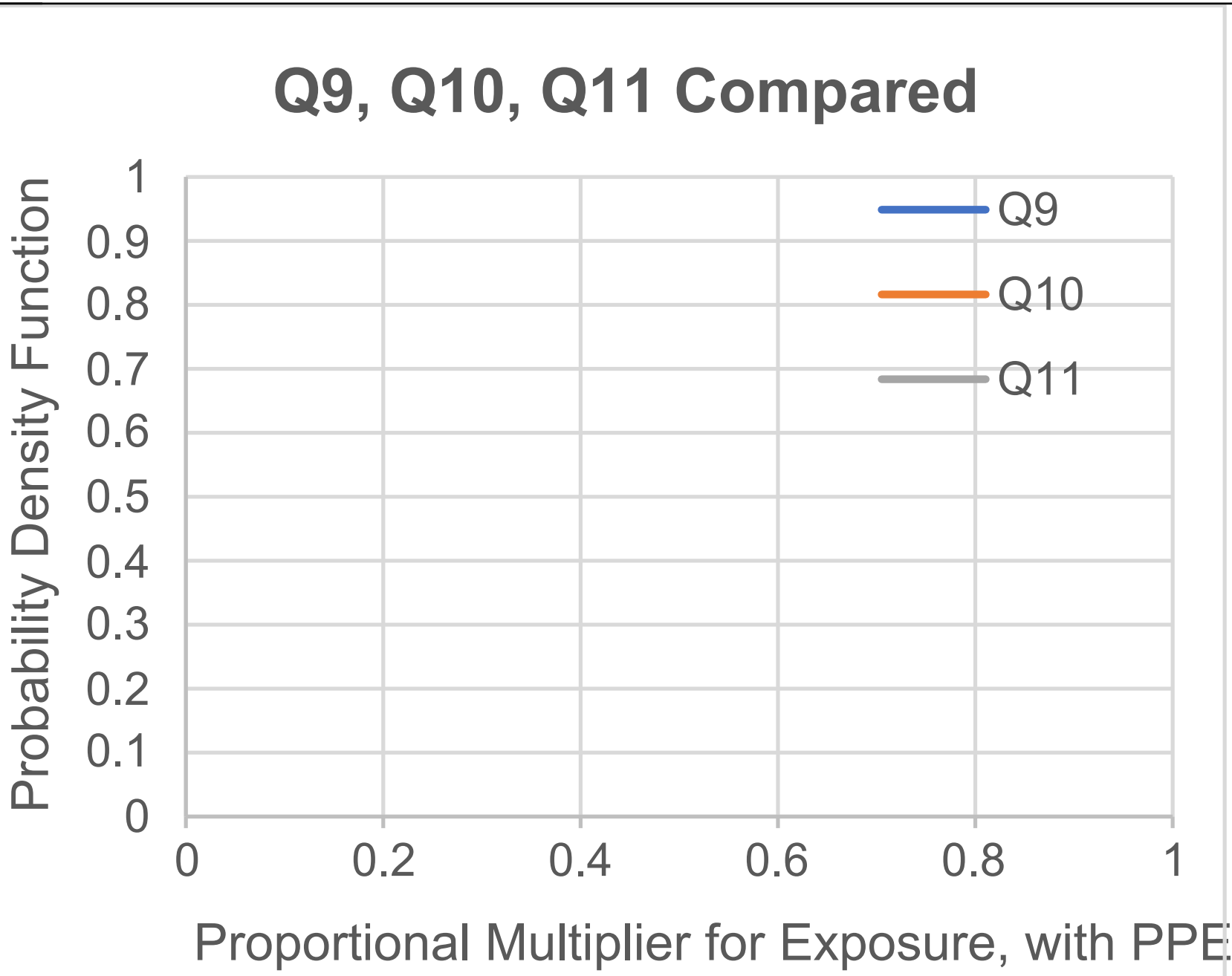
20
40
60
80
100
Number of Exposed Bats out of 100

Best-fit Probability Distribution for Your Responses

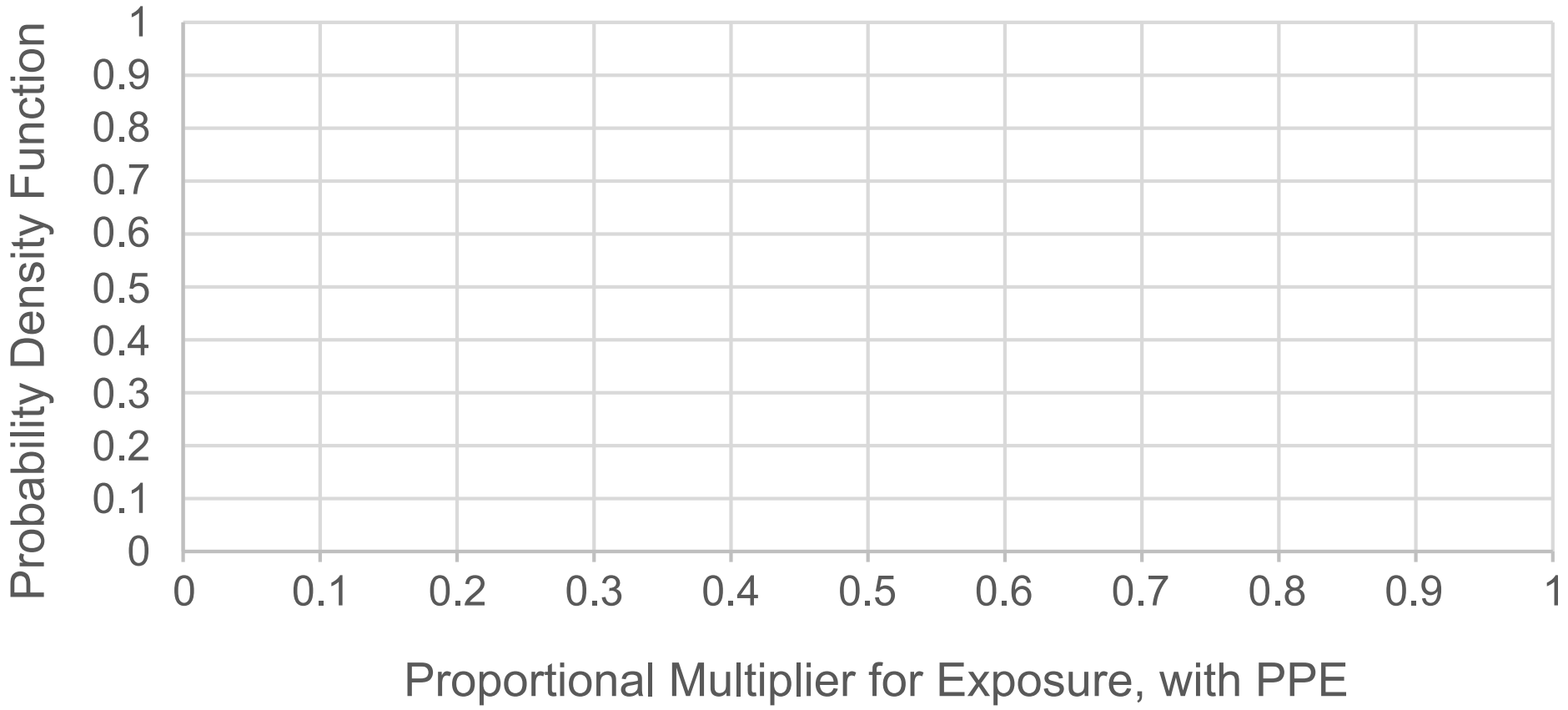


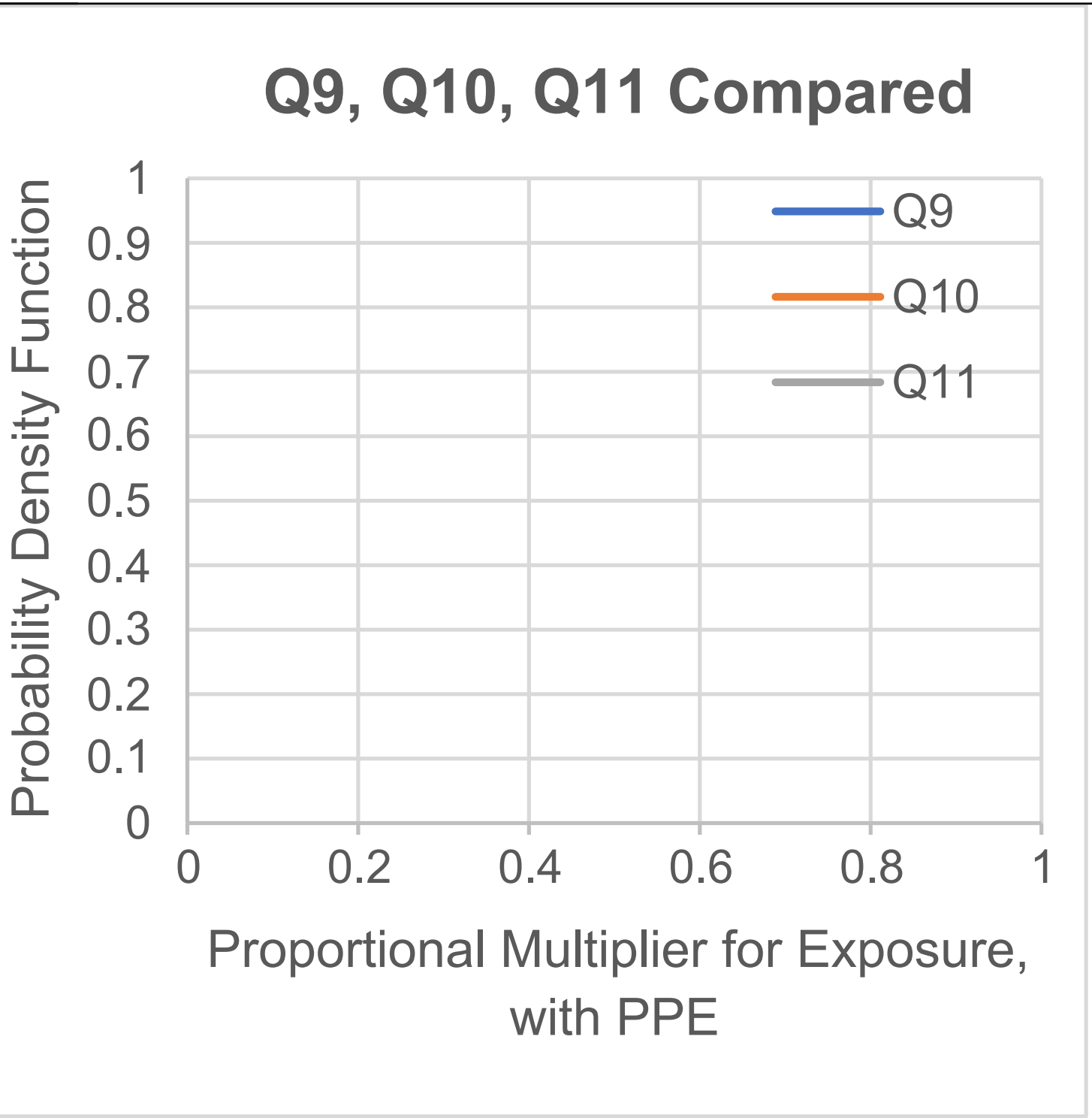
Best-fit Probability Distribution for Your Responses




Q9, Q10, Q11 Compared
Probability Density Function
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
0.2
0.4
0.6
0.8
1
Q9
Q10
Q11
Proportional Multiplier for Exposure, with PPE

Best-fit Probability Distribution for Your Responses




Q9, Q10, Q11 Compared
Probability Density Function
1
0.9
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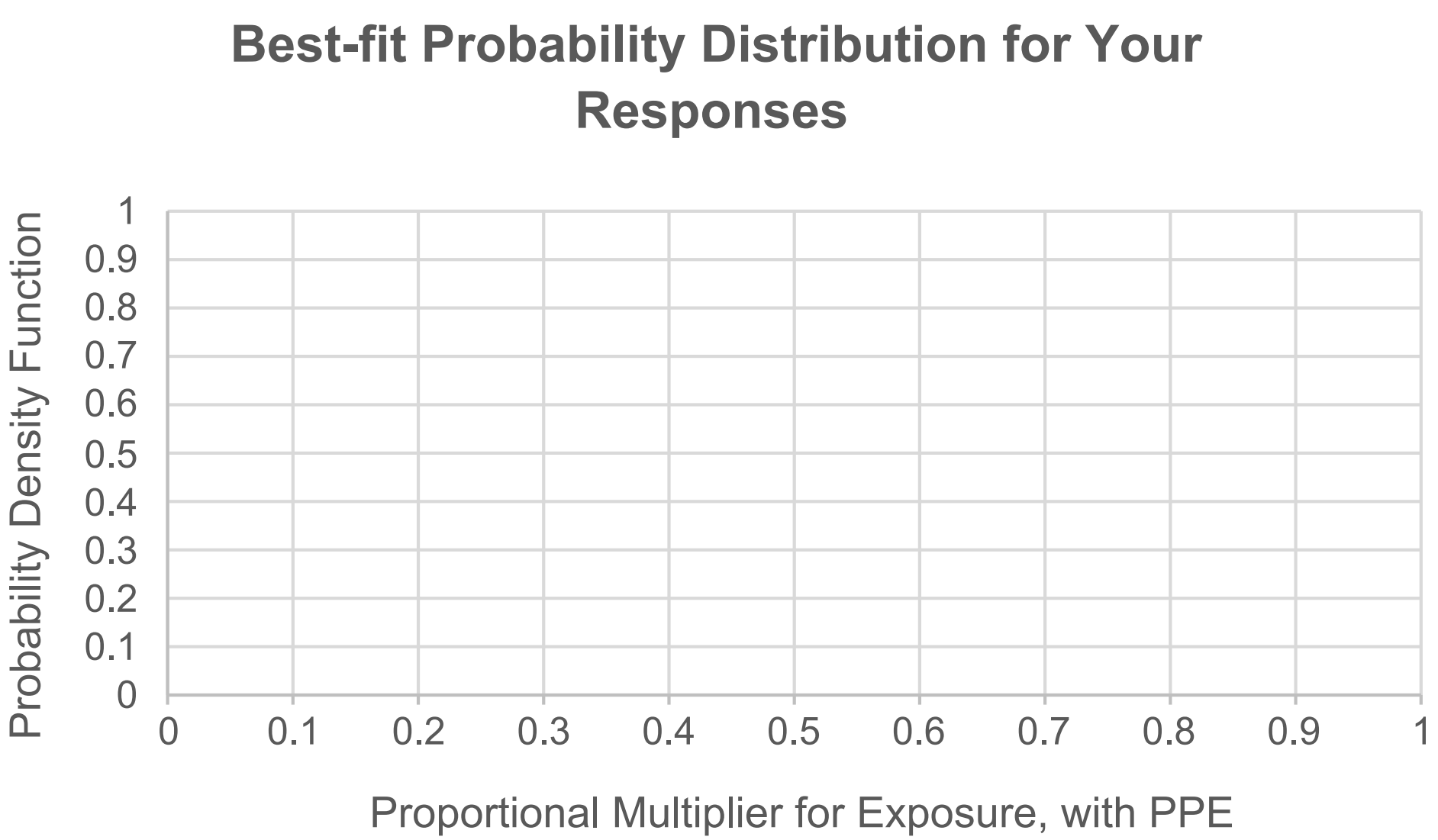
Q9
Q10
Q11
Proportional Multiplier for Exposure, with PPE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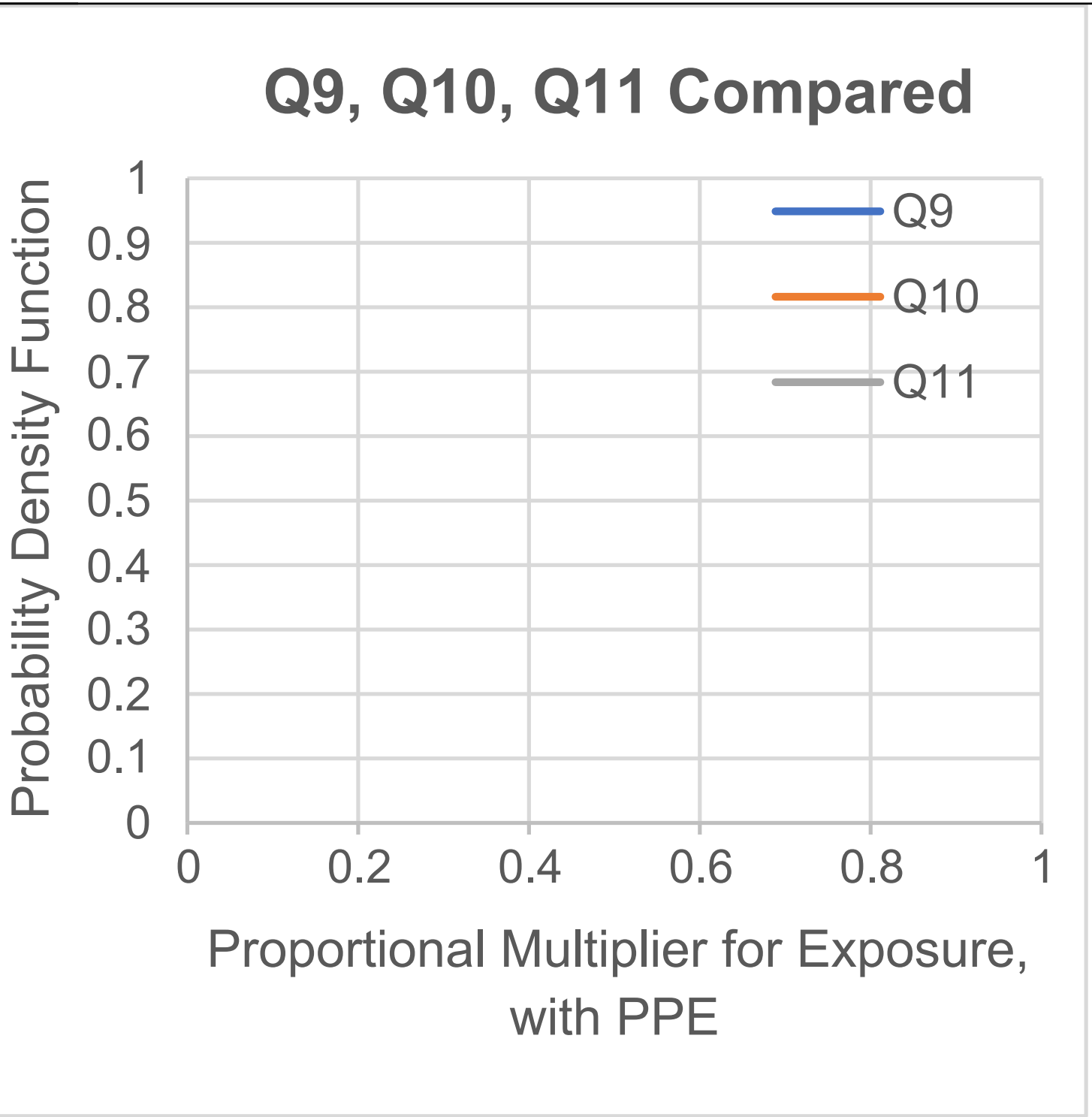
0.9
1
Proportional Multiplier for Exposure, with PPE


Q9, Q10, Q11 Compared
Probability Density Function
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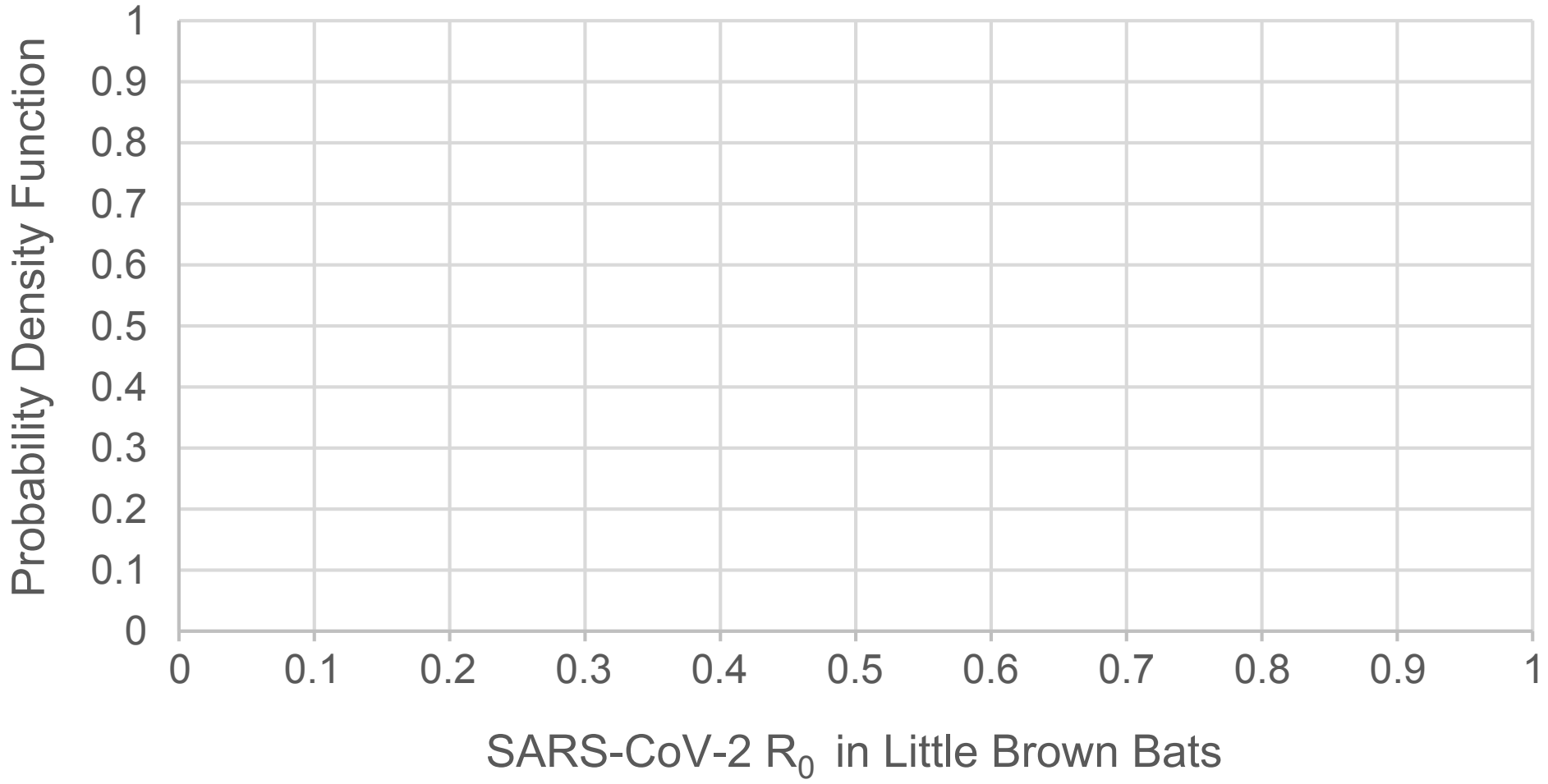
Q9
Q10
Q11
Proportional Multiplier for Exposure, with PPE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0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
SARS-CoV-2 R_0 in Little Brown Bats

From: DeeAnn Reeder [redacted]
Sent: Wednesday, April 15, 2020 7:31 PM EDT
To: Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) [redacted] >
CC: Coleman, Jeremy T [redacted]; Cryan, Paul [redacted]; Daniel Streicker [redacted] Gibbs, Samantha [redacted] Gilbert, Amy T - Aphis [redacted] >; Grant, Evan H [redacted] >; Hopkins, Maria-Richetta (Camille) C [redacted]; epstein [redacted] ecohealthalliance.org>; Lorch, Jeffrey M [redacted] >; O'Shea, Thomas [redacted] >; Kading,Rebekah [redacted] Runge, Michael C [redacted] Sleeman, Jonathan M [redacted]; a.pee[redacted]; castlek[redacted]; ckjohnsor[redacted] kate.e.jones[redacted]; linfa.wang[redacted] >; oliva[redacted] ecohealthalliance.org>; raina.plowright[redacted]; rbaric[redacted]; sja[redacted]; wfrick[redacted]
Subject: Re: Expert judgement for SARS-CoV-2 risk assessment for North American bats

Thanks Jon!

On Wed, Apr 15, 2020 at 7:15 PM Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) [redacted] wrote:

> Some food for thought while considering the effectiveness (or not) of bat workers/researchers putting on some kind of respiratory protection. This data, collected pre-COVID19, basically shows that putting on surgical masks can be effective for minimizing the spread of human coronaviruses, although the total number of patients tested was still pretty low and we don't know the extent to which COVID-19 can be spread in aerosolized form. Note that the masks weren't that effective for rhinoviruses or aerosolized flu.
>
> Jon

From: Daniel Streicker [redacted]
Sent: Wednesday, April 15, 2020 2:04 PM
To: Jon Epstein [redacted] ecohealthalliance.org>
Cc: Grant, Evan H [redacted] >; castlek[redacted]; O'Shea, Thomas [redacted] >; raina.plowright[redacted]; dreeder[redacted]; sja[redacted] kate.e.jones[redacted] ckjohnson[redacted]; wfrick[redacted]; linfa.wang[redacted]; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) [redacted] a.peel[redacted]; rbaric[redacted] Rebekah.Kading[redacted]; Gilbert, Amy T - Aphis [redacted]; Lorch, Jeffrey M [redacted] >; Runge, Michael C [redacted] Cryan, Paul [redacted] ecohealthalliance.org; Sleeman, Jonathan M [redacted] >; Coleman, Jeremy T [redacted] >; Gibbs, Samantha [redacted]; Hopkins, Maria-Richetta (Camille) C [redacted]
Subject: Re: Expert judgement for SARS-CoV-2 risk assessment for North American bats

Hi Jon,

Thanks for passing this along. So others don't have to dig through all of the the 2.5 page table full of abbreviations, here are some scores (matching residues of the 20 key AAs considered) for a few selected species which might be relevant to judging the susceptibility of Myotis lucifugus, which had a score of 11/20:

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Sus scrofa (15/20), in vitro evidence of infection

Mustela putorius furo (15/20), in vivo susceptibility confirmed

Rhinolophus macrotis (13/20), susceptible?

Rhinolophus pusillus (14/20), susceptible?

Rhinolophus ferrumequinum (12/20), susceptible?

Desmodus rotundus (12/20), possibly susceptible (same family as Artibeus, which was not included in the study)?

So, Myotis is relatively low on the list, but so are bats which are related to the presumed reservoir and known susceptible species like ferrets are not too much higher up on the list. I'd be curious to know how others with more knowledge than myself interpret these numbers. Is this measure of ACE-2 affinity something we should use and how low is too low for a host to be susceptible?

Best,

Daniel

On 15 Apr 2020, at 17:35, Jon Epstein [redacted]ecohealthalliance.org> wrote:

Hi All,

Here's the ACE-2 affinity paper.

Cheers,

Jon

On Thu, Apr 9, 2020 at 5:39 PM Grant, Evan H[redacted] wrote:

Hello experts,

Thank you for volunteering your time and expertise to help estimate the risk of SARS-CoV-2 to North American bats. Mike Runge and I (Evan Grant), with the U.S. Geological Survey Patuxent Wildlife Research Center, are facilitating this effort in collaboration with the USGS National Wildlife Health Center, USGS Fort Collins Science Center, USFWS, and EcoHealth Alliance. We are conducting a rapid assessment of the risks for transmission of SARS-CoV-2 from humans to bats. The goal is to provide scientific information that will guide wildlife management agency response to this potential risk, including development of management recommendations and mitigation strategies.

Attached please find two documents: (1) an introduction to expert elicitation with some background on the issue we are addressing, and (2) a spreadsheet <BatEE Practice Questions v2.xlsx> with calibration questions. There are three tabs (corresponding to the three questions) in the accompanying spreadsheet, and a fourth tab that summarizes the responses and the calculated mean and standard deviation for each question.

We have a very tight timeline to provide guidance to U.S. management agencies, so we thank you for your participation along the following timeline:

i. Respond to ehgrant[redacted] with your responses to the calibration questions in the attached spreadsheet (due by 12 PM ET 10 Apr)

ii. Review the background information and elicitation questions (we will send these additional documents to you by 6 pm ET 10 Apr)

iii. Respond with your initial responses to the questions (due by 6 PM ET 13 Apr)

iv. Be available for a 2-hr conference call to discuss initial responses and share insights (4 PM ET 14 Apr – and/or – 4 PM ET 15 Apr)

v. Revise and send your second-round responses to the questions (due 24 hours after the last conference call)

Thank you in advance for your participation. If you have questions – please contact Evan (ehgrant[redacted]

Kindest regards,

Evan and Mike

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street, Ste. 1701

New York, NY 10001

[redacted]

web: ecohealthalliance.org

[redacted]

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

<SARS-CoV 2 spike protein favors ACE2 from Bovidae and Cricetidae_Luan et al 2020.pdf>

--
DeeAnn M. Reeder, PhD
Professor
Department of Biology
Bucknell University
Lewisburg, PA 17837

http://deeannreeder.scholar.bucknell.edu
[redacted]

From: Kevin Castle [redacted]>
Sent: Friday, April 17, 2020 9:52 AM EDT
To: Grant, Evan H [redacted]>
CC: wfrick [redacted]; Plowright, Raina [redacted]>; dreeder [redacted]; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) [redacted]; Coleman, Jeremy T [redacted]; Cryan, Paul [redacted]; Daniel Streicker [redacted]>; Gibbs, Samantha [redacted]>; Gilbert, Amy T - Aphis [redacted]; Hopkins, Maria-Richetta (Camille) C [redacted]>; epstein [redacted]ecohealthalliance.org>; Kading,Rebekah [redacted]>; Runge, Michael C [redacted]>; Sleeman, Jonathan M [redacted] a.pee [redacted] ckjohnson [redacted]; kate.e.jones [redacted]>; oliva [redacted] [redacted]ecohealthalliance.org>; sja [redacted]< [redacted] Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) [redacted]>; Reichard, Jonathan D [redacted]
Subject: Re: Expert judgement for SARS-CoV-2 risk assessment for North American bats

Thanks Evan and Mike, and thanks Jeremy et al. for getting the additional WCO information, it was helpful.
Kevin

On Thu, Apr 16, 2020 at 4:21 PM Grant, Evan H [redacted] wrote:

> Hi Experts,
>
> Thanks for all your work on this. The 2 conference calls were very helpful in understanding how you were thinking about the questions we posed, and I hope that you gained some insights during the discussions.
>
> I attach here 2 documents. The first is the summary of your responses (Mike showed this on the calls). The second is clarifications of the question we were asking. This should be reviewed prior to revising your estimates. We have tried to add the necessary detail to help understand the context under which we are seeking your opinions for the questions.
>
> Please send me your revised estimates by this time tomorrow (you can revise your estimates and send the revised spreadsheet). Please take note that we are asking for your estimates of the most likely values and range for each of the questions. In particular, you can think about the estimate of confidence you are reporting by calculating and evaluating the complement (e.g., 70% confidence means that there is a 15% probability the true value lies below the lowest value you provided, and a 15% probability it is above the highest value).
>
> Thanks again for lending your expertise during what I expect is an exceptionally busy time for all of you.
>
> Kindest regards,
>
> Evan and Mike

--
Kevin T. Castle, DVM, MS
Wildlife Veterinary Consulting, LLC
[redacted]

From: Daniel Streicker [redacted]>
Sent: Wednesday, April 15, 2020 2:03 PM EDT
To: epstein [redacted]ecohealthalliance.org>
CC: Grant, Evan H [redacted]>; castlek[redacted]; O'Shea, Thomas [redacted]>; raina.plowright[redacted]; dreeder[redacted]>; sja[redacted]>; kate.e.jones[redacted]>; ckjohnson[redacted]; wfrick[redacted]>; linfa.wang[redacted]; jit[redacted]a.pee[redacted]; rbaric[redacted]>; Kading,Rebekah [redacted]>; Gilbert, Amy T - Aphis [redacted]>; Lorch, Jeffrey M [redacted]>; Runge, Michael C [redacted]Cryan, Paul [redacted]oliva[redacted]ecohealthalliance.org>; Sleeman, Jonathan M [redacted]>; Coleman, Jeremy T [redacted]; Gibbs, Samantha [redacted]>; Hopkins, Maria-Richetta (Camille) C [redacted]>
Subject: Re: Expert judgement for SARS-CoV-2 risk assessment for North American bats

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Best,
Daniel

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Cheers,
Jon

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>
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>
> i. Respond to [redacted] with your responses to the calibration questions in the attached spreadsheet (due by 12 PM ET 10 Apr)

ii. Review the background information and elicitation questions (we will send these additional documents to you by 6 pm ET 10 Apr)

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v. Revise and send your second-round responses to the questions (due 24 hours after the last conference call)

Thank you in advance for your participation. If you have questions – please contact Evan [redacted].

Kindest regards,

Evan and Mike

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street, Ste. 1701

New York, NY 10001

[redacted]

web: ecohealthalliance.org

[redacted]

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

<SARS-CoV 2 spike protein favors ACE2 from Bovidae and Cricetidae_Luan et al 2020.pdf>

From: Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)
Sent: Monday, April 20, 2020 9:18 AM EDT
To: Plowright, Raina DeeAnn Reeder
CC: Coleman, Jeremy T ; Cryan, Paul Daniel Streicker ; Gibbs, Samantha ; Gilbert, Amy T - Aphis Grant, Evan H ; Hopkins, Maria-Richetta (Camille) C ; epstein ecohealthalliance.org>; Lorch, Jeffrey M ; O'Shea, Thomas ; Kading,Rebekah ; Runge, Michael C >; Sleeman, Jonathan M >; a.pee >; castlekt@gmail.com ; ckjohnson >; kate.e.jones ; linfa.wang ; oliva ecohealthalliance.org>; rbaric >; sja ; wfrick
Subject: RE: Expert judgement for SARS-CoV-2 risk assessment for North American bats
Attachment(s): "Damas_bioRxiv_2020.pdf"

If you haven't seen it.
Jon

From: Plowright, Raina
Sent: Wednesday, April 15, 2020 9:29 PM
To: DeeAnn Reeder ; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)
Cc: Coleman, Jeremy T >; Cryan, Paul >; Daniel Streicker >; Gibbs, Samantha >; Gilbert, Amy T - Aphis >; Grant, Evan H ; Hopkins, Maria-Richetta (Camille) C Jon Epstein ecohealthalliance.org>; Lorch, Jeffrey M ; O'Shea, Thomas ; Rebekah.Kading ; Runge, Michael C >; Sleeman, Jonathan M >; a.pee ; castlekt ; ckjohnson ; kate.e.jones ; linfa.wang ecohealthalliance.org; rbaric sja wfrick
Subject: Re: Expert judgement for SARS-CoV-2 risk assessment for North American bats

Great discussion! Thanks for forwarding the paper Jon, and thanks for summarizing the data Dan.
Receptor binding studies are a great and practical first step, however, susceptibility is far more complex than receptor binding. Many processes must be overcome to infect a new species and experiments are probably the only way to definitively determine susceptibility.
I reached out to Tony S to see if he had insights about Artibeus jamaicensis (susceptible) with respect to the AA considered in the paper – he looked through his transcriptome data and noted it has 13 matched AAs.
I look forward to more discussion tomorrow.
Raina

> **From:** DeeAnn Reeder >
> **Date:** Wednesday, April 15, 2020 at 5:31 PM
> **To:** "Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)"
> **Cc:** "Coleman, Jeremy T", "Cryan, Paul" >, Daniel Streicker , "Gibbs, Samantha" >, "Gilbert, Amy T - Aphis" , "Grant, Evan H" >, "Hopkins, Maria-Richetta (Camille) C" >, Jon Epstein ecohealthalliance.org>, "Lorch, Jeffrey M" >, "O'Shea, Thomas" >, "Rebekah.Kading " >, "Runge, Michael C" >, "Sleeman, Jonathan M" >, "a.peel " , "castlekt " >, "ckjohnson " >, "kate.e.jones " , "linfa.wang >, "oliva " , Raina Plowright >, "rbaric " >, "sja " >, "wfrick " >
> **Subject:** Re: Expert judgement for SARS-CoV-2 risk assessment for North American bats
>
> Thanks Jon!
>
> On Wed, Apr 15, 2020 at 7:15 PM Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) > wrote:
>
> > Some food for thought while considering the effectiveness (or not) of bat workers/researchers putting on some kind of respiratory protection. This data, collected pre-COVID19, basically shows that putting on surgical masks can be effective for minimizing the spread of human coronaviruses, although the total number of patients tested was still pretty low and we don't know the extent to which COVID-19 can be spread in aerosolized form. Note that the masks weren't that effective for rhinoviruses or aerosolized flu.
> >
> > Jon

From: Daniel Streicker >
Sent: Wednesday, April 15, 2020 2:04 PM
To: Jon Epstein ecohealthalliance.org>
Cc: Grant, Evan H >; castlekl ; O'Shea, Thomas ; raina.plowright ; dreeder ; sja ; kate.e.jones ckjohnson ; wfrick ; linfa.wang ; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) >; a.peel ; rbaric ; Rebekah.Kading Gilbert, Amy T - Aphis ; Lorch, Jeffrey M ; Runge, Michael C Cryan, Paul ; ecohealthalliance.org; Sleeman, Jonathan M Coleman, Jeremy T ; Gibbs, Samantha >; Hopkins, Maria-Richetta (Camille) C

Subject: Re: Expert judgement for SARS-CoV-2 risk assessment for North American bats

Hi Jon,

Thanks for passing this along. So others don't have to dig through all of the the 2.5 page table full of abbreviations, here are some scores (matching residues of the 20 key AAs considered) for a few selected species which might be relevant to judging the susceptibility of Myotis lucifugus, which had a score of 11/20:

Homo sapiens (20/20)
Sus scrofa (15/20), in vitro evidence of infection
Mustela putorius furo (15/20), in vivo susceptibility confirmed
Rhinolophus macrotis (13/20), susceptible?
Rhinolophus pusillus (14/20), susceptible?
Rhinolophus ferrumequinum (12/20), susceptible?
Desmodus rotundus (12/20), possibly susceptible (same family as Artibeus, which was not included in the study)?

So, Myotis is relatively low on the list, but so are bats which are related to the presumed reservoir and known susceptible species like ferrets are not too much higher up on the list. I'd be curious to know how others with more knowledge than myself interpret these numbers. Is this measure of ACE-2 affinity something we should use and how low is too low for a host to be susceptible?

Best,
Daniel

On 15 Apr 2020, at 17:35, Jon Epstein ecohealthalliance.org> wrote:

Hi All,
Here's the ACE-2 affinity paper.
Cheers,
Jon

On Thu, Apr 9, 2020 at 5:39 PM Grant, Evan H wrote:

> Hello experts,
>
> Thank you for volunteering your time and expertise to help estimate the risk of SARS-CoV-2 to North American bats. Mike Runge and I (Evan Grant), with the U.S. Geological Survey Patuxent Wildlife Research Center, are facilitating this effort in collaboration with the USGS National Wildlife Health Center, USGS Fort Collins Science Center, USFWS, and EcoHealth Alliance. We are conducting a rapid assessment of the risks for transmission of SARS-CoV-2 from humans to bats. The goal is to provide scientific information that will guide wildlife management agency response to this potential risk, including development of management recommendations and mitigation strategies.
>
> Attached please find two documents: (1) an introduction to expert elicitation with some background on the issue we are addressing, and (2) a spreadsheet <BatEE Practice Questions v2.xlsx> with calibration questions. There are three tabs (corresponding to the three questions) in the accompanying spreadsheet, and a fourth tab that summarizes the responses and the calculated mean and standard deviation for each question.
>
> We have a very tight timeline to provide guidance to U.S. management agencies, so we thank you for your participation along the following timeline:
>
> i. Respond to ehgrant with your responses to the calibration questions in the attached spreadsheet (due by 12 PM ET 10 Apr)
>
> ii. Review the background information and elicitation questions (we will send these additional documents to you by 6 pm ET 10 Apr)
>
> iii. Respond with your initial responses to the questions (due by 6 PM ET

13 Apr)

iv. Be available for a 2-hr conference call to discuss initial responses and share insights (4 PM ET 14 Apr – and/or – 4 PM ET 15 Apr)

v. Revise and send your second-round responses to the questions (due 24 hours after the last conference call)

Thank you in advance for your participation. If you have questions – please contact Evan (ehgrant .

Kindest regards,
Evan and Mike

--
Jonathan H. Epstein DVM, MPH, PhD
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web: ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

<SARS-CoV 2 spike protein favors ACE2 from Bovidae and Cricetidae_Luan et al 2020.pdf>

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Broad Host Range of SARS-CoV-2 Predicted by Comparative and Structural Analysis of ACE2 in Vertebrates

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[1]These authors contributed equally to this work.

Abstract

The novel coronavirus SARS-CoV-2 is the cause of Coronavirus Disease-2019 (COVID-19). The main receptor of SARS-CoV-2, angiotensin I converting enzyme 2 (ACE2), is now undergoing extensive scrutiny to understand the routes of transmission and sensitivity in different species. Here, we utilized a unique dataset of 410 vertebrates, including 252 mammals, to study cross-species conservation of ACE2 and its likelihood to function as a SARS-CoV-2 receptor. We designed a five-category ranking score based on the conservation properties of 25 amino acids important for the binding between receptor and virus, classifying all species from *very high* to *very low*. Only mammals fell into the *medium* to *very high* categories, and only catarrhine primates in the *very high* category, suggesting that they are at high risk for SARS-CoV-2 infection. We employed a protein structural analysis to qualitatively assess whether amino acid changes at variable residues would be likely to disrupt ACE2/SARS-CoV-2 binding, and found the number of predicted unfavorable changes significantly correlated with the binding score. Extending this analysis to human population data, we found only rare (<0.1%) variants in 10/25 binding sites. In addition, we observed evidence of positive selection in ACE2 in multiple species, including bats. Utilized appropriately, our results may lead to the identification of intermediate host species for SARS-CoV-2, justify the selection of animal models of COVID-19, and assist the conservation of animals both in native habitats and in human care.

Keywords: SARS-CoV-2, COVID-19, ACE2, comparative genomics, host range, species conservation, evolution

Introduction

The 2019-novel coronavirus (2019-nCoV, also, SARS-CoV-2 and COVID-19 virus) is the cause of Coronavirus Disease-2019 (COVID-19), a major pandemic that threatens millions of lives and the global economy (1). Comparative analysis of SARS-CoV-2 and related coronavirus sequences has shown that SARS-CoV and SARS-CoV-2 likely originated in bats, followed by transmission to an intermediate host, and that both viruses may have an extended host range that includes primates and other mammals (1–3). However, the immediate source population/species for SARS-CoV and SARS-CoV-2 viruses has not yet been identified. Several mammalian species host coronaviruses, and these infections are frequently associated with severe clinical diseases, such as respiratory and enteric disease in pigs and cattle (4, 5). Molecular phylogenetics revealed that at least one human coronavirus (HCov-OC43), may have originated in cattle or swine (6), and that this virus was associated with a human pandemic that emerged in the late 19th century (7). Recent data indicate that coronaviruses can move from bats to other wildlife species and humans (8) and from humans to tigers (9) and pigs (10). Therefore, understanding the host range of SARS-CoV-2 and related coronaviruses is essential for improving our ability to predict and control future pandemics. It is also crucial for protecting populations of wildlife species in native habitats and under human care, particularly non-human primates, who may also be susceptible to COVID-19 (11).

The angiotensin I converting enzyme 2 (ACE2) serves as a functional receptor for the spike protein (S) of SARS-CoV and SARS-CoV-2 (12, 13). Under normal physiological conditions, ACE2 is a dipeptidyl carboxypeptidase that catalyzes the conversion of angiotensin I into angiotensin 1-9, a peptide of unknown function, and angiotensin II, a vasoconstrictor that is important in the regulation of blood pressure (14). ACE2 also converts angiotensin II into angiotensin 1-7, a vasodilator that affects the cardiovascular system (14) and may regulate other components of the renin-angiotensin system (15). The host range of SARS-CoV-2 may be extremely broad due to the conservation of ACE2 in mammals (2, 13) and its expression on ciliated bronchial epithelial cells and type II pneumocytes (10). While coronaviruses related to SARS-CoV-2 use ACE2 as a primary receptor, coronaviruses may use other proteases as receptors, such as CD26 (DPP4) for MERS-CoV (16), thus limiting or extending their host range.

In humans, ACE2 may be a cell membrane protein or it may be secreted (14). The secreted form is created primarily by enzymatic cleavage of surface-bound ACE2 by ADAM17 and other proteases (14). Sequence variation in *ACE2* affects the protein's functions. *ACE2* is polymorphic in humans, with many

synonymous and nonsynonymous mutations identified, although most are rare at the population level (17) and few are believed to affect cellular susceptibility to human coronavirus infections (18). Site-directed mutagenesis and co-precipitation of SARS-CoV constructs have revealed critical residues on the ACE2 tertiary structure that are essential for binding to the virus receptor binding domain (RBD) (19). These findings have been strongly supported by co-crystallization and the structural determination of the SARS-CoV and SARS-CoV-2 S proteins with human ACE2 (13, 20, 21), as well as binding-affinity with heterologous ACE2 (19). The RBD of human coronaviruses may mutate to change the binding affinity of S for ACE2, and thus lead to adaptation in humans or other hosts. The best studied example is the palm civet, believed to have been the intermediate host between bats and humans for SARS-CoV (2). To date, an intermediate host for SARS-CoV-2 has not been identified definitively, although Malayan pangolins (*Manis javanica*) have been proposed as a possible reservoir (22).

Comparative analysis of ACE2 nucleotide and protein sequences can predict their ability to bind SARS-CoV-2 S and therefore will yield important insights into the biology and potential zoonotic transmission of SARS-CoV-2 infection. Recent work has examined ACE2 from different vertebrate species and predicted its ability to bind SARS-CoV-2 S, but phylogenetic sampling was extremely limited (11, 23). Here, we made use of sequenced genomes of 410 vertebrates and protein structural analysis, to identify ACE2 homologs in all vertebrate classes (fishes, amphibians, birds, reptiles, and mammals) that have the potential to serve as a receptor for SARS-CoV-2, and to understand the evolution of ACE2 SARS-CoV-2 S binding sites. Our results reinforce earlier findings on the natural host range of SARS-CoV-2, and predict a broader group of species that may serve as a reservoir or intermediate host for this virus. Importantly, many threatened and endangered species were found to be at potential risk for SARS-CoV-2 infection, suggesting that as the pandemic spreads, humans could inadvertently introduce a potentially devastating new threat to these already vulnerable populations, especially for great apes and other primates.

Results

Comparison of vertebrate ACE2 sequences and their predicted ability to bind SARS-CoV-2. We identified 410 unique vertebrate species with *ACE2* orthologs (Dataset S1) that included representatives of all vertebrate taxonomic classes. Among these were 252 mammals, 72 birds, 65 fishes, 17 reptiles and 4 amphibians. Twenty-five amino acids corresponding to known SARS-CoV-2 S-binding residues (11, 13, 21) were examined for their similarity to the residues in human ACE2 (Fig. 1, Dataset S1). On the basis of

known interactions between specific residues on ACE2 and the RBD of SARS-CoV-2 S, a set of rules was developed for predicting the likelihood of S binding to ACE2 from each species (see Materials and Methods). Five score categories were predicted: *very high*, *high*, *medium*, *low* and *very low*. Results for all species and all SARS-CoV-2 S binding scores are shown in Dataset S1, and results for mammalian species are also shown in Fig. 1. The *very high* classification had at least 23/25 ACE2 residues identical to their human homolog and other constraints on substitutions at SARS-CoV-2 S binding hot spots (see Materials and Methods). The 18 species predicted as *very high* were all Old World primates and apes completely identical to human across the 25 ACE2 binding residues. The ACE2 proteins of 28 species were classified as having a *high* likelihood of binding the S RBD. Among them are twelve cetaceans, seven rodents, three cervids (deer), three lemuriform primates, two representatives of the order Pilosa (Giant anteater and Southern tamandua), and one Old World primate (Angola colobus, Fig. 1). Fifty-seven species scored as *medium* for the ability of their ACE2 to bind SARS-CoV-2 S. Like the *high* score, this category has at least 20/25 residues identical to human ACE2 but more relaxed constraints for critical binding residues. All species with *medium* score are mammals distributed across six orders.

Among Carnivora, 9/43 scored *medium*, 9/43 scored *low*, and 25/43 scored *very low* (Fig. 1). The carnivores scoring *medium* were only felids, including the domestic cat and Siberian tiger. Among the 13 Primates scoring *medium* there were 10 New World primates and three lemurs. Of 45 Rodentia species, 11 scored *medium*. Twenty-one Artiodactyls scored *medium*, including several important wild and domesticated ruminants, such as domesticated cattle, bison, sheep, goat, water buffalo, Masai giraffe, and Tibetan antelope. Species scoring *medium* also included 2/3 Lagomorphs and one Cetacean (sperm whale).

All chiropterans (bats) scored *low* (N=8) or *very low* (N=29) (Fig. 1), including the Chinese rufous horseshoe bat (*Rhinolophus sinicus*), from which a coronavirus very similar to SARS-CoV-2 was identified (1). Only 7.7% (3/39) primate species' ACE2 scored *low* or *very low,* and 61% of rodent species scored *low* (10/46) or *very low* (18/46). All monotremes (N=1) and marsupials (N=4) scored *very low*. All birds, fish, amphibians, and reptiles scored *very low*, with less than 18/25 ACE2 residues identical to the human and many non-conservative residues at the remaining non-identical sites (Dataset S1). Notable species scoring *very low* include the Chinese pangolin (*Manis pentadactyla*), Sunda pangolin (*Manis javanica*), and white-bellied pangolin (*Phataginus tricuspis*) (Fig. 1, Dataset S1).

Structural analysis of the ACE2/SARS-CoV-2 S binding interface. We complemented the sequence-identity based scoring scheme with a qualitative approach that combined structural homology

modeling and best fit rotamer positioning. We examined the 25 ACE2 binding residues in a subset of 28 representative species (Fig. S1) and 17 sites were variable and not glycosylation sites. First, we assessed the similarity of every contact at the binding interface between two recently solved crystal structures for the human ACE2/SARS-CoV-2 S RBD complex in humans, 6M0J and 6WV1 (13, 21). Both structures were in agreement except for the position of S19, which was excluded from subsequent analysis (24). We then generated homology models, and aligned them to the human ACE2/SARS-CoV-2 S RBD 6M0J structure. This showed a high degree of similarity along the Cα backbone (25) for each of the 28 species. We selected the most favorable rotamer at each residue using CHIMERA (Fig. S2).

We examined a total of 55 substitutions and assigned each to one of three types: *neutral* (N; likely to maintain similar contacts; 18 substitutions); *weaken* (W; likely to weaken the interaction; 14 substitutions); or *unfavorable* (U; likely to introduce unfavorable interactions; 23 substitutions) (Fig. S1). Our assignments show good agreement with those made in a second study (26) based on experimental data, with 83.4% of the 55 substitutions evaluated concordant between the two approaches (Fig. S1). The structural homology binding assessments support the sequence identity analysis, with the fraction of residues ranked as U, correlating very strongly with the substitution scoring scheme (Spearman correlation rho=0.76; $p< 2.2e-16$; Fig. 2).

Structural analysis of variation in human *ACE2*. We applied the same approach used to compare species, sequence identity and protein structural analysis, to examine the variation in ACE binding residues within humans, some of which have been proposed to alter binding affinity (18, 27–30). We integrated data from six different sources: dbSNP (31), 1KGP (32), Topmed (33), UK10K (34) and CHINAMAP (28), and identified a total of 11 variants in ten of the 25 ACE2 binding residues (Dataset S2). All variants found are rare, with allele frequency less than 0.01 in any populations, and less than 0.0007 over all populations. Three of the 11 variants were synonymous changes, seven were conservative missense variants, and one, S19P, was a semi-conservative substitution. S19P has the highest allele frequency of the 11 variants, with a global frequency of 0.0003 (17). We evaluated, by structural homology, six missense variants. Four were *neutral* and two weakening (E35K, frequency=0.000016; E35D, frequency=0.000279799). S19P was not included in our structural homology assessment, but a recent study predicted it would increase binding affinity (26). Thus, with an estimated summed frequency of 0.001, genetic variation in the ACE2 S-binding interface is overall rare, and it is unclear whether the variation that does exist increases or decreases susceptibility to infection.

Evolution of ACE2 across mammals. We next investigated the evolution of ACE2 variation in vertebrates, including how patterns of positive selection compare between bats, a mammalian lineage known to harbor a diversity of coronaviruses (35), and other mammalian clades. We first inferred the phylogeny of *ACE2* using our 410-vertebrate alignment and IQTREE, using the best-fit model of sequence evolution (JTT+F+R7) and rooting the topology on fishes (Dataset S3; Fig. S3). We then assayed sequence conservation with PhyloP (36). The majority of ACE2 codons are significantly conserved across vertebrates and across mammals, likely reflecting its critical function in the renin-angiotensin system (37) (Dataset S4.1), with ten residues in the ACE2 binding domain exceptionally conserved in Chiroptera and/or Rodentia (Dataset S4.2).

We next used phyloP and CODEML to test for acceleration and positive selection (36). PhyloP compares the rate of evolution at each codon to the expected rate in a model estimated from third nucleotide positions of the codon, and is agnostic to synonymous versus nonsynonymous substitutions (dN/dS). CODEML uses ω=dN/dS>1 and Bayes Empirical Bayes (BEB) scores to identify codons under positive selection, and was run on a subset of 64 representative mammals (see Materials and Methods).

ACE2 shows significant evidence of positive selection across mammals (ω=1.83, LRT=194.13, p<0.001; Dataset S4.3, 4.4). Almost 10% of codons (N=73; 9 near the RBD) are accelerated within mammals (Dataset S4.1, 4.5), and 18 of these have BEB scores greater than 0.95, indicating positively selected residues (Dataset S4.5, 4.6, Fig. S4). Nineteen accelerated residues, including two positively-selected codons (Q24, H34), are critical for the binding of the ACE2 RBD and SARS-CoV-2 S (Dataset S4.5; Fig. 3; Fig. S5). Q24 has not been observed to be polymorphic within the human population, and H34 harbors a synonymous polymorphism (AF=0.00063) but no non-synonymous polymorphisms (Dataset S2).

This pattern of acceleration and positive selection in *ACE2* also holds for individual mammalian lineages. Using CODEML, positive selection was detected within the orders Chiroptera (LRT=346.40, ω=3.44 p<0.001), Cetartiodactyla (LRT=92.86, ω=3.83, p<0.001), Carnivora (LRT=65.66, ω=2.27. p<0.001), Primates (LRT=72.33, ω=3.16, p<0.001) and Rodentia (LRT=91.26, ω=1.77, p<0.001). Overall, bats had more positively selected sites with significant BEB scores (29 sites in Chiroptera compared to 10, 8, 7 and 15 sites in Cetartiodactyla, Carnivora, Primates and Rodentia, respectively). Positive selection at key sites for the binding of ACE2 and SARS-CoV-2 was only found in the bat-specific alignment. PhyloP was used to assess shifts in evolutionary rate within mammalian lineages, for each assessing signal relative to a neutral model trained on species from the specified lineage (Dataset S4.6-11, Fig. S6). We discovered six important binding residues, five of which showed evidence for positive selection, that are accelerated in

one or more of Chiroptera, Rodentia, or Carnivora, with G354 accelerated in all of these lineages (Dataset S4.12).

Given pervasive signatures of adaptive evolution in *ACE2* across mammals, we next sought to test if any mammalian lineages are evolving particularly rapidly compared to the others. CODEML branch-site tests identified positive selection in both the ancestral Chiroptera branch (1 amino acid, ω=26.7, LRT= 4.22, p=0.039) and ancestral Cetartiodactyla branch (2 amino acids, ω=10.38, LRT= 7.89, p=0.004, Dataset S4.3) using 64 mammals. These residues did not correspond to known viral binding sites. We found no evidence for lineage-specific positive selection in the ancestral primate, rodent or carnivore lineages. PhyloP identified lineage-specific acceleration in Chiroptera, Carnivora, Rodentia, Artiodactyla and Cetaceans relative to mammals (Dataset S4.13-17, Fig. S7). Bats have a particularly high level of accelerated evolution (18 codons; $p<0.05$). Of these accelerated residues, T27 and M82 are known to be important for binding SARS-CoV-2, with some bat subgroups having amino acids predicted to lead to less favorable binding of SARS-CoV-2 (Fig. S1, Fig. S8). Surprisingly, a residue that is conserved overall in our 410 species alignment and in the mammalian subset, Q728, is perfectly conserved in all 37 species of bats except for fruit bats (Pteropodidae), which have a substitution from Q to E. These results support the theory that *ACE2* is under lineage-specific selective pressures in bats relative to other mammals.

Positive selection in SARS-CoV-2 S protein. Positive selection was found using CODEML at sites L455, E484, F490 and S494 in the SARS-CoV-2 S sequence (ω=1.15, LRT=116.7, $p<0.001$); however this signal was not particularly high, possibly due to the small sample size (N=8). All of these sites lie within or near the ACE2 SARS-CoV-2 S RBD binding sites (Fig. 3) (38).

Discussion

Phylogenetic analysis of coronaviruses has demonstrated that SARS-CoV-2 most likely originated in a bat species (1). However, whether SARS-CoV-2 or the progenitor of this virus was transmitted directly to humans or through an intermediary host is not yet resolved. To determine if amino acid substitution analysis and structural information could be used to identify candidate intermediate host species, we undertook a deep comparative genomic, evolutionary and structural analysis of ACE2, the SARS-CoV-2 receptor in humans. To accomplish this we drew on the rapidly growing dataset of annotated vertebrate genomes as well as predicted protein sequences from recently acquired whole genome sequences produced by the Genomes 10K-affiliated Bat1K Consortium, Zoonomia, and Vertebrate

Genomes Project, and other sources (39, 40). We conducted a phylogenetic analysis of ACE2 orthologs from 410 vertebrate species and made predictions of their likelihood to bind the SARS-CoV-2 S using a score that was based on amino acid substitutions at 25 consensus human ACE2 binding residues (13, 21). We supported these predictions with comprehensive homology modeling of the ACE2 binding site. We also tested the hypothesis that the ACE2 receptor is under selective constraints in different mammalian lineages, and correlated these results with data on the known species distribution of coronaviruses.

Several recent studies examined the role of ACE2 in SARS-CoV-2 binding and cellular infection, and its relationship to experimental and natural infections in different species (30, 41–46). Our study design differs substantially from those studies in several aspects: 1) we analyzed a larger number of primates, carnivores, rodents, cetartiodactyls and other mammalian orders, and an extensive phylogenetic sampling of fishes, birds, amphibians and reptiles; 2) we analyzed the full complement of S-binding residues across the ACE2 binding site, which was based on a consensus set from two independent studies (13, 21); 3) we used different methodologies to assess ACE2 binding capacity for SARS-CoV-2 S; and, 4) our study tested for selection and accelerated evolution across the entire ACE2 protein. While our results are strongly consistent with the results and conclusions of Melin and colleagues (44) on the predicted susceptibility of primates to SARS-CoV-2, particularly Old World primates, our work made predictions for a larger number of primates (N=39 vs N=27), bats (N=37 vs N=7), other mammals (N=176 vs N=5) and other vertebrates (N=158 vs N=0). When ACE2 from species in our study were compared with results of other studies there were many consistencies, such as for rodents, but some predictions that differ, such as the relatively high risk described for SARS-CoV-2 binding in pangolin and horse (45), civet (46), *Rhinolophus sinicus* bats (46) and turtles (45). In one recent study, binding affinity of soluble ACE2 for the SARS-CoV-2 S RBD was analyzed by saturation mutagenesis (26). Results obtained at each ACE2 binding residue were generally consistent with ours, particularly in the binding hotspot region of ACE2 residues 353-357. Importantly, as compared with other studies, our results greatly expanded the potential number of intermediate hosts and identified many more threatened species that could be infected by SARS-CoV-2 via their ACE2 receptors.

Evolution of *ACE2*. Variation of *ACE2* in the human population is rare (17). We examined a large set of *ACE2* variants for their potential differences in binding to SARS-CoV-2 S and their relationship to selected and accelerated sites. We found rare variants that would result in missense mutations in 7 out of the 25 binding residues (Dataset S2). Some of those (e.g. E35K with an AF of 0.00001636) could reduce the virus binding affinity, thus potentially lowering the susceptibility to the virus in a very small fraction of

the population. The analysis suggests that some variants (e.g. D38E) might not affect the binding while others (e.g. S19P) have uncertain effects. Further studies are needed to confirm and correctly address recent discoveries (18, 27, 28) and the data presented here, investigating the possible effect of these rare variants in specific populations.

When exploring patterns of codon evolution in ACE2, we found that a number of sites are evolving at different rates in the different lineages represented in our 410-species vertebrate alignment. Multiple ACE2 RBD residues important for the binding of SARS-CoV-2 are evolving rapidly across mammals, with two (Q24 and H34) under positive selection (Fig. 3, Fig. S5). Relative to other lineages analyzed, Chiroptera has a greater proportion of accelerated versus conserved residues, particularly at the SARS-CoV-2 S RBD, suggesting the possibility of selective forces on these codons in Chiroptera driven by their interactions with SARS-CoV-2-like viruses (Dataset S4.12, Fig. S8). Indeed, distinct signatures of positive selection found in bats and in the SARS-CoV S protein support this hypothesis that bats are evolving to tolerate SARS-CoV-2-like viruses.

Relationship of the ACE2 binding score to known infectivity of SARS-CoV-2. Data on susceptibility of wild animals to SARS-CoV-2 is still very limited. It has been reported that a captive Malayan tiger was infected by SARS-CoV-2 (9) and that domestic cats, ferrets (47), rhesus macaques (48) and Syrian golden hamsters (49) are susceptible to experimental infection by SARS-CoV-2. These results agree with our predictions of ACE2 binding ability to SARS-CoV-2 S (Fig. 1, Dataset S1); 4/5 five species with demonstrated susceptibility to SARS-CoV-2 score *very high* (Rhesus macaque) or *medium* (domestic cat, tiger and Golden hamster). The only inconsistency was observed for ferrets, which had a *low* ACE2 binding score. This inconsistency could be related to the high infectivity dose used for experimental infection that likely does not correspond to virus exposure in nature. Dogs have low susceptibility to SARS-CoV-2 under experimental conditions (47), and score *low* for binding of their ACE2 to SARS-CoV-2 S. However, kidney cell lines derived from dog showed ACE2-dependent SARS-CoV-2 S entry, suggesting that *in vitro* experiments may be overestimating true infectivity potential (39, 50). Pigs (*low*), ducks (*very low*) and chickens (*very low*) were similarly exposed to SARS-CoV-2 and showed no susceptibility (47), providing further support of our methodology. A recent publication reporting that SARS-CoV-2 could use pig, masked palm civet and Chinese rufous horseshoe bat ACE2 expressed in HeLa cells were inconsistent with our predictions, while data for mouse was in agreement (1). Indeed, while mouse ACE2 scored *very low* in our analysis, pig and Chinese rufous horseshoe bat score *low*, while the masked palm civet scored *very low*. As for the ferret, high-level exposure to the virus *in vitro* could potentially result in infection via low affinity interactions with ACE2. Another possibility is that other cellular machinery

present in the human HeLa cells is facilitating the infection, and that infectivity does not relate directly to ACE2 differences in these species. Confirmation of *in vitro* and *in vivo* susceptibility of these species under physiological conditions and with proper controls is clearly necessary. In addition, the expression of ACE2 varies across animal age, cell types, tissues and species (51, 52), which may lead to discrepancies between SARS-CoV-2 susceptibility gleaned from experimental infections or laboratory experiments and predictions made from the ACE2-based binding score.

Mammals with high predicted risk of SARS-CoV-2 infection. Of the 19 catarrhine primates analyzed, 18/19 scored *very high* for binding of their ACE2 to SARS-CoV-2 S and one scored *high* (the Angola colobus); the 18 species scoring *very high* had 25/25 identical binding residues to human ACE2, including rhesus macaques (*Macaca mulatta*), which are known to be infected by SARS-CoV-2 and develop COVID-19-like clinical symptoms (3, 48). Our analysis predicts that all Old World primates are susceptible to infection by SARS-CoV-2 via their ACE2 receptors. Thus, many of the 21 primate species native to China could be a potential reservoir for SARS-CoV-2. The remaining primate species were scored as *high* or *medium*, with only the Gray mouse lemur and the Philippine tarsier scoring as *low*.

We were surprised to find that all three species of Cervid deer and 12/14 cetacean species have *high* scores for binding of their ACE2s to SARS-CoV-2 S. There are 18 species of Cervid deer found in China. Therefore, Cervid deer cannot be ruled out as an intermediate host for SARS-CoV-2. While coronavirus sequences have been found in white tailed deer (53) and gammacoronaviruses have been found in beluga whales (54, 55) and bottlenose dolphins (56) and are associated with respiratory diseases, the cellular receptor used by these viruses is not known.

Other artiodactyls. A relatively large fraction (21/30) of artiodactyl mammals were classified with *medium* score for ACE2 binding to SARS-CoV-2 S. These include many species that are commonly found in Hubei Province and around the world, such as domesticated cattle, sheep and goats, as well as many species commonly found in zoos and wildlife parks (e.g., Masai giraffe, okapi, hippopotamus, water buffalo, scimitar horned oryx, and Dama gazelle). Although cattle MDBK cells were shown in one study to be resistant to SARS-CoV-2 *in vitro* (50), we propose immediate surveillance of common artiodactyl species for SARS-CoV-2 and studies of cellular infectivity, given our predictions. If ruminant artiodactyls can serve as a reservoir for SARS-CoV-2, it would have significant epidemiological implications as well as implications for food production and wildlife management (see below). It is noteworthy that camels and pigs, known for their ability to be infected by coronaviruses (35), both score *low* in our analysis. These

data are consistent with results (discussed above) indicating that pigs cannot be infected with SARS-CoV-2 both *in vivo* (47) and *in vitro* (50).

Rodents. Among the rodents, 7/46 species score *high* for ACE2 binding to SARS-CoV-2 S, with the remaining 11, 10 and 18 scoring *medium*, *low* or *very low*, respectively. Brown rats *(Rattus norvegicus*) and the house mouse (*Mus musculus*), scored *very low*, consistent with infectivity studies (1, 50). Given that wild rodent species likely come in contact with bats as well as with other predicted high risk species, we urge surveillance of *high* and *medium* binding likelihood rodents for the presence of SARS-CoV-2.

Bats and other species of interest. Chiroptera (bats) represent a clade of mammals that are of high interest in COVID-19 research because several bat species are known to harbor coronaviruses, including those most closely related to the betacoronavirus SARS-CoV-2 (1). We analyzed ACE2 from 37 bat species of which 8 and 29 scored *low* and *very low*, respectively. These results were unexpected because the three *Rhinolophus* spp. including the Chinese rufous horseshoe bat are major suspects in the transmission of SARS-CoV-2, or a closely related virus, to humans (1). Globally, bats have been shown to harbour the highest diversity of betacoronaviruses in mammals tested (35) and show little pathology carrying these viruses (57). We found evidence for accelerated evolution at six RBD binding domain residues within the bat lineage, which is more than in any other lineage tested. Bats also had far more sites showing evidence of positive selection, including four binding domain residues, compared to other mammalian orders. This suggests that the diversity observed in bat ACE2 sequences may be driven by selective pressure from coronaviruses. Our results suggest that SARS-CoV-2 is not likely to use the ACE2 receptor in bats, which challenges a recent study showing that SARS-CoV-2 can infect HeLa cells expressing *Rhinolophus sinicus* ACE2 (1). If bats can be infected with SARS-CoV-2, the virus likely uses a different receptor. For example, the MERS-CoV, a betacoronavirus, uses CD26/DPP4 (16) while the porcine transmissible enteritis virus, an alphacoronavirus uses aminopeptidase N (ANPEP) (58). As detailed above, further *in vitro* and *in vivo* infectivity studies are required to fully understand the mode of transmission of susceptibility of bats to SARS-CoV-2.

Carnivores. Recent reports of a Malayan tiger and a domestic cat infected by SARS-CoV-2 suggest that the virus can be transmitted to other felids (9, 47). Our results are consistent with these studies; 9/9 felids we analyzed scored *medium* for ACE2 binding of SARS-CoV-2 S. However, the masked palm civet (*Paguma larvata*), a member of the Viverridae family that is related to but distinct from Felidae, scored as *very low*. These results are inconsistent with transfection studies using civet ACE2 receptors expressed in HeLa cells (1), although these experiments have limitations as discussed above. While

carnivores closely related to dogs (dingos, wolves and foxes) all scored *low*, experimental data supporting infection in dogs were inconsistent (47, 50, 59) so no conclusions can be drawn.

Pangolins. Considerable controversy surrounds reports that pangolins can serve as an intermediate host for SARS-CoV-2. Pangolins were proposed as a possible intermediate host (22) and have been shown to harbor related coronaviruses. In our study, ACE2 of Chinese pangolin (*Manis pentadactyla*), Sunda pangolin (*Manis javanica*), and white bellied pangolin (*Phataginus tricuspis*) had *low* or *very low* binding score for SARS-CoV-2 S. Neither experimental infection nor *in vitro* infection with SARS-CoV-2 has been reported for pangolins. As for ferrets and bats, if SARS-CoV-2 infects pangolins it may be using a receptor other than ACE2, based on our analysis.

Other vertebrates. Our analysis of 29 orders of fishes, 29 orders of birds, 3 orders of reptiles and 2 orders of amphibians predicts that the ACE2 proteins of species within these vertebrate classes are not likely to bind SARS-CoV-2 S. Thus, vertebrate classes other than mammals are not likely to be an intermediate host or reservoir for the virus, despite predictions reported in a recent study (45), unless SARS-CoV-2 can use another receptor for infection. With many different non-mammal vertebrates sold in the seafood and wildlife markets of Asia and elsewhere, it is still important to determine if SARS-CoV-2 can be found in non-mammalian vertebrates.

Relevance to Threatened Species. Among the 103 species that scored *very high*, *high* and *medium* for ACE2 SARS-CoV-2 S RBD binding, 41 (40%) are classified in one of three 'Threatened' categories (*Vulnerable*, *Endangered*, and *Critically Endangered*) on the IUCN Red List of Threatened Species, five are classified as *Near Threatened*, and two species are classified as *Extinct in the Wild* (Dataset S1)(60). This represents only a small fraction of the threatened species potentially susceptible to SARS-CoV-2. For example, all 20 catarrhine primate species in our analysis, representing three families (Cercopithecidae, Hylobatidae, and Hominidae) scored *very high*, suggesting that all 185 species of catarrhine primates, most of which are classified Threatened (62), are potentially susceptible to SARS-CoV-2. Similarly, all three species of deer, representatives of a family of ~92 species (Cervidae), scored as *high* risk, as did species representing Cetacea (baleen and toothed whales), and both groups contain a number of threatened species. Toothed whales have potential for viral outbreaks and have lost function of a gene key to the antiviral response in other mammalian lineages (61). If they are susceptible to SARS-CoV-2 , human-to-animal transmission could pose a risk through sewage outfall (62) and contaminated refuse from cities, commercial vessels and cruise liners (63). In contrast, some threatened species scored *low* or *very low*, such as the giant panda (*low*), potentially positive news for these at risk populations.

Our results have practical implications for populations of threatened species in the wild and those under human care (including those in zoos). Established guidelines for minimizing potential human to animal transmission should be implemented and strictly followed. Guidelines for field researchers working on great apes established by the IUCN have been in place since 2015 in response to previous human disease outbreaks (64) and have received renewed attention because of SARS-CoV-2 (64–66). For zoos, guidelines in response to SARS-CoV-2 have been distributed by several Taxon Advisory Groups of the North American Association of Zoos and Aquariums (AZA), the American Association of Zoo Veterinarians (AAZV), and the European Association of Zoo and Wildlife Veterinarians (EAZWV), and these organizations are actively monitoring and updating knowledge of species in human care considered to be potentially sensitive to infection (67, 68). Although *in silico* studies suggest potential susceptibility of diverse species, verification of infection potential is warranted, using cell cultures, stem cells, organoids, and other methods that do not require direct animal infection studies. Zoos and other facilities that maintain living animal collections are in a position to provide such samples for generating crucial research resources by banking tissues, and cryobanking viable cell cultures in support of these efforts.

Animal models for COVID-19. A variety of animal models have been developed for studying SARS and MERS coronavirus infections (69). Presently, there is a tremendous need for animal models for studying SARS-CoV-2 infection and pathogenesis, as the only species currently known to be infected and show similar symptoms of COVID-19 is rhesus macaque. Non-human primate models have proven to be highly valuable for other infectious diseases, but are expensive to maintain and numbers of experimental animals are limited. Our results provide an extended list of potential species that might be useful as animal models for SARS-CoV-2 infection and pathogenesis, including Chinese hamster and Syrian/Golden hamster (49), and large animals maintained for biomedical and agricultural research (e.g., domesticated sheep and cattle).

Conclusions. We predict that species scored as *very high* and *high* for SARS-CoV-2 S binding to ACE2 will have a high probability of becoming infected by the virus. We also predict that many species having a *medium* score have some risk of infection, and species scored as *very low* and *low* are unlikely to be infected by SARS-CoV-2 via the ACE2 receptor. Importantly, our predictions are based solely on *in silico* analyses and must be confirmed by direct experimental data. Until such time, other than for species in which SARS-CoV-2 infection has been demonstrated to occur using ACE2, we urge caution not to over-interpret the predictions made in the present study. This is especially important with regards to species, endangered or otherwise, in human care. While species ranked *high* or *medium* may be

susceptible to infection based on the features of their ACE2 residues, pathological outcomes may be very different among species depending on other mechanisms that could affect virus replication and spread to target cells, tissues, and organs within the host. Furthermore, we cannot exclude the possibility that infection in any species occurs via another cellular receptor, as has been shown for other betacoronaviruses. Nonetheless, our predictions provide a useful starting point for selection of appropriate animal models for COVID-19 research and for identification of species that may be at risk for human-to-animal or animal-to-animal transmissions by SARS-CoV-2. The approach we used for ACE2 can be extended to other cellular proteins known to be involved in coronavirus infection and immunity to better understand infection, transmission, inflammatory responses and disease progression.

Materials and Methods

Angiotensin I converting enzyme 2 (ACE2) coding and protein sequences. All human ACE2 orthologs for vertebrate species, and their respective coding sequences, were retrieved from NCBI Protein (March 20, 2020) (70). ACE2 coding DNA sequences were extracted from available or recently sequenced unpublished genome assemblies for 123 other mammalian species, with the help of genome alignments and the human or within-family ACE2 orthologs. The protein sequences were predicted using AUGUSTUS v3.3.2 (71) or CESAR v2.0 (72) and the translated protein sequences were checked against the human ACE2 orthologue. ACE2 gene predictions were inspected and manually curated if necessary. For four bat species (*Micronycteris hirsuta*, *Mormoops blainvillei*, *Tadarida brasiliensis* and *Pteronotus parnellii*) the ACE2 coding region was split into two scaffolds which were merged, and for *Eonycteris spelaea* a putative 1bp frameshift base error was corrected. Eighty ACE2 predictions were obtained from the Zoonomia project, 19 from the Hiller Lab, 12 from the Koepfli lab, 8 from the Lewin lab and 4 from the Zhou lab. The source, and accession numbers for the genomes or proteins retrieved from NCBI are listed in Dataset S1. The final set of ACE2 sequences comprises 410 vertebrate species. To assure alignment robustness, the full set of coding and protein sequences were aligned independently using Clustal Omega (73), MUSCLE (74) and COBALT (75) all with default parameters. All resulting protein alignments were identical. Clustal Omega alignments were used in the subsequent analysis. Each amino acid replacement present in our dataset was classified as neutral, semi-conservative and non-conservative as in Clustal Omega.

Identification of ACE2 residues involved in binding to SARS-CoV-2 S protein. We identified 22 ACE2 protein residues that were previously reported to be critical for the effective binding of ACE2 RBD and

SARS-CoV-2 S (13, 21). These residues include S19, Q24, T27, F28, D30, K31, H34, E35, E37, D38, Y41, Q42, L45, L79, M82, Y83, N330, K353, G354, D355, R357, and R393. All these residues were identified from the co-crystallization and structural determination of SARS-CoV-2 S and ACE2 RBD (13, 21). The known human ACE2 RBD glycosylation sites N53, N90 and N322 were also included in the analyzed residue set (11).

ACE2 and SARS-CoV-2 binding ability prediction. Based on the known interactions of ACE2 and SARS-CoV-2 residues, we developed a set of rules for predicting the likelihood of the SARS-CoV-2 S binding to ACE2. Each species was classified in one of five categories: *very high*, *high*, *medium*, *low* or *very low* likelihood of binding SARS-CoV-2 S. Species in the *very high* category have at least 23/25 critical residues identical to the human; have K353, K31, E35, M82, N53, N90 and N322; do not have N79; and have only conservative substitutions among the non-identical 2/25 residues. Species in the *high* group have at least 20/25 residues identical to the human; have K353; have only conservative substitutions at K31 and E35; do not have N79; and can only have one non-conservative substitution among the 5/25 non-identical residues. Species scoring *medium* have at least 20/25 residues identical to the human; can only have conservative substitutions at K353, K31, and E35; and can have up to two non-conservative substitutions in the 5/25 non-identical residues. Species in the *low* category have at least 18/25 residues identical to the human; can only have conservative substitutions at K353; can have up to three non-conservative substitutions on the remaining 7/25 non-identical residues. Lastly, species in the *very low* group have less than 18/25 residues identical to the human or have at least four non-conservative substitutions in the non-identical residues.

Protein structure analysis. We applied an orthogonal approach to assess the likelihood of binding of a sampling of species that were predicted to bind SARS-CoV-2 across the categories of *high*, *medium*, *low* or *very low* likelihood of binding. ACE2 amino acid sequences from 28 species were extracted from the multiway alignment and loaded into SWISS-MODEL (25) in order to generate homology derived models. The output files were aligned to the crystal structure 6MOJ (13) in order to assess the overall similarities to human ACE2. We used two recently solved crystal structures of the complex for ACE2 and SARS-CoV-2 S RBD, 6MOJ (13) and 6VW1 (21) as ground truth for the human ACE2/SARS-CoV-2 S interaction. In the program CHIMERA (76), we utilized the rotamer function to model each individual variant that species exhibit separately, and chose the rotamer with the least number of clashes, retaining the most initial hydrogen bonds and containing the highest probability of formation as calculated by CHIMERA from the Dunbrack 2010 backbone-dependent rotamer library (77). The rotamer was then evaluated in the context of its structural environment and assigned a score based on likelihood of interface disruption.

Neutral (N) was assigned if the residue maintained a similar environment as the original residue, and was predicted to maintain or in some cases increase affinity. Weakened (W) was assigned if hydrophobic contacts were lost and contacts that appear disruptive are introduced that are not technically clashes. Unfavorable (U) was assigned if clashes are introduced and/or a hydrogen bond is broken. Additional structural visualizations were generated in Pymol (78).

Human variants analysis. All variants at the 25 residues critical for effective SARS-CoV-2-ACE2 binding (11, 21, 79) were compiled from from dbSNP (31), 1KGP (32), Topmed (33), UK10K (34) and CHINAMAP (28). Specific population frequencies were obtained from gnomAD v.2.1.1 (17).

Phylogenetic reconstruction of the vertebrate *ACE2* species tree. The multiple sequence alignment of 410 ACE2 orthologous protein sequences from mammals, birds, fishes, reptiles and amphibians was used to generate a gene tree using the maximum likelihood method of reconstruction, as implemented in IQTREE (80). The best fit model of sequence evolution was determined using ModelFinder (81) and used to generate the species phylogeny. A total of 1000 bootstrap replicates were used to determine node support using UFBoot (82).

Identifying sites undergoing positive selection. Signatures of site-specific positive selection in the *ACE2* receptor were explored using CODEML, part of the Phylogenetic Analysis using Maximum Likelihood (PAML, (83)) suite of software. Given CODEML's computational complexity, a smaller subset of mammalian taxa (N=64, Dataset S1), which included species from all prediction categories mentioned above, was used for selection analyses. To calculate likelihood-derived dN/dS rates (ω), CODEML utilises both a species tree and a codon alignment. The species tree for all 64 taxa was calculated using IQTREE (80) and the inferred best-fit model of sequence evolution (JTT+F+R4). This gene topology was generally in agreement with the 410 taxa tree, however bats were now sister taxa to Perissodactyla. Therefore all selection analyses were run using both the inferred gene tree, and a modified tree with the position of bats manually modified to reflect the 410 taxa topology. All species trees used were unrooted. A codon alignment of the 64 mammals was generated using pal2nal (84) with protein alignments generated with Clustal Omega (73) and their respective CDS sequences.

Site-models M7 (null model) and M8 (alternative model) were used to identify *ACE2* sites undergoing positive selection in mammals. Both M7 and M8 estimate ω using a beta distribution and 10 rate categories per site with ω<=1 (neutral or purifying selection), but with an additional 11^{th} category allowing ω >1 (positive selection) in M8. A likelihood ratio test (LRT) calculated as $2*(\ln L_{alt} - \ln L_{null})$, comparing the fit of both null and alternative model likelihoods was carried out, with a p-value

calculated assuming a chi-squared distribution. Sites showing evidence of positive selection were identified by a significant (>0.95) Bayes Empirical Bayes (BEB) score, and validated by visual inspection of the protein alignment. To explore order-specific instances of positive selection, separate multiple sequence alignments and gene trees for Chiroptera (N=37), Cetartiodactyla (N=45), Carnivora (N=44), Rodentia (N=46) and Primates (N=39) were also generated and explored using M7 vs. M8 in CODEML.

In addition to site-models, branch-site model A1 (null model) and model A (alternative model) were also implemented targeting various mammalian orders, specifically Chiroptera, Cetartiodactyla, Rodentia and Primates, to identify lineage-specific positive selection in the *ACE2* receptor sequence. Branch-site Model A1 constrains both the target foreground branch (Carnivora, Chiroptera, Cetartiodactyla, Rodentia and Primates) and background branches to $\omega<=1$, while the alternative Model A allows positive selection to occur in the foreground branch. Null and alternative models were compared using LRTs as above, with significant BEB sites identified.

We also looked for positively selected sites in the viral spike protein, using SARS-CoV-2 (MN908947.3), Bat coronavirus RaTg13 (MN996532.1), Bat SARS-like coronavirus isolate Rs4231 (KY417146.1), SARS-related coronavirus strain BtKY72 (KY352407.1), SARS coronavirus Urbani (AY278741.1), SARS coronavirus PC4-227 (AY613950.1), Coronavirus BtRs-BetaCoV/YN2018B (MK211376.1) and the more divergent Bat Hp-betacoronavirus/Zhejiang2013 (NC_025217.1) viral strains. Protein and codon alignments were generated as above, with the viral species tree inferred using full genome alignments of all strains generated with Clustal Omega (73). Site-test models were applied using CODEML, and significant BEB sites identified.

Analysis for departure from neutral evolutionary rate in ACE2 with PHAST. Neutral models were trained on the specified species sets (Dataset S4) using the REV nucleotide substitution model implemented in phyloFit using an expectation maximization algorithm for parameter optimization. The neutral model fit was based on third codon positions to approximate the neutral evolution rate specific to the *ACE2* gene, using a 410-species phylogenetic tree generated by IQTREE as described above and rooted on fishes. The program phyloP was then used to identify codons undergoing accelerated or conserved evolution relative to the neutral model using --features to specify codons, --method LRT --mode CONACC, and --subtree for lineage-specific tests, with p-values thus assigned per codon based on a likelihood ratio test. P-values were corrected for multiple testing using the Benjamini-Hochberg method (36) and sites with a corrected p-value less than 0.05 were considered significant. PhyloFit and phyloP are both part of the PHAST package v1.4 (85, 86).

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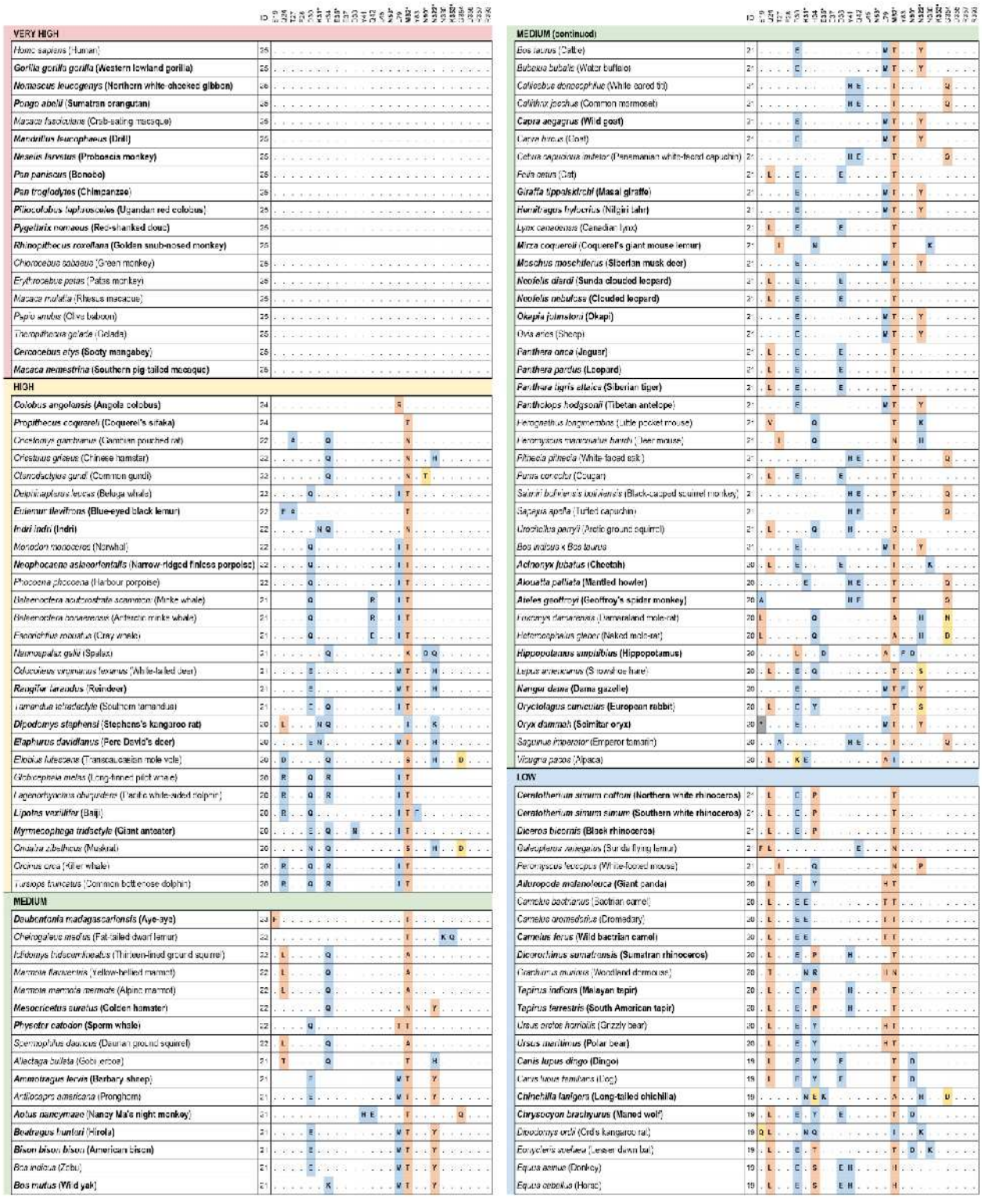
Figures and Tables



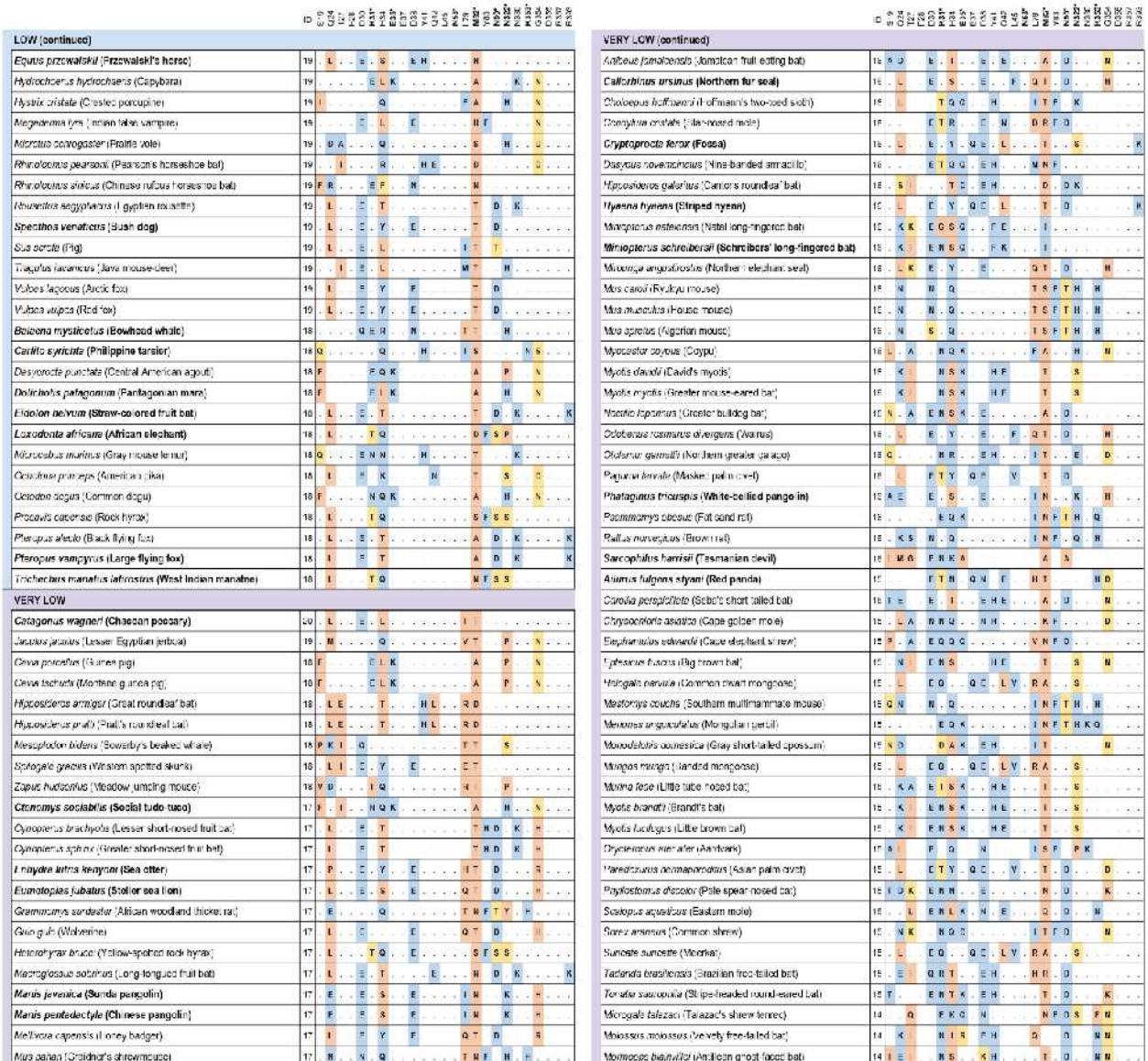


Figure 1. Cross-species conservation of ACE2 and predictions of SARS-CoV-2 susceptibility. Species are sorted by binding score of ACE2 for SARS-CoV-2 S. The 'ID' column depicts the number of amino acids identical to human binding residues. Bold amino acid positions (also labeled with *) represent residues at binding hotspots and constrained in the scoring scheme. Each amino acid substitution is colored according to its classification as non-conservative (orange), semi-conservative (yellow) or neutral (blue), as compared to the human residue. Bold species names depict species with threatened IUCN risk status. The 410 vertebrate species dataset is available in Dataset S1.

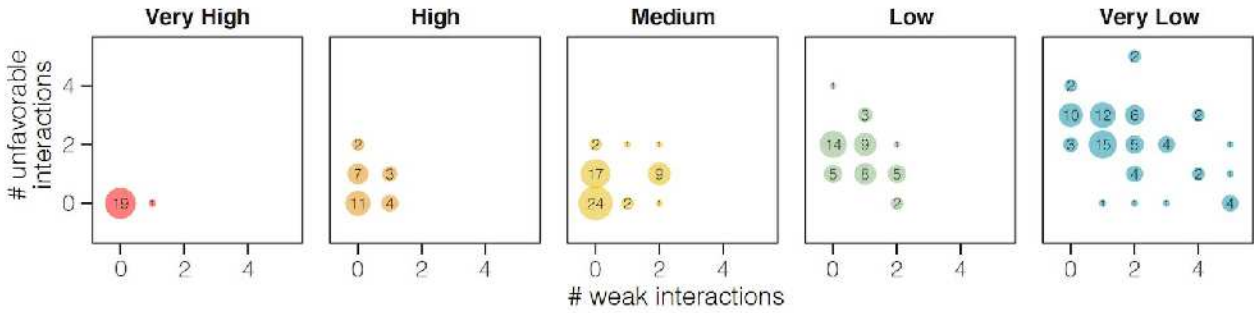


Figure 2. Congruence between binding score and structural homology analysis. Species classified by sequence identity to human ACE2 as *very high* (red) or *high* binding score (orange) have significantly fewer amino acid substitutions rated as potentially altering the binding interface between ACE2 and SARS-CoV-2 through protein structural analysis, as compared to *low* (green) or *very low* (blue) species. The more severe *unfavorable* variants are counted on y-axis and less severe *weaken* variants on the x-axis. Black numerical labels indicate species count.

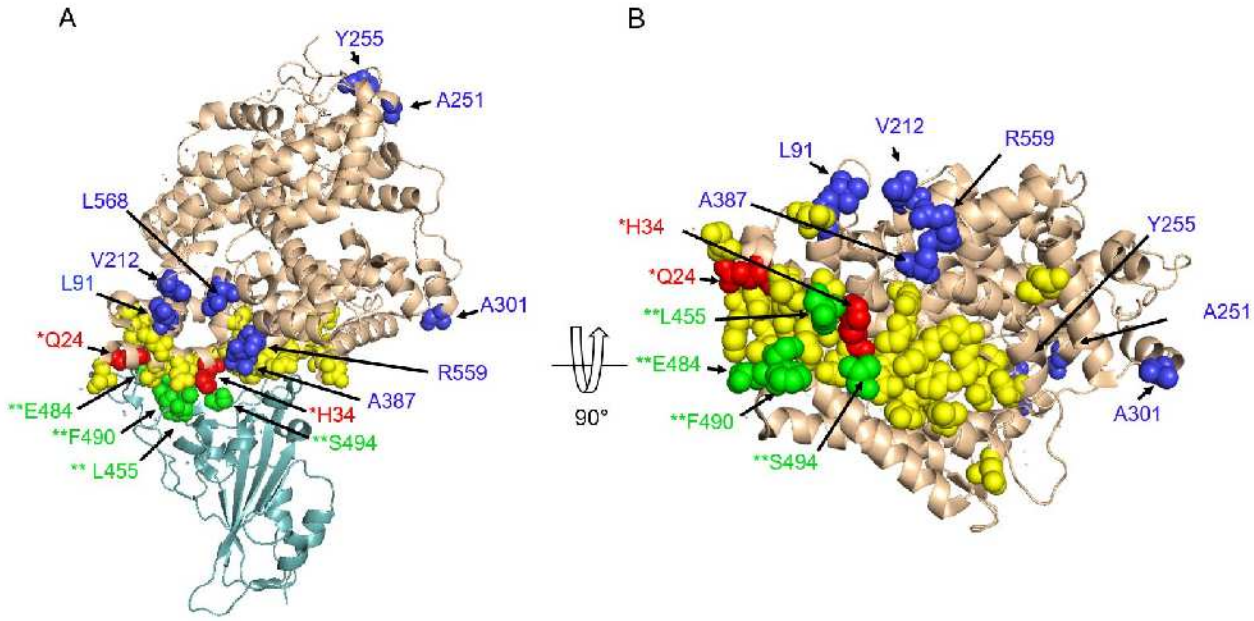


Figure 3. Residues under positive selection detected with CODEML and acceleration with phyloP in mammals. (**A**) ACE2 is represented in wheat cartoon with residues involved in the binding interface shown in yellow spheres. Dark blue and red spheres indicate residues in ACE2 that are accelerated and under positive selection. Red spheres represent residues that overlap with positions in the binding interface and are labeled with (*). The spike RBD is shown in light teal cartoon. Green spheres indicate residues on the SARS-CoV-2 spike protein under positive selection and are labeled with (**). (**B**) 90 degree rotation of the ACE2 protein.

From: Kevin Olival ecohealthalliance.org>
Sent: Thursday, April 16, 2020 10:26 PM EDT
To: Jonathan S. Towner <jit8@CDC.GOV>
CC: Daniel Streicker epstein ecohealthalliance.org>; Grant, Evan H ; castlekl >; O'Shea, Thomas ; raina.plowright ; dreeder ; sja >; kate.e.jones >; Christine Kreuder Johnson >; wfrick ; linfa.wang ; a.peel >; Ralph S. Baric ; Kading,Rebekah ; Amy Gilbert ; Lorch, Jeffrey M ; Runge, Michael C ; Paul Cryan Jonathan M Sleeman ; Jeremy Coleman >; Gibbs, Samantha >; Hopkins, Maria-Richetta (Camille) C
Subject: Re: Expert judgement for SARS-CoV-2 risk assessment for North American bats
Attachment(s): "preprints202004.0203.v1.pdf"

Here's another review (preprint) on mask efficacy.

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

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EcoHealth Alliance develops science-based solutions to prevent pandemics *and* promote conservation

> On Apr 15, 2020, at 7:15 PM, Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) > wrote:
>
> Some food for thought while considering the effectiveness (or not) of bat workers/researchers putting on some kind of respiratory protection. This data, collected pre-COVID19, basically shows that putting on surgical masks can be effective for minimizing the spread of human coronaviruses, although the total number of patients tested was still pretty low and we don't know the extent to which COVID-19 can be spread in aerosolized form. Note that the masks weren't that effective for rhinoviruses or aerosolized flu.
>
> Jon
>
> ---
>
> **From:** Daniel Streicker
> **Sent:** Wednesday, April 15, 2020 2:04 PM
> **To:** Jon Epstein ecohealthalliance.org>
> **Cc:** Grant, Evan H ; castlekl ; O'Shea, Thomas >; raina.plowright ; dreeder sja kate.e.jones ; ckjohnson wfrick linfa.wang ; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) >; a.peel ; rbaric ; Rebekah.Kading Gilbert, Amy T - Aphis >; Lorch, Jeffrey M >; Runge, Michael C >; Cryan, Paul ; ecohealthalliance.org; Sleeman, Jonathan M Coleman, Jeremy T ; Gibbs, Samantha >; Hopkins, Maria-Richetta (Camille) C
>
> **Subject:** Re: Expert judgement for SARS-CoV-2 risk assessment for North American bats
>
> Hi Jon,
>
> Thanks for passing this along. So others don't have to dig through all of the the 2.5 page table full of abbreviations, here are some scores (matching residues of the 20 key AAs considered) for a few selected species which might be relevant to judging the susceptibility of Myotis lucifugus, which had a score of 11/20:

Homo sapiens (20/20)
Sus scrofa (15/20), in vitro evidence of infection
Mustela putorius furo (15/20), in vivo susceptibility confirmed
Rhinolophus macrotis (13/20), susceptible?
Rhinolophus pusillus (14/20), susceptible?
Rhinolophus ferrumequinum (12/20), susceptible?
Desmodus rotundus (12/20), possibly susceptible (same family as Artibeus, which was not included in the study)?

So, Myotis is relatively low on the list, but so are bats which are related to the presumed reservoir and known susceptible species like ferrets are not too much higher up on the list. I'd be curious to know how others with more knowledge than myself interpret these numbers. Is this measure of ACE-2 affinity something we should use and how low is too low for a host to be susceptible?

Best,
Daniel

On 15 Apr 2020, at 17:35, Jon Epstein ecohealthalliance.org> wrote:

Hi All,
Here's the ACE-2 affinity paper.
Cheers,
Jon

On Thu, Apr 9, 2020 at 5:39 PM Grant, Evan H > wrote:

> Hello experts,
>
> Thank you for volunteering your time and expertise to help estimate the risk of SARS-CoV-2 to North American bats. Mike Runge and I (Evan Grant), with the U.S. Geological Survey Patuxent Wildlife Research Center, are facilitating this effort in collaboration with the USGS National Wildlife Health Center, USGS Fort Collins Science Center, USFWS, and EcoHealth Alliance. We are conducting a rapid assessment of the risks for transmission of SARS-CoV-2 from humans to bats. The goal is to provide scientific information that will guide wildlife management agency response to this potential risk, including development of management recommendations and mitigation strategies.
>
> Attached please find two documents: (1) an introduction to expert elicitation with some background on the issue we are addressing, and (2) a spreadsheet <BatEE Practice Questions v2.xlsx> with calibration questions. There are three tabs (corresponding to the three questions) in the accompanying spreadsheet, and a fourth tab that summarizes the responses and the calculated mean and standard deviation for each question.
>
> We have a very tight timeline to provide guidance to U.S. management agencies, so we thank you for your participation along the following timeline:
>
> i. Respond to ehgrant with your responses to the calibration questions in the attached spreadsheet (due by 12 PM ET 10 Apr)
>
> ii. Review the background information and elicitation questions (we will send these additional documents to you by 6 pm ET 10 Apr)
>
> iii. Respond with your initial responses to the questions (due by 6 PM ET 13 Apr)
>
> iv. Be available for a 2-hr conference call to discuss initial responses and share insights (4 PM ET 14 Apr – and/or – 4 PM ET 15 Apr)
>
> v. Revise and send your second-round responses to the questions (due 24 hours after the last conference call)
>
> Thank you in advance for your participation. If you have questions – please contact Evan (ehgrant@usgs.gov).
>
> Kindest regards,
> Evan and Mike

--
Jonathan H. Epstein DVM, MPH, PhD
Vice President for Science and Outreach
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)

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EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

<SARS-CoV 2 spike protein favors ACE2 from Bovidae and Cricetidae_Luan et al 2020.pdf>

<Leung NHL et al. 2020 Resp virus shedding in exhaled breath and efficacy of face masks Nature Medicine.pdf>

Face Masks Against COVID-19: An Evidence Review

Jeremy Howard[a,c,1], Austin Huang[b], Zhiyuan Li[k], Zeynep Tufekci[m], Vladimir Zdimal[e], Helene-Mari van der Westhuizen[f,g], Arne von Delft[o,g], Amy Price[n], Lex Fridman[d], Lei-Han Tang[j,l], Viola Tang[l], Gregory L. Watson[h], Christina E. Bax[s], Reshama Shaikh[q], Frederik Questier[r], Danny Hernandez[p], Larry F. Chu[n], Christina M. Ramirez[h], and Anne W. Rimoin[t]

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This manuscript was compiled on April 12, 2020

The science around the use of masks by the general public to impede COVID-19 transmission is advancing rapidly. Policymakers need guidance on how masks should be used by the general population to combat the COVID-19 pandemic. Here, we synthesize the relevant literature to inform multiple areas: 1) transmission characteristics of COVID-19, 2) filtering characteristics and efficacy of masks, 3) estimated population impacts of widespread community mask use, and 4) sociological considerations for policies concerning mask-wearing. A primary route of transmission of COVID-19 is likely via small respiratory droplets, and is known to be transmissible from presymptomatic and asymptomatic individuals. Reducing disease spread requires two things: first, limit contacts of infected individuals via physical distancing and contact tracing with appropriate quarantine, and second, reduce the transmission probability per contact by wearing masks in public, among other measures. The preponderance of evidence indicates that mask wearing reduces the transmissibility per contact by reducing transmission of infected droplets in both laboratory and clinical contexts. Public mask wearing is most effective at stopping spread of the virus when compliance is high. The decreased transmissibility could substantially reduce the death toll and economic impact while the cost of the intervention is low. Thus we recommend the adoption of public cloth mask wearing, as an effective form of source control, in conjunction with existing hygiene, distancing, and contact tracing strategies. We recommend that public officials and governments strongly encourage the use of widespread face masks in public, including the use of appropriate regulation.

COVID-19 | SARS-CoV-2 | Masks | Pandemic

Policymakers need urgent guidance on the use of masks by the general population as a tool in combating SARS-CoV-2, the respiratory virus that causes COVID-19. Masks have been recommended as a potential tool to tackle the COVID-19 pandemic since the initial outbreak in China (1), although usage during the outbreak varied by time and province (2). Globally, countries are grappling with translating the evidence of public mask wearing to their contexts. These policies are being developed in a complex decision-making environment, with a novel pandemic, rapid generation of new research, and exponential growth in cases and deaths in many areas. There is currently a global shortage of N95 or FFP2 respirators and surgical masks for use in hospitals. Simple cloth masks present a pragmatic solution for use by the public. This has been supported by the United States and European Centres for Disease Control. We present a literature review on the role of simple cloth masks and policies in reducing COVID-19 transmission.

1. Components to Evaluate for Public Mask Wearing

In order to identify whether public mask wearing is an appropriate policy, we need to consider these questions:

1. Do asymptomatic or presymptomatic patients pose a risk of infecting others?
2. Would a face mask likely decrease the number of people infected by an infectious mask wearer?
3. Are there alternative face covers that will not disrupt the medical supply chain, e.g. homemade cloth masks?
4. Will wearing a mask impact the probability of the wearer becoming infected themselves?
5. Does mask use reduce compliance with other recommended strategies, such as physical distancing and quarantine?

Significance Statement

Governments are evaluating the use of non-medical masks in the community amidst conflicting guidelines from health organizations. This review synthesizes available evidence to provide clarity, and advances the use of the 'precautionary principle' as a key consideration in developing policy around use of non-medical masks in public.

Jeremy Howard prepared the initial literature list; Reshama Shaikh prepared the initial literature summaries; Frederik Questier did additional literature searches and summaries; Zhiyuan Li, Violet Tang, Lei-Han Tang, and Danny Hernandez did impact modeling; Zeynep Tufekci provided sociological research and analysis; Helene-Mari van der Westhuizen and Arne von Delft provided analysis of additional impacts; Christina Bax provided review and feedback; All authors contributed to the writing.

Anne W. Rimoin is an editor of the British Medical Journal. Larry F. Chu is a member of the editorial advisory board of the British Medical Journal.

[1]To whom correspondence should be addressed. E-mail: jphoward@usfca.edu

6. Are there any other potential benefits to universal mask wearing such as reducing stigma, signaling solidarity, and increased compliance with other measures?

We will evaluate each consideration in turn.

2. Transmission Characteristics of COVID-19

A primary route of transmission of SARS-CoV-2 is likely via small droplets that are ejected when speaking, coughing or sneezing. The most common droplet size threshold has a minimum at 5 µm to 10 µm (3, 4). There is much debate about whether these droplets should sometimes be considered an aerosol (5). An added complexity is that aerosols are not consistently defined in the literature.

Although earlier studies assumed that droplets were spread mainly through coughing, a more recent analysis has found that transmission through talking may be a key vector, with louder speech creating increasing quantities and sizes of droplets, which are associated with a higher viral load (6).

SARS-CoV-2 is highly transmissible, with a replication number estimated to be approximately 2.4 (7) although estimates vary (8) and will likely change as improved measurements of asymptomatic spread become available. Many COVID-19 patients are asymptomatic, and nearly all have a pre-symptomatic incubation period ranging from 2 to 15 days, with a median length of 5.1 days (9). Patients are most infectious during the initial days of infection (10–15), when symptoms are mildest or not present. This characteristic differentiates SARS-CoV-2 (COVID-19) from SARS-CoV, as replication is activated early in the upper respiratory tract (14, 16). High viral titers of SARS-CoV-2 are reported in the saliva of COVID-19 patients. These titers have been highest at time of patient presentation and viral levels are just as high in asymptomatic or presymptomatic patients (11, 16).

A consequence of these disease characteristics is that any successful intervention policy must properly address transmission due to infectious patients that display few or no symptoms and may not realize that they are infected.

3. Filtering Capability of Masks

Masks can be made of different materials and designs (17) which influence their filtering capability. There are rigorous standards evaluating masks used in healthcare settings but these focus on personal protective equipment (PPE) efficacy, that is, the ability of the mask to protect the wearer from infectious particles. N95 (the American standard; the equivalent in Europe is FFP2) respirators are recommended for health workers conducting aerosol-generating procedures during clinical care of COVID-19 patients. While it has been shown that N95 or FFP2 respirators perform well as PPE, they can become a scarce resource during a pandemic. Toner and Waldhorn (2006) (18) point out that shortages of N95 or FFP2 respirators should be anticipated, and say that if no other masks are available, surgical masks, which will provide droplet protection, should be used. One approach that has been studied for handling N95 or FFP2 respirator shortages is sterilization and re-use, which can be effective (19).

Masks can also be used for source control, which refers to blocking droplets ejected by the wearer, as well as PPE. Although we consider both of these as important, our focus in this paper is on source control, because if everyone is wearing masks to decrease the chance that they themselves are unknowingly infecting someone, everyone ends up being more protected.

Multiple studies show the filtration effects of cloth masks relative to surgical masks. Particle sizes for speech are on the order of 1 µm (20) while typical definitions of droplet size are 5 µm-10 µm (5). Generally available household materials had between a 49% and 86% filtration rate for 0.02 µm exhaled particles whereas surgical masks filtered 89% of those particles (21). In a laboratory setting, household materials had 3% to 60% filtration rate for particles in the relevant size range, finding them comparable to some surgical masks (22). In another laboratory setup, a tea cloth mask was found to filter 60% of particles between 0.02 µm to 1 µm, where surgical masks filtered 75% (23). Dato et al (2006) (24), note that "quality commercial masks are not always accessible." They designed and tested a mask made from heavyweight T-shirts, finding that it "offered substantial protection from the challenge aerosol and showed good fit with minimal leakage".Although cloth and surgical masks are primarily targeted towards droplet particles, some evidence suggests they may have a partial effect in reducing viral aerosol shedding (25).

When considering the relevance of these studies of ingress, it's important to note that they are likely to substantially underestimate effectiveness of masks for source control. When someone is breathing, speaking, or coughing, only a tiny amount of what is coming out of their mouths is already in aerosol form. Nearly all of what is being emitted is droplets. Many of these droplets will then evaporate and turn into aerosolized particles that are 3 to 5-fold smaller. The point of wearing a mask as source control is largely to stop this process from occurring, since big droplets dehydrate to smaller aerosol particles that can float for longer in air (26).

Anfinrud et al (6) used laser light-scattering to sensitively detect droplet emission while speaking. Their analysis showed that virtually no droplets were "expelled" with a homemade mask consisting of a washcloth attached with two rubber bands around the head, while significant levels were expelled without a mask. The authors stated that "wearing any kind of cloth mouth cover in public by every person, as well as strict adherence to distancing and handwashing, could significantly decrease the transmission rate and thereby contain the pandemic until a vaccine becomes available."

An important focus of analysis for public mask wearing is droplet source control. This refers to the effectiveness of blocking droplets from an infectious person, particularly during speech, when droplets are expelled at a lower pressure and are not small enough to squeeze through the weave of a cotton mask. Many recommended cloth mask designs also include a layer of paper towel or coffee filter, which could increase filter effectiveness for PPE, but does not appear to be necessary for blocking droplet emission (6, 27, 28).

In summary, there is laboratory-based evidence that household masks have some filtration capacity in the relevant droplet size range, as well some efficacy in blocking droplets and particles from the wearer (26). That is, these masks help people keep their droplets to themselves.

4. Mask Efficacy Studies

Although no randomized controlled trials (RCT) on the use of masks as source control for SARS-CoV-2 has been published, a number of studies have attempted to indirectly estimate the efficacy of masks. Overall, an evidence review (29) finds "moderate certainty evidence shows that the use of handwashing plus masks probably reduces the spread of respiratory viruses."

The most relevant paper (30), with important implications for public mask wearing during the COVID-19 outbreak, is one that compares the efficacy of surgical masks for source control for seasonal coronavirus, influenza, and rhinovirus. With ten participants, the masks were effective at blocking coronavirus droplets of all sizes for every subject. However, masks were far less effective at blocking rhinovirus droplets of any size, or of blocking small influenza droplets. The results suggest that masks may have a significant role in source control for the current coronavirus outbreak. The study did not use COVID-19 patients, and it is not yet known whether seasonal coronavirus behaves the same as SARS-CoV-2; however, they are of the same genus, so similar behavior is likely.

Another relevant (but under-powered, with n=4) study (31) found that a cotton mask blocked 96% (reported as 1.5 log units or about a 36-fold decrease) of viral load on average, at eight inches away from a cough from a patient infected with COVID-19. If this is replicated in larger studies it would be an important result, because it has been shown (32) that "every 10-fold increase in viral load results in 26% more patient deaths" from "acute infections caused by highly pathogenic viruses".

A comparison of homemade and surgical masks for bacterial and viral aerosols (21) observed that "the median-fit factor of the homemade masks was one-half that of the surgical masks. Both masks significantly reduced the number of microorganisms expelled by volunteers, although the surgical mask was 3 times more effective in blocking transmission than the homemade mask." Research focused on aerosol exposure has found all types of masks are at least somewhat effective at protecting the wearer. Van der Sande et al (33) found that "all types of masks reduced aerosol exposure, relatively stable over time, unaffected by duration of wear or type of activity", and concluded that "any type of general mask use is likely to decrease viral exposure and infection risk on a population level, despite imperfect fit and imperfect adherence". Overall however, analysis of particle filtration is likely to underestimate the effectiveness of masks, since the fraction of particles that are emitted as aerosol (vs. droplet) is quite small (26). Analysis of seasonal coronavirus compared to rhinovirus (30) suggests that filtration of COVID-19 may be much more effective, especially for source control.

The importance of using masks for health care workers has been observed (34) in three Chinese hospitals where, in each hospital, medical staff wearing masks (mainly in quarantine areas) had no COVID-19 infections, despite being around COVID-19 patients far more often, whilst other medical staff had 10 or more infections in each of the three hospitals.

Masks seem to be effective for source control in the controlled setting of an airplane. One case report (35) describes a man who flew from China to Toronto and then tested positive for COVID-19. He was wearing a mask during the flight. The 25 people closest to him on plane/flight attendants were tested and all were negative. Nobody has been reported from that flight as getting COVID-19. Another case study involving a masked influenza patient on an airplane (36) found that "wearing a face mask was associated with a decreased risk for influenza acquisition during this long-duration flight".

Guideline development for health worker personal protective equipment have focused on whether surgical masks or N95 respirators should be recommended. Most of the research in this area focuses on influenza. At this point, it is not known to what extent findings from influenza studies apply to COVID-19 filtration. Wilkes et al (37) found that "filtration performance of pleated hydrophobic membrane filters was demonstrated to be markedly greater than that of electrostatic filters." However, even substantial differences in materials and construction do not seem to impact the transmission of droplet-borne viruses in practice, such as a meta-analysis of N95 respirators compared to surgical masks (38) that found "the use of N95 respirators compared with surgical masks is not associated with a lower risk of laboratory-confirmed influenza." Johnson et al (39) showed that "surgical and N95 masks were equally effective in preventing the spread of PCR-detectable influenza". Radonovich et al (40) found in an outpatient setting that "use of N95 respirators, compared with medical masks... resulted in no significant difference in the rates of laboratory-confirmed influenza."

One of the most frequently mentioned papers evaluating the benefits and harms of cloth masks have been by MacIntyre et al (41). Findings have been misinterpreted, and therefore justify detailed discussion here. The authors "caution against the use of cloth masks" for healthcare professionals compared to the use of surgical masks and regular procedures, based on an analysis of transmission in hospitals in Hanoi. We emphasize the setting of the study - health workers using masks to protect themselves against infection. The study compared a "surgical mask" group which received 2 new masks per day, to a "cloth mask" group that received 5 masks for the entire 4 week period and were required to wear the masks all day, to a "control group" which used masks in compliance with existing hospital protocols, which the authors describe as a "very high level of mask use". It is important to note that the authors did not have a "no mask" control group because it was deemed "unethical to ask participants to not wear a mask." The study does not inform policy pertaining to public mask wearing as compared to the absence of masks in a community setting, since there is not a "no mask" group. The results of the study show that the group with a regular supply of new surgical masks each day had significantly lower infection of rhinovirus than the group that wore a limited supply of cloth masks. This paper lends support to the use of clean, surgical masks by medical staff in hospital settings to avoid rhinovirus infection by the wearer, and is consistent with other studies that show cloth masks provide poor filtration for rhinovirus (30). Its implementation does not inform the effect of using cloth masks versus not using masks in a community setting for source control of SARS-CoV-2, which is of the same genus as seasonal coronavirus, which has been found to be effectively filtered by cloth masks in a source control setting (30).

A. Studies of Impact on Community Transmission. When evaluating the available evidence for the impact of masks on community transmission, it is critical to clarify the setting of the research study (health care facility or community), the res-

piratory illness being evaluated and what reference standard was used (no mask or surgical mask). There are no RCTs that have been done to evaluate the impact of masks on community transmission during a coronavirus pandemic. While there is some evidence from influenza outbreaks, the current global pandemic poses a unique challenge. A review (42) of 67 studies including randomized controlled trials and observational studies found that simple and lowcost interventions would be useful for reducing transmission of epidemic respiratory viruses. The review recommended that "the following effective interventions should be implemented, preferably in a combined fashion, to reduce transmission of viral respiratory disease: 1. frequent handwashing with or without adjunct antiseptics; 2. barrier measures such as gloves, gowns, and masks with filtration apparatus; and 3. suspicion diagnosis with the isolation of likely cases". However, it cautioned that routine longterm implementation of some measures assessed might be difficult without the threat of an epidemic.

Seuess et al conducted an RCT (43)that suggests household transmission of influenza can be reduced by the use of non-pharmaceutical interventions, namely the use of face masks and intensified hand hygiene, when implemented early and used diligently. Concerns about acceptability and tolerability of the interventions should not be a reason against their recommendation (43). Cowling et al (44) investigated hand hygiene and face masks in an RCT that seemed to prevent household transmission of influenza virus when implemented within 36 hours of index patient symptom onset. These findings suggest that non-pharmaceutical interventions are important for mitigation of pandemic and inter-pandemic influenza.

RCT findings by Aiello et al (45) "suggest that face masks and hand hygiene may reduce respiratory illnesses in shared living settings and mitigate the impact of the influenza A (H1N1) pandemic". A randomized intervention trial (46) found that "face masks and hand hygiene combined may reduce the rate of ILI [influenza-like illness] and confirmed influenza in community settings. These non-pharmaceutical measures should be recommended in crowded settings at the start of an influenza pandemic." The authors noted that their study "demonstrated a significant association between the combined use of face masks and hand hygiene and a substantially reduced incidence of ILI during a seasonal influenza outbreak. If masks and hand hygiene have similar impacts on primary incidence of infection with other seasonal and pandemic strains, particularly in crowded, community settings, then transmission of viruses between persons may be significantly decreased by these interventions."

An observational study in Hong Kong on SARS (47) found "frequent mask use in public venues, frequent hand washing, and disinfecting the living quarters were significant protective factors (OR 0.36 to 0.58)". An important observation was that "members of the case group [infected with SARS] were less likely than members of the control group [not infected] to have frequently worn a face mask in public venues (27.9% vs. 58.7%)".

B. Implementation and Sociolological Considerations. For a novel disease where much is unknown, it is important to examine the context of studies closely and also distinguish "absence of evidence" from "evidence of absence" (2). We discuss estimates of cloth mask filtering performance in Filtering Capability of Masks and summarize modelling on population impact in Estimating Population Impacts.

Some of the concerns about public mask wearing have not been around primary evidence for the efficacy of source control, but concerns about how they will be used. We present some considerations for the translation of evidence about public mask wearing to diverse countries across the globe, outside of the parameters of a controlled research setting:

B.1. Supply chain management of N95 respirators and surgical masks. There has been a global shortage of protective equipment for health workers, with health workers falling ill and dying of occupationally acquired COVID-19 disease (48). Public messaging encouraging mask use and depleting critical supplies have been a major concern. Some regions, like South Korea and Taiwan, have decided to promote surgical mask use on a mass scale and opted to address potential stock issues through rapidly increasing production of surgical masks. In regions where surgical mask supplies are scarce, cloth masks may be a pragmatic temporary alternative to surgical masks for the public.

B.2. Sociological considerations and anticipating population-level behavior changes. It is difficult to predict the behavior change that would accompany regulations encouraging public mask use. One concern around public health messaging promoting the use of face-covering has been that members of the public may use risk compensation behavior and neglect physical distancing based on overvaluing the protection a surgical mask may offer due to an exaggerated or false sense of security (49). Similar arguments have previously been made for HIV prevention strategies (50) (51) and other safety devices and mandates such as motorcycle helmet laws (52) and seat-belts (53). However, research on these topics finds no such increase in adverse outcomes at the population level but rather improvements in safety and well-being, suggesting that even if risk compensation occurs in some individuals, that effect is dwarfed by the increased safety at the population level (53, 54). Further, even for deliberately high-risk recreational activities such as alpine skiing and snowboarding, wearing a helmet was generally associated with risk reduction oriented-behavior (55), suggesting safety devices are both compatible with and perhaps encourage safety-oriented behavior. Even for high-risk recreational activities like alpine skiing and snowboarding, helmet use has greatly reduced injury rates (56).

In general, various forms of risk compensation theories have been proposed for many different safety innovations, but have been not found to have empirical support (57) at the population level. These findings strongly suggest that, instead of withholding a preventative tool, accompanying it with accurate messaging that combines different preventative measures would display trust in the general public's ability to act responsibly and empower citizens, and risk compensation is unlikely to undo the positive benefits at the population level (58).

At the height of the 2009 influenza epidemic in Mexico City it was found (59) that mandatory mask requirements increased compliance compared to voluntary recommendations. Voluntary compliance was strongly influenced by public perception regarding the effectiveness of the recommended measures.

For many infectious diseases, including, for example, tuberculosis, health authorities recommend masks only for those

infected or people who are taking care of someone infected. However, research shows that many sick people are reluctant to wear a mask if it identifies them as sick, and thus end up not wearing them at all in an effort to avoid the stigma of illness (60, 61). Stigma is a powerful force in human societies, and many illnesses come with stigma for the sick as well as fear of them, and managing the stigma is an important part of the process of controlling epidemics as stigma also leads to people avoiding treatment as well as preventive measures that would "out" their illness (62). Many health authorities have recommended wearing masks for COVID-19 only if people are sick; however, reports of people wearing masks being attacked, shunned and stigmatized have already been observed (63). Having masks worn only by the suspected/confirmed infected also has led to employers in high-risk environments like grocery stores and prisons, and even hospitals, banning employees from wearing one sometimes with the idea that it would scare the customer or the patients (64, 65). Further, in many countries, minorities suffer additional stigma and assumptions of criminality (66). In that vein, black people in the United States have reported that they were reluctant to wear masks in public during this pandemic for fear of being mistaken as criminals (67, 68). Even if it were possible to encourage only infected people to wear masks, given the lack of access to testing in many countries, it is not possible for many people to know for sure if they are infected or not (69). Thus, while this paper has shown the importance of masks for source-control – preventing asymptomatic and presymptomatic people from infecting others – it may not even be possible to have infected/sick people wear masks due to stigma, employer restrictions, or simple lack of knowledge of ones status without mask-wearing becoming universal policy.

Another important benefit of recommending universal mask wearing would be to serve as a visible signal and reminder of the pandemic, and given the importance of ritual and solidarity in human societies (70), it is plausible that visible, public signaling via mask wearing can potentially increase compliance with other health measures as well, such as keeping distance and hand-washing. Health, especially during an epidemic, is a form of public good in that everyone else's health behaviors improve the health odds of everyone else, and that it is non-rivalrous in that one person's health does not diminish the health of anyone else (71, 72). Visible signals play an important role in human societies (73). As such, signaling participation in health behaviors by wearing a mask as well as visible enforcement (for example, shops asking customers to wear masks) can increase compliance (74). Further, historically epidemics are a time of fear, confusion and helplessness (75, 76). Mask-wearing and even mask-making or distribution can provide feelings of empowerment and self-efficacy (77), which would in turn also suggest masks could increase compliance in other health-behaviors as well by increasing self-efficacy. In Hong Kong, for example, a community-driven focus on epidemic prevention started in the early days of COVID-19, and included community activists acquiring and distributing masks especially to those without resources and the elderly, even before it was officially declared a pandemic or before their own government had taken strong steps (78). Currently, Hong Kong has not only a relatively contained epidemic compared with many other countries, but a significant reduction in influenza cases as well which their health authorities attribute, among other factors, to the near-universal mask wearing and strong norms around it (79–81).

C. Universal or near-universal mask wearing. Estimating adherence to regulations for public mask wearing is a key input for modeling the impact of public mask wearing. Telephone surveys during the SARS-CoV-2 outbreak in Hong Kong reported enhanced adherence to public mask wearing as the pandemic progressed over three weeks, with 74.5% self reported mask wearing when going out increasing to 97.5%, without mandatory requirements (82). Similar surveys reported face mask use in Hong Kong during the SARS outbreak in 2003 as 79% (83), and approximately 10% during the influenza A(H1N1) pandemic in 2009 (84). This suggests that the public have enhanced awareness of their risk, and display higher adherence levels to prevention strategies than during other epidemics. Cloth masks could be an additional tool to enhance awareness of the importance of physical distancing in public places, serving as a visual reminder. Should masks be reserved solely for use in symptomatic patients, they become a symbol of illness and could lead to public stigmatization that discourages use, as has been described for patients with tuberculosis (61). Countries like the Czech Republic and Hong Kong offer interesting perspectives on the role of citizen advocacy and on the acceptability of face-covering in public.

D. Balancing potential harm of cloth masks with additional benefits for concurrent epidemic. Based on our detailed discussion above, cloth masks have not been shown to increase the risk of infection in people using them compared to not wearing any mask. While the focus of this article has been on preventing the spread of COVID-19 disease through public mask wearing, many low-middle income countries face concurrent epidemics of diseases like tuberculosis. Tuberculosis kills 1.5 million people globally per year, and in 2018, 10 million people fell ill (85). Face covering has been shown to also reduce the transmission of tuberculosis (86) and offer additional benefits to public mask wearing. Similarly, influenza transmissibility in the community was found to have declined by 44% in Hong Kong after the implementation of changes in population behaviors, including social distancing and increased mask wearing, enforced in most stores, during the COVID-19 outbreak (82).

It has been noted (87) that ensuring compliance with non-pharmaceutical interventions can be challenging: "Mask wearing is a promising non-pharmaceutical intervention to reduce risk of secondary transmission of viral URI [upper respiratory infections], but it is likely that adherence to mask wearing would occur only if there was a major pandemic that resulted in a heightened level of community concern and fear." Many regions have now passed laws to ensure compliance. The first RCT (2008) on mask use (88) "found compliance to be low, but compliance is affected by the perception of risk. In a pandemic, we would expect compliance to improve." The authors noted that "in compliant users, masks were highly efficacious."

5. Estimating Population Impacts

At the national and global scale, effective local interventions are aggregated into epidemiological parameters of disease spread. The standard epidemiological measure of spread is known as the reproduction number R_0 which parameterizes

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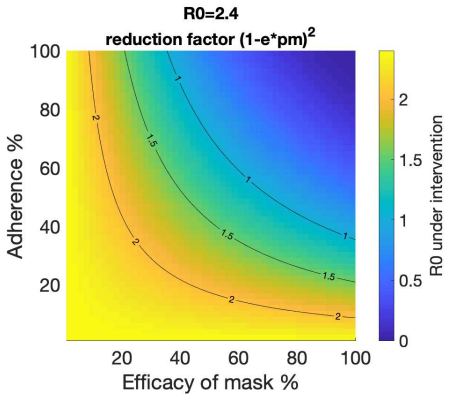

Fig. 1. Impact of public mask wearing under the full range of mask adherence and efficacy scenarios. The color indicates the resulting reproduction number R_0 from an initial R_0 of 2.4 (7).

the number of cases infected by one case,in a completely susceptible population. R_0 determines the rate of growth, with a superlinear effect. The goal of any related healthcare policy is to have an aggregate effect of reducing R_0 to below 1.0.

Efficacy of face masks within local interventions would have an aggregate effect on the reproduction number of the epidemic. What is the magnitude of such an effect? The HKBU COVID-19 Modelling Group developed a transmission model that incorporated mask wearing and mask efficacy as a factor in the model (89). They estimate reductions in the basic reproduction number R_0 under common intervention measures. For wearing masks, they find that wearing masks reduces R_0 by a factor $(1 - ep_m)^2$, where e is the efficacy of trapping viral particles inside the mask, and p_m is the percentage of the population that wears masks. When combined with contact tracing, the two effects multiply.

A conservative assessment applied to the COVID-19 estimated R_0 of 2.4 (7) might posit 50% mask usage and a 50% mask efficacy level, reducing R_0 to 1.35, an order of magnitude impact rendering spread comparable to the reproduction number of seasonal influenza. To put this in perspective, 100 cases at the start of a month becomes 31,280 cases by the month's end ($R_0 = 2.4$) vs. only 584 cases ($R_0 = 1.35$). Such a slowdown in case-load protects healthcare capacity and renders a local epidemic amenable to contact tracing interventions that can eliminate the spread entirely.

A full range of efficacy e and adherence p_m is shown with the resulting R_0 in Figure 1, illustrating regimes in which growth is halted entirely ($R_0 < 1$) as well as pessimistic regimes (e.g. due to poor implementation or population compliance) that nonetheless result in a beneficial effect in suppressing the exponential growth of the pandemic.

Yan et al (90) provide an additional example of an incremental impact assessment of respiratory protective devices using an augmented variant of a traditional SIR model in the context of influenza with N95 respirators. They showed that a sufficiently high adherence rate (~ 80% of the population) resulted in the elimination of the outbreak with most respiratory protective devices.

Qualitative comparisons of outcomes between countries (91, 92) are suggestive of policy differences leading to differences in disease spread of up to three orders of magnitude. Although between-country comparisons do not allow for causal attribution, they suggest mask wearing to be a low-risk measure with a potentially large positive impact, with many countries with widespread use of masks in public keeping deaths below one in a million.

Abaluck et al (93) extend the between-country analyses from a cost perspective, estimating the marginal benefit per cloth mask worn to range from $3,000-$6,000. They also found that "the average daily growth rate of confirmed positives is 18% in countries with no preexisting mask norms and 10% in countries with such norms." and "that the growth rate of deaths is 21% in countries with no mask norms and 11% in countries with such norms."

6. Discussion and Recommendations

Our review of the literature offers evidence in favor of widespread mask use to reduce community transmission: non-medical masks use materials that obstruct droplets of the necessary size; people are most infectious in the initial period post-infection, where it is common to have few or no symptoms (10–16); non-medical masks have been effective in reducing transmission of influenza; non-medical masks have been shown to be effective in small trials at blocking transmission of coronavirus; and places and time periods where mask usage is required or widespread have shown substantially lower community transmission.

The available evidence suggests that near-universal adoption of non-medical masks when out in public, in combination with complementary public health measures could successfully reduce effective-R to below 1.0, thereby stopping community spread. Economic analysis suggests that the impact of mask wearing could be thousands of US dollars saved per person per mask (93).

Interventions to reduce COVID-19 spread should be prioritized in order of their expected multiple on effective R divided by their cost. By this criterion experimentation with and deployment of universal masks look particularly promising. When used in conjunction with widespread testing, contact tracing, quarantining of anyone that may be infected, hand washing, and physical distancing, face masks are a valuable tool to reduce community transmission. All of these measures, through their effect on R_0, have the potential to reduce the period of lockdown required. As governments talk about relaxing lockdowns, keeping transmissions low enough to preserve health care capacity will be critical until a vaccine can be developed. Mask wearing may be critical to preventing a second wave of infections from overwhelming the health care system – further research is urgently needed here.

UNESCO states that "when human activities may lead to morally unacceptable harm that is scientifically plausible but uncertain, actions shall be taken to avoid or diminish that harm" (94). This is known as the "precautionary principle". The World Charter for Nature, which was adopted by the UN General Assembly in 1982, was the first international endorsement of the precautionary principle. It was implemented in an international treaty in the 1987 Montreal Protocol. The loss of life and economic destruction that has been seen already from COVID-19 is a "morally unacceptable harm". The positive impact of public mask wearing on this is "scientifically plausible but uncertain". This notion is reflected in Figure 1 - while researchers may reasonably disagree on the magnitude of transmissibility reduction and compliance, seemingly

modest benefits can be massively beneficial in the aggregate due to the exponential character of the transmission process. Therefore, the action of ensuring widespread use of masks in the community should be taken, based on this principle (95).

Models suggest that public mask wearing is most effective at stopping spread of the virus when compliance is high. This is the same situation as we see with vaccines - the more people are vaccinated, the higher the benefit to the whole population including those who cannot be vaccinated like infants or immuno-compromised people. A common policy response to this conundrum is to ensure compliance by using laws and regulations, such as widespread state laws in the US which require vaccinations to attend school. Research shows that the strength of the mandate to vaccinate greatly influences compliance rates for vaccines and that policies that set a higher bar for vaccine exemptions result in higher vaccination rates. (96) The same approach is now being used in many jurisdictions to increase mask wearing compliance, by mandating mask use in a variety of settings (such as public transportation or grocery stores or even at all times outside the home). Early results suggest that these laws are effective at increasing compliance and slowing or stopping the spread of COVID-19 (91). We recommend that mask use requirements are implemented by governments, or when governments do not, by organizations that provide public-facing services, such as transit service providers or stores, as "no mask, no service" rules. Such mandates must be accompanied by measures to ensure access to masks, possibly including distribution and rationing mechanisms so that they do not become discriminatory but remain focused on the public health benefit. Given the value of the source control principle, especially for presymptomatic people, it is not good enough for only employees to wear masks, customers must wear masks as well.

It is also important for health authorities to provide clear guidelines for the production, use and sanitization or re-use of face masks, and consider their distribution as shortages allow. A number of countries have distributed surgical masks (South Korea, Taiwan) from early on while Japan and Singapore are now distributing cloth masks to their whole population. Clear and implementable guidelines can help increase compliance, and bring communities closer to the goal of reducing and ultimately stopping the spread of COVID-19.

Materials and Methods

A community-driven approach was used for building the paper list used in this literature review. A multidisciplinary community of researchers used online tools to review and actively discuss publications related to the question of the effectiveness and policy of public mask wearing.

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From: Kevin Olival ecohealthalliance.org>
Sent: Wednesday, January 31, 2018 9:09 AM EST
To: S Wacharapluesadee
CC: Katie Leahy <katie.leahy >; lance.r.brooks >; Newman, Carl I CIV DTRA J3-7 (US) Lancaster, Mary J CIV (US) christopher.r.lewis ; Kading,Rebekah >; DeeAnn Reeder >; Cryan, Paul Vivek Kapur ; Gavin James Smith Tigga Kingston ; abelwade >; Ian Mendenhall ; tamar kutateladze Keti Sidamonidze ; Lela Urushadze ; joram.buza c demetria >; Jon Epstein ecohealthalliance.org>; cryan.paul ; Stokes, Martha M CIV (US)
Subject: Re: Field trip

Wow, I just barely made the cutoff! Did we loose anyone on the far right!?

It was an amazing trip Supaporn! I speak on behalf of all the BPERNet and PMAC delegates when I say THANK YOU !

You and the team did an amazing job organizing this.

Best regards,
Kevin

> On Jan 31, 2018, at 7:50 PM, S Wacharapluesadee wrote:
>
> For your memory!
>
> Thank you,
> Supaporn
>
>
>
>

> Katie Leahy
>
> lance.r.brooks "Newman, Carl I CIV DTRA J3-7 (US)"
, "Lancaster, Mary J CIV (US)" ,
christopher.r.lewis "Kading,Rebekah" , DeeAnn Reeder
, "Cryan, Paul" , Vivek Kapur , Gavin James
Smith , Tigga Kingston , abelwade , Ian
Mendenhall >, tamar kutateladze , Keti Sidamonidze
< >, Lela Urushadze , joram.buz ,
c demetria , Kevin Olival < econealthalliance.org>, Jon Epstein
econealthalliance.org>, cryan.paul
> Cc: "Stokes, Martha M CIV (US)" >, Simmi Ghai
S Wacharapluesadee
> Afternoon Session
>
> All,
>
> Here are slides to start filling out for the afternoon session.
>
> V/r,
>
> Katie Leahy
>
> From: Katie Leahy >
> Date: Tuesday, January 30, 2018 at 10:30 AM
> To: "lance.r.brooks " , "Newman, Carl I CIV DTRA J3-7 (US)"
, "Lancaster, Mary J CIV (US)" ,
"christopher.r.lewis , "Kading,Rebekah"
>, DeeAnn Reeder "Cryan, Paul" ,
Vivek Kapur , Gavin James Smith Tigga Kingston
, "abelwade " >, Ian Mendenhall
>, "tamar_kutateladze " , Keti
Sidamonidze , Lela Urushadze , "joram.buza
>, "c_demetria " , Kevin Olival
econealthalliance.org>, Jon Epstein econealthalliance.org>, Jason Rao
, "cryan.paul "
> Cc: "Stokes, Martha M CIV (US)" >, Simmi Ghai ,
S Wacharapluesadee >

> Subject: NEW SLIDES
>
> Here are the working group slides that were live-edited for your use in break-out groups.
>
> V/r,
>
> Katie Leahy
>
> From: Katie Leahy >
> Date: Monday, January 29, 2018 at 9:01 PM
> To: "lance.r.brooks " >, "Newman, Carl I CIV DTRA J3-7 (US)" "Lancaster, Mary J CIV (US)" , "christopher.r.lewis >, "Kading,Rebekah" >, <vkapur.psu , Gavin James Smith Trigga Kingston , "abelwade " , Ian Mendenhall , "tamar_kutateladze " < >, Keti Sidamonidze , Lela Urushadze >, "joram.buza " , "c_demetria " Kevin Olival econealthalliance.org>, Jon Epstein @econealthalliance.org>, Jason Rao >, "cryan.paul "
> Cc: "Stokes, Martha M CIV (US)" , Simmi Ghai >, S Wacharapluesadee
> Subject: Update to the BPERNet Slides
>
> Hi, everyone! We made a couple changes to the slides for tomorrow. Nothing substantive, just our approach to conducting the brief-out discussions and the order of a couple of the initial slides.
>
> A reminder again to please be in the lobby at 0745, the bus will depart for Chulalongkorn promptly at 0800.
>
> V/r,
>
> Katie Leahy
>
> From: Katie Leahy >
> Date: Monday, January 29, 2018 at 10:28 AM
> To: "lance.r.brooks >, "Newman, Carl I CIV DTRA J3-7 (US)" , "Lancaster, Mary J CIV (US)" , "christopher.r.lewis " >, "Kading,Rebekah" , DeeAnn Reeder , "Cryan, Paul" Vivek Kapur >, Gavin James Smith , Trigga Kingston , "abelwade " , Ian Mendenhall >, "tamar_kutateladze " >, Keti Sidamonidze >, Lela Urushadze , "joram.buza " , "c_demetria " , Kevin Olival @econealthalliance.org>, Jon Epstein econealthalliance.org>
> Cc: "Stokes, Martha M CIV (US)" , Simmi Ghai < >, S Wacharapluesadee <
> Subject: BPERNet: Transportation Times and Other Useful Information (30 and 31 January 2017)
>
> Hello, everyone! Welcome to Bangkok. On behalf of the Executive Committee (Dr. Martha Stokes and Dr. Mary Lancaster), we are so pleased that you are able to join us this week for our BPERNet planning meeting and other PMAC activities.
>
> Please use this email as your resource for information regarding transportation, logistics, and other coordinating information for 30 January â€“ 31 January.
>
> 30 January â€“ BPERNet Meeting at Chulalongkorn Hospital
>
> 1. The bus will depart from the Renaissance Hotel promptly at 0800; please be in the lobby for head count at 0745
> 2. We will provide coffee and light refreshment during the meeting; you will take lunch at one of the many canteen options at the hotel; please bring about 200 - 300 thai baht (~10 USD) for lunch
>
> 31 January â€“ PMAC / BPERNet Field Trip
>
> 1. The bus will depart from the Renaissance Hotel promptly at 0630; please be in the lobby for head count at 0615; please make sure that you are on time, as we are caravanning with a delegation from the Centara Hotel and will receive a police escort to move us quickly through traffic
> 2. We will provide a box breakfast for the bus ride
> 3. Please make sure that you dress appropriately for this field trip; we strongly suggest covered shoes and loose, comfortable clothing; in addition to this mode of dress we also suggest that you bring accompaniments for spending a day outdoors amongst bat roosts; such as:
>   * Hat
>   * Sunscreen

>   *   Sunglasses
>   *   Bug spray
>   *   Water bottle
>
> We will provide information regarding the Ambassadorâ€™s reception at the close of tomorrowâ€™s meeting.
>
> Again, we are so excited to have you all here. Please do not hesitate to reach out to me or Megan Hudson (copied) if you have any questions.
>
> V/r,
>
> Katie Leahy
>
> [cid:image001.png@01D399CC.51F40100]
>
> Katie Leahy
> Program Manager | Global Systems Engineering
> 6303 Little River Turnpike, Suite 208
> Alexandria, VA 22305
>
> http://globalsyseng.com<http://globalsyseng.com/>
>
>
> Note: This email and any attachments may contain confidential or proprietary information.
> If you are not the intended recipient, any use or distribution is prohibited; please notify the sender and delete from your system.
>
> <image001.png>
> <1517399433493.jpg>

From: Kingston, Tigga >
Sent: Monday, February 26, 2018 12:22 PM EST
To: Katie Leahy ; Tamar Kutateladze Kading,Rebekah ; DeeAnn Reeder >; Cryan, Paul Vivek Kapur <vkapur.psu >; Gavin James Smith abelwade Ian Mendenhall >; Keti Sidamonidze >; Lela Urushadze >; c_demetria >; Jon Epstein ecohealthalliance.org>; cryan.paul ; S Wacharapluesadee >; Kevin Olival ecohealthalliance.org>
CC: Stokes, Martha M CIV (US) ; Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) ; Megan Hudson
Subject: RE: Final BPERNet Read-out

Understood, thanks
Tigga

From: Katie Leahy [mailto:katie.leahy
Sent: Monday, February 26, 2018 11:21 AM
To: Kingston, Tigga ; Tamar Kutateladze ; Kading,Rebekah ; DeeAnn Reeder ; Cryan, Paul ; Vivek Kapur >; Gavin James Smith >; abelwade Ian Mendenhall ; Keti Sidamonidze ; Lela Urushadze c_demetria ; Jon Epstein ecohealthalliance.org>; cryan.paul ; S Wacharapluesadee Kevin Olival ecohealthalliance.org>
Cc: Stokes, Martha M CIV (US) ; Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) >; Megan Hudson >
Subject: Re: Final BPERNet Read-out

Hi, Tigga, the document has not yet been approved by DTRA Public Affairs, so it is not available to the public. We are submitting to Marty and Mary today, I will let everyone know when it is available for wider distribution.

V/r,

Katie Leahy

From: "Kingston, Tigga"
Date: Monday, February 26, 2018 at 12:16 PM
To: Katie Leahy >, Tamar Kutateladze >, "Kading,Rebekah" , DeeAnn Reeder >, "Cryan, Paul" , Vivek Kapur , Gavin James Smith , "abelwade " , Ian Mendenhall , Keti Sidamonidze >, Lela Urushadze < , "c_demetria >, Jon Epstein ecohealthalliance.org>, "cryan.paul , S Wacharapluesadee , Kevin Olival ecohealthalliance.org>
Cc: "Stokes, Martha M CIV (US)" "Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US)" , Megan Hudson >
Subject: RE: Final BPERNet Read-out

Katie
Is this document open to the public now? I.e. can I share it?
Tigga

From: Katie Leahy
Sent: Wednesday, February 21, 2018 1:23 PM
To: Tamar Kutateladze ; Kading,Rebekah >; DeeAnn Reeder >; Cryan, Paul >; Vivek Kapur ; Gavin James Smith >; abelwade ; Ian Mendenhall >; Keti Sidamonidze >; Lela Urushadze >; c_demetria ; Jon Epstein ecohealthalliance.org>; cryan.paul ; Kingston, Tigga >; S Wacharapluesadee >; Kevin Olival ecohealthalliance.org>
Cc: Stokes, Martha M CIV (US) >; Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) >; Megan Hudson
Subject: Final BPERNet Read-out

All,

Please find the final BPERNet read-out for your files. To everyone who provided feedback, we thank you very much for your responses.

A couple housekeeping items:

1. In the next several weeks, we will begin making plans for our next meeting to take place around the One Health Congress in Saskatoon, Canada.

The event feedback you provided will help shape this event and that we anticipate building a 2-day program that includes a scenario-based exercise and presentations.

2. One action item from our Bangkok meeting was to begin discussion about a new name for the network; **please participate in this survey monkey poll to find our new name https://www.surveymonkey.com/r/PQXTHCV**. Please note that the group's will assist the group with establishing a web presence for better communications and outreach, so we depend on your feedback to meet these goals. Please let us know through the survey if you do not feel we are using the right words to communicate the group's core mission.

Thank you again for your participation in these polls and feedback on the report. Please let us know if you have any questions or concerns.

Katie Leahy
Program Manager | Global Systems Engineering
6303 Little River Turnpike, Suite 208
Alexandria, VA 22305

http://globalsyseng.com

From: Kevin Olival ecohealthalliance.org>
Sent: Thursday, April 30, 2020 11:19 AM EDT
To: Kading,Rebekah
CC: Paul Cryan >
Subject: Re: Final version of North American bat/SARS2 ms - PLEASE REVIEW

Thanks Rebekah… long week indeed!

On Apr 29, 2020, at 7:07 PM, Kading,Rebekah wrote:

p.s. Kevin AND Paul, I mean to say in my previous email. Sorry, it's been a long week already! Thanks to both of you!!
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kading,Rebekah
Sent: Wednesday, April 29, 2020 5:05 PM
To: Kevin Olival ecohealthalliance.org>; 'Paul Cryan'
Subject: Re: Final version of North American bat/SARS2 ms - PLEASE REVIEW

Hi Kevin,

Very nice job on this! Only spotted a couple small things.
1) "highlights" is misspelled on line 128.
2) looks like a ref is still needed in line 342 regarding PPE usage in the field. This ref might fit...it's more broadly on wildlife professionals though (PMID: 31993824)
3) don't forget to delete the [...] on line 421

Yes, I would be delighted to be a co-author.

My ORCID is 0000-0002-4996-915X.

Thanks so much!
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kevin Olival ecohealthalliance.org>
Sent: Sunday, April 26, 2020 10:11 PM
To: Paul Cryan ; Brian R. Amman ; Ralph S. Baric ; David S Blehert ; Cara Brook ; Charles H Calisher ; Kevin Castle ; Jeremy Coleman >; Peter Daszak ecohealthalliance.org>; epstein ecohealthalliance.org>; Hume Field ecohealthalliance.org>; Winifred F Frick, Ph.D. >; Gilbert, Amy T - APHIS >; David Hayman ; Hon S Ip >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson Kading,Rebekah ; Tigga Kingston < ; Lorch, Jeffrey M ; Ian Mendenhall >; alisonpeel ; Kendra Phelps >; Plowright, Raina <raina. >; DeeAnn Reeder ; Jonathan D Reichard ; Jonathan M Sleeman <| >; Daniel Streicker ; Jonathan S. Towner >
Subject: Final version of North American bat/SARS2 ms - PLEASE REVIEW

Dear Esteemed Colleagues,

Please review the attached penultimate draft of our manuscript (now entitled: " **Possible risks of SARS-CoV-2 spillover to free-ranging wildlife: a case study of bats")**, together with the supplementary table and refs. Our plan is to submit to *Lancet Infectious Diseases* as a review article (correct length and they allow 150 refs) in the next week - references are currently formatted for that journal. We would also like to post it on bioRxiv as a pre-print once we get it submitted to *Lancet ID*. Please let me know if you have any concerns with that plan.

Thank you all for your excellent comments and edits on the previous draft. Paul and I have gone back and forth on several rounds of revisions since then (and multiple late night texts), aiming to take each and every suggestion into account, and we believe it's a much better manuscript now! Very excited about this one, and looking forward to getting it published!

By Thursday April 30th (or ASAP), could you each please:

1. Confirm that you agree to be a co-author.
2. Double check your name and affiliation, and send me your ORCID number if you have one.
3. Read through the ms and send any important, last minute changes or edits you feel are necessary. Please use track changes. If you're okay with the ms as is, please just confirm so.
4. For my Federal US Gov't friends (USFWS, USGS, CDC, USDA) - please let us know what we need to do for approval on your end. I know Paul is working with USGS now to hopefully get rapid clearance.

No need to cc all if you don't want, but please include both me and Paul on your response.

Looking forward to hearing from you all soon!

Cheers,
Kevin and Paul

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
460 West 34th Street, Suite 1701
New York, NY 10001

www.ecohealthalliance.org
EcoHealth Alliance develops science-based solutions to prevent pandemics *and* promote conservation

From: DeeAnn Reeder
Sent: Friday, July 28, 2017 12:46 AM EDT
To: Jon Epstein ecohealthalliance.org>
CC: Wade Abel ; l.urushadze Kading,Rebekah >; c_demetria >; spwa >; Lancaster, Mary J CIV (US) ; Stokes, Martha M CIV (US) ; gavin.smith ; tigga.kingston ; nisreen.hmoud ; Caitlin Devaney ; Sander, William E CTR (US) >; joram.buza Gamboa, Omar Maj USAF DTRA J3-7 (US) Katie Leahy >; vkapur ; lelincdc ; kityrob ian.mendenhall >; ecohealthalliance.org ; tamar_kutateladze ; cryanp
Subject: Re: GBA Products and Action Items

Hi Katie et al.,

I too strongly support the January meeting for the reasons that Jon outlined and also because my teaching is in the fall semester and it would be hard for me to attend the meeting in Doha.

I support Jon's RABEZ suggestion. In reference to our colleagues in bat conservation, we need to have the pathogen component in the title. And, we can't, from a grammatical perspective be an alliance FOR bat pathogens, rather an alliance for the study of bat pathogens.

Thanks, DeeAnn

On Jul 28, 2017 3:42 AM, "Jon Epstein" ecohealthalliance.org> wrote:

> Hi Katie,
> I propose meeting at the Prince Mahidol Award Conference (PMAC) in Bangkok, late January 2018. Primarily, I think November might be slightly early for our next meeting, given that we're working through governance and committee population. Also, PMAC is a big One Health meeting that at least three of us on the steering committee will already be attending, so there's some efficiency to it in terms of scheduling and expense, as well as having thematic relevance to our group.
>
> Potential names:
> 1) Bat Ecology Research Network (BERN)
>
> 2) Bat Research Coordination Network (BRCN)
>
> 3) Global Alliance for Bat Research (GABR)
>
> 4) Research Alliance for Bat-borne Emerging Zoonoses (RABEZ)
>
> Cheers,
> Jon
>
> Jonathan Epstein DVM, MPH, PhD
>
> Vice President for Science and Outreach
>
> EcoHealth Alliance
> New York

On Jul 25, 2017 9:18 AM, "Katie Leahy" > wrote:

Note: this email is best viewed in HTML

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Katie Leahy

Program Manager | Global Systems Engineering

5881 Leesburg Pike, Suite 506

Baileys Crossroads, VA 22041

http://globalsyseng.com

From: Kingston, Tigga
Sent: Tuesday, August 01, 2017 8:32 AM EDT
To: Tamar Kutateladze ; Katie Leahy ; kityrob ian.mendenhall >; joram.buza < ; vkapur oliva >; epstein >; Kading,Rebekah >; lelincdc ; l.urushadze <l.urushadze >; spwa >; abelwade >; c_demetria >; cryanp < ; dreeder >; gavin.smith >; nisreen.hmoud >
CC: Stokes, Martha M CIV (US) >; Lancaster, Mary J CIV (US) Gamboa, Omar Maj USAF DTRA J3-7 (US) ; Sander, William E CTR (US) >; Caitlin Devaney
Subject: RE: GBA Products and Action Items

Hi everyone

Bat-associated Pathogen and Ecology Research Network (BPERN) also gets my vote (if RABEZ is off the table – but I think that actually was the best description).

The PENAPH Conference works best for me

Tigga

Tigga Kingston, PhD
Associate Professor
Department of Biological Sciences
Texas Tech University
Lubbock, TX 79409-3131
USA

http://kingstonlab.org
http://seabcru.org

From: Tamar Kutateladze |
Sent: Monday, July 31, 2017 11:41 AM
To: Katie Leahy ; kityrob ; ian.mendenhall ; joram.buza vkapur ; ecohealthalliance.org; ecohealthalliance.org; rebekah.kading lelincdc ; l.urushadze ; spwa abelwade ; c_demetria ; Kingston, Tigga ; cryanp dreeder gavin.smith ; nisreen.hmoud
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Yours sincerely,

Tamar

Tamar Kutateladze
MD PhD
R. Lugar Center for Public Health Research
National Center for Disease Control & Public Health
16 Kakheti Highway, Tbilisi 0152, Georgia

On Tuesday, July 25, 2017, 5:18:11 PM GMT+4, Katie Leahy < > wrote:

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Program Manager | Global Systems Engineering

5881 Leesburg Pike, Suite 506

Baileys Crossroads, VA 22041

http://globalsyseng.com

From: Lela Urushadze
Sent: Thursday, July 27, 2017 6:05 AM EDT
To: Katie Leahy
CC: kityrob >; ian.mendenhall ;
joram.buza ; vkapur >;
@ecohealthalliance.org ; ecohealthalliance.org
; Kading,Rebekah >; l.urushadze
>; tamar_kutateladze ; spwa
; abelwade ; c demetria
; tigga.kingston >; cryanp ;
dreeder ; gavin.smith
nisreen.hmoud ; Stokes, Martha M CIV (US) Lancaster,
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>
Subject: Re: GBA Products and Action Items

Dear Katie
Thank you for your email
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As for network name -Global Alliance for Bat-born Pathogens (GBAP)
For next meeting I vote for (PENAPH) Thailand
All the best
Lela

On Tue, Jul 25, 2017 at 5:18 PM, Katie Leahy< wrote:

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5881 Leesburg Pike, Suite 506

Baileys Crossroads, VA 22041

http://globalsyseng.com

--

Lela Urushadze M.Sc.
Senior specialist
National Center for Disease Control and Public Health (NCDC) of Georgia
9M. Asatiani str. Tbilisi, 0177, Georgia

From: Jon Epstein @ecohealthalliance.org>
Sent: Friday, July 28, 2017 11:49 AM EDT
To: Kingston, Tigga >
CC: DeeAnn Reeder ; Wade Abel >; l.urushadze >; Kading,Rebekah >; c_demetria >; spwa ; Lancaster, Mary J CIV (US) ; Stokes, Martha M CIV (US) ; gavin.smith >; nisreen.hmoud ; Caitlin Devaney >; Sander, William E CTR (US) >; joram.buza >; Gamboa, Omar Maj USAF DTRA J3-7 (US) < >; Katie Leahy >; vkapur >; lelincdc kityrob ; ian.mendenhall ecohealthalliance.org ecohealthalliance.org>; tamar_kutateladze cryanp >
Subject: Re: GBA Products and Action Items

My RABEZ suggestion was slightly tongue-in-cheek. In retrospect, I worry that it might be outwardly confusing to others if we become the "Rabies network" when we won't actually be doing much with rabies.
With sensitivity to the bat conservation community, I suggest the "Bat Viral Ecology Research Network" or something along that line.

Cheers,
Jon

On Fri, Jul 28, 2017 at 8:19 AM, Kingston, Tigga > wrote:

> Greetings everyone
>
> Jon is there a link for the Prince Mahidol Award Conference (PMAC)? And dates? I will be teaching that semester, and it can be a bit manic taking time off at the beginning, but not impossible.
>
> For all the reasons pointed out by DeeAnn, I too like:
>
> Research Alliance for Bat-borne Emerging Zoonoses
>
> (RABEZ)
>
> Best wishes
>
> Tigga
>
> **From:** DeeAnn Reeder
> **Sent:** Thursday, July 27, 2017 11:47 PM
> **To:** Jon Epstein ecohealthalliance.org >
> **Cc:** Wade Abel ; l.urushadze ; rebekah.kading ; c_demetria spwa ; Lancaster, Mary J CIV (US) ; Stokes, Martha M CIV (US) ; gavin.smith ; Kingston, Tigga >; nisreen.hmoud ; Caitlin Devaney >; Sander, William E CTR (US) >; joram.buza ; Gamboa, Omar Maj USAF DTRA J3-7 (US) ; Katie Leahy ; vkapur ; lelincdc ; kityrob ; ian.mendenhall ; ecohealthalliance.org; tamar_kutateladze ; cryanp
> **Subject:** Re: GBA Products and Action Items
>
> Hi Katie et al.,
>
> I too strongly support the January meeting for the reasons that Jon outlined and also because my teaching is in the fall semester and it would be hard for me to attend the meeting in Doha.
>
> I support Jon's RABEZ suggestion. In reference to our colleagues in bat conservation, we need to have the pathogen

component in the title. And, we can't, from a grammatical perspective be an alliance FOR bat pathogens, rather an alliance for the study of bat pathogens.

Thanks, DeeAnn

On Jul 28, 2017 3:42 AM, "Jon Epstein" ecohealthalliance.org > wrote:

> Hi Katie,
>
> I propose meeting at the Prince Mahidol Award Conference (PMAC) in Bangkok, late January 2018. Primarily, I think November might be slightly early for our next meeting, given that we're working through governance and committee population. Also, PMAC is a big One Health meeting that at least three of us on the steering committee will already be attending, so there's some efficiency to it in terms of scheduling and expense, as well as having thematic relevance to our group.
>
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> Jon
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> EcoHealth Alliance
> New York
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--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

web: ecohealthalliance.org

Twitter: @epsteinjon

-

From: Ian Mendenhall
Sent: Thursday, August 03, 2017 8:06 PM EDT
To: Kading,Rebekah ; Cryan, Paul >; Kingston, Tigga >
CC: Tamar Kutateladze ; Katie Leahy kityrob ; joram.buza ; vkapur ; ecohealthalliance.org ; ecohealthalliance.org >; lelincdc l.urushadze ; spwa ; abelwade ; c_demetria ; dreeder ; Gavin James Smith ; nisreen.hmoud ; Stokes, Martha M CIV (US) >; Lancaster, Mary J CIV (US) < >; Gamboa, Omar Maj USAF DTRA J3-7 (US) Sander, William E CTR (US) ; Caitlin Devaney
Subject: Re: GBA Products and Action Items

My preference is meeting in Thailand and the name Bat-associated Pathogen and Ecology Research Network (BPERN).

Ian

Sent from my Samsung Galaxy smartphone.

-------- Original message --------
From: "Kading,Rebekah"
Date: 03/08/2017 23:28 (GMT+08:00)
To: "Cryan, Paul" >, "Kingston, Tigga" >
Cc: Tamar Kutateladze , Katie Leahy >, kityrob Ian Mendenhall , joram.buza , vkapur , ecohealthalliance.org, , lelincdc , l.urushadze , spwa , abelwade , c_demetria dreeder , Gavin James Smith >, nisreen.hmoud , "Stokes, Martha M CIV (US)" "Lancaster, Mary J CIV (US)" , "Gamboa, Omar Maj USAF DTRA J3-7 (US)" , "Sander, William E CTR (US)" >, Caitlin Devaney >
Subject: RE: GBA Products and Action Items

I agree with Paul and Tigga.
Thanks!
Rebekah

From: Cryan, Paul
Sent: Tuesday, August 01, 2017 11:43 AM
To: Kingston, Tigga
Cc: Tamar Kutateladze ; Katie Leahy ; kityrob ian.mendenhall joram.buza vkapur ; ecohealthalliance.org; ecohealthalliance.org; Kading,Rebekah ; lelincdc ; l.urushadze ; spwa abelwade ; c_demetria ; dreeder gavin.smith nisreen.hmoud Stokes, Martha M CIV (US) Lancaster, Mary J CIV (US) >; Gamboa, Omar Maj USAF DTRA J3-7 (US) ; Sander, William E CTR (US) ; Caitlin Devaney >
Subject: Re: GBA Products and Action Items

Hi All,

I prefer a meeting in Thailand and like the name Bat-associated Pathogen and Ecology Research Network (BPERN).

Thanks,
Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info
ORCID

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Associate Professor
Department of Biological Sciences
Texas Tech University
Lubbock, TX 79409-3131
USA

http://kingstonlab.org
http://seabcru.org

From: Tamar Kutateladze
Sent: Monday, July 31, 2017 11:41 AM
To: Katie Leahy >; kityrob ; ian.mendenhall ; joram.buza vkapur ; ecohealthalliance.org; ecohealthalliance.org; rebekah.kading lelincdc l.urushadze ; spwa abelwade ; c_demetria Kingston, Tigga >; cryanp dreeder gavin.smit nisreen.hmoud
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Sent: Monday, July 31, 2017 12:41 PM EDT
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Katie Leahy

Program Manager | Global Systems Engineering

5881 Leesburg Pike, Suite 506

Baileys Crossroads, VA 22041

http://globalsyseng.com

From: catalino demetria
Sent: Wednesday, July 26, 2017 8:54 PM EDT
To: Wade Abel ; Katie Leahy
CC: kityrob >; ian.mendenhall >; joram.buza >; vkapur ; olival ; epstein >; Kading,Rebekah >; lelincdc ; l.urushadze ; tamar_kutateladze ; spwa >; tigga.kingston ; cryanp ; dreeder gavin.smith ; nisreen.hmoud ; Stokes, Martha M CIV (US) ; Lancaster, Mary J CIV (US) Gamboa, Omar Maj USAF DTRA J3-7 (US) ; Sander, William E CTR (US) Caitlin Devaney >
Subject: Re: GBA Products and Action Items

Hi Katie,

Thank you for the email. I have successfully created an account on the link provided. I like the name GABP for the group, and I also prefer DOHA, QATAR for the next meeting.

Sincerely,

Catalino S. Demetria, DVM
Section Head
Rabies and Special Pathogens Laboratory

Veterinary Research Department
Research Institute for Tropical Medicine
9002 Research Drive, FCC, Alabang, Muntinlupa City
1771 PHILIPPINES

On Wednesday, July 26, 2017, 4:14:39 AM GMT+8, Wade Abel > wrote:

Dear Katie,

Thanks for your message. The system failed to create an APAN account for me, will try other way. However, I would like to response to the 2 points. My suggestions are:

a. Next meeting during International Congress on Pathogens at the Human and Animal Interface (ICOPHAI) 7-9 November 2017, Doha, Qatar https://icophai.org/
b. Network name: Global Alliance for Bat-borne Pathogens (GABP)

kind regards

On 25 July 2017 at 14:18, Katie Leahy wrote:

> ***Note: this email is best viewed in HTML***
>
> Greetings, GBA Steering Committee!
>
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>
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Katie Leahy

Program Manager | Global Systems Engineering

5881 Leesburg Pike, Suite 506

Baileys Crossroads, VA 22041

http://globalsyseng.com

--

Dr Abel WADE
Director of the National Veterinary Laboratory (LANAVET) annex inYaounde
Ministry of Livestock, Fisheries and Animal Industries (MINEPIA)
Yaounde-Cameroon

www.lanavet.com; www.minepia.org.cm

From: Kevin Olival, PhD ecohealthalliance.org>
Sent: Friday, July 28, 2017 12:18 PM EDT
To: Katie Leahy
CC: kityrob ; Ian MENDENHALL PhD ; joram.buza >; Vivek Kapur ; Jon Epstein ecohealthalliance.org>; Kading,Rebekah ; lelincdc >; l.urushadze >; tamar kutateladze >; Supaporn Wacharapluesadee >; abelwade >; c_demetria >; Tigga Kingston >; Paul Cryan >; DeeAnn Reeder ; gavin.smith >; nisreen.hmoud >; Martha M CIV Stokes ; Mary J. Lancaster Ph.D. >; Gamboa, Omar Maj USAF DTRA J3-7 (US) >; Sander, William E CTR (US) >; Caitlin Devaney
Subject: Re: GBA Products and Action Items

Dear Katie and all,

I have set up the APAN account, and confirmed with Will Sander.

I also support PMAC in Thailand (end of Jan) as a good meeting suggestion, and already plan to attend this. I would available for Doha (ICOPHAI) too if others/DTRA feel this is best.

Good name suggestions out there. I also thought Jon's RABEZ suggestion was clever, but agree with him it could cause some confusion. I really like Mary's recent suggestion of: **Bat-associated Pathogen and Ecology Research Network (BPERN).** Think this accurately captures the focus on pathogens and also the ecology of those pathogens, and avoids confusion with the conservation community that the more generic names caused.

Cheers,
Kevin

Kevin J. Olival, PhD

Associate Vice President for Research

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

www.ecohealthalliance.org

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

On Jul 25, 2017, at 9:18 AM, Katie Leahy > wrote:

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<image001.png> **Katie Leahy**
Program Manager | Global Systems Engineering
5881 Leesburg Pike, Suite 506
Baileys Crossroads, VA 22041

http://globalsyseng.com

<GBA Executive Summary_rev2.docx><TORFTA_GBA_v14.docx><GBA_TORFTA Editing Form.xlsx>

From: Cryan, Paul >
Sent: Tuesday, August 01, 2017 1:42 PM EDT
To: Kingston, Tigga >
CC: Tamar Kutateladze ; Katie Leahy ;
kityrob ; ian.mendenhall
joram.buza ; vkapur ;
olival >; epstein
Kading,Rebekah ; lelincdc
; l.urushadze >; spwa
abelwade ; c_demetria >;
dreeder >; gavin.smith ;
nisreen.hmoud ; Stokes, Martha M CIV (US) ; Lancaster,
Mary J CIV (US) ; Gamboa, Omar Maj USAF DTRA J3-7 (US)
Sander, William E CTR (US) ; Caitlin Devaney
>
Subject: Re: GBA Products and Action Items

Hi All,

I prefer a meeting in Thailand and like the name Bat-associated Pathogen and Ecology Research Network (BPERN).

Thanks,
Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info
ORCID

On Tue, Aug 1, 2017 at 6:32 AM, Kingston, Tigga< wrote:

> Hi everyone
>
> Bat-associated Pathogen and Ecology Research Network (BPERN) also gets my vote (if RABEZ is off the table – but I think that actually was the best description).
>
> The PENAPH Conference works best for me
>
> Tigga
>
> Tigga Kingston, PhD
>
> Associate Professor
>
> Department of Biological Sciences
>
> Texas Tech University
>
> Lubbock, TX 79409-3131
>
> USA
>
> http://kingstonlab.org
>
> http://seabcru.org

From: Tamar Kutateladze
Sent: Monday, July 31, 2017 11:41 AM
To: Katie Leahy >; kityrob ; ian.mendenhall ; joram.buza ; vkapur ecohealthalliance.org; ecohealthalliance.org; rebekah.kading ; lelincdc ; l.urushadze ; spwa abelwade ; c_demetria Kingston, Tigga <tigga.kingston >; cryanp ; dreeder gavin.smith ; nisreen.hmoud
Cc: Stokes, Martha M CIV (US) ; Lancaster, Mary J CIV (US) <mary.j.lancaster Gamboa, Omar Maj USAF DTRA J3-7 (US) ; Sander, William E CTR (US) ; Caitlin Devaney
Subject: Re: GBA Products and Action Items

Dear Katie, Dear Colleagues,

Thank you for your email.

I have successfully created an APAN account.

As for network name - I like Mary's suggestion - Bat-associated Pathogen and Ecology Research Network, or Global Alliance for Bat-born Pathogens (GBAP)

For the next meeting I vote for (PENAPH) Thailand.

Yours sincerely,

Tamar

Tamar Kutateladze
MD PhD
R. Lugar Center for Public Health Research
National Center for Disease Control & Public Health
16 Kakheti Highway, Tbilisi 0152, Georgia

T

On Tuesday, July 25, 2017, 5:18:11 PM GMT+4, Katie Leahy < > wrote:

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Katie Leahy

Program Manager | Global Systems Engineering

5881 Leesburg Pike, Suite 506

Baileys Crossroads, VA 22041

http://globalsyseng.com

From: Kingston, Tigga
Sent: Friday, July 28, 2017 11:53 AM EDT
To: Jon Epstein ecohealthalliance.org>
CC: DeeAnn Reeder ; Wade Abel ; l.urushadze >; Kading,Rebekah ; c_demetria >; spwa ; Lancaster, Mary J CIV (US) >; Stokes, Martha M CIV (US) >; gavin.smith ; nisreen.hmoud >; Caitlin Devaney Sander, William E CTR (US) joram.buza >; Gamboa, Omar Maj USAF DTRA J3-7 (US) >; Katie Leahy ; vkapur ; lelincdc ; kityrob >; ian.mendenhall ; olival tamar_kutateladze ; cryanp
Subject: RE: GBA Products and Action Items

I've been in TX too long, I gave it a Spanish pronunciation and missed the rabies thing entirely haha!

From: Jon Epstein
Sent: Friday, July 28, 2017 10:50 AM
To: Kingston, Tigga >
Cc: DeeAnn Reeder >; Wade Abel >; l.urushadze ; rebekah.kading c_demetria ; spwa ; Lancaster, Mary J CIV (US) >; Stokes, Martha M CIV (US) l>; gavin.smith ; nisreen.hmoud Caitlin Devaney >; Sander, William E CTR (US) ; joram.buza ; Gamboa, Omar Maj USAF DTRA J3-7 (US) ; Katie Leahy >; vkapur lelincdc ; kityrob ian.mendenhall ; ecohealthalliance.org; tamar_kutateladze ; cryanp
Subject: Re: GBA Products and Action Items

My RABEZ suggestion was slightly tongue-in-cheek. In retrospect, I worry that it might be outwardly confusing to others if we become the "Rabies network" when we won't actually be doing much with rabies.
With sensitivity to the bat conservation community, I suggest the "Bat Viral Ecology Research Network" or something along that line.

Cheers,
Jon

On Fri, Jul 28, 2017 at 8:19 AM, Kingston, Tigga > wrote:

> Greetings everyone
> Jon is there a link for the Prince Mahidol Award Conference (PMAC)? And dates? I will be teaching that semester, and it can be a bit manic taking time off at the beginning, but not impossible.
>
> For all the reasons pointed out by DeeAnn, I too like:
> Research Alliance for Bat-borne Emerging Zoonoses
> (RABEZ)
>
> Best wishes
> Tigga
>
> **From:** DeeAnn Reeder
> **Sent:** Thursday, July 27, 2017 11:47 PM
> **To:** Jon Epstein < ecohealthalliance.org>
> **Cc:** Wade Abel < >; l.urushadze rebekah.kading ; c_demetria ; spwa Lancaster, Mary J CIV (US) <mary.j.lancaste ; Stokes, Martha M CIV (US) ; gavin.smith ; Kingston, Tigga >; nisreen.hmoud Caitlin Devaney >; Sander, William E CTR (US) < >; joram.buza Gamboa, Omar Maj USAF DTRA J3-7 (US) ; Katie Leahy >; vkapur .edu; lelincdc ; kityrob ; ian.mendenhall ; ecohealthalliance.org; tamar_kutateladze cryanp
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I support Jon's RABEZ suggestion. In reference to our colleagues in bat conservation, we need to have the pathogen component in the title. And, we can't, from a grammatical perspective be an alliance FOR bat pathogens, rather an alliance for the study of bat pathogens.

Thanks, DeeAnn

On Jul 28, 2017 3:42 AM, "Jon Epstein" > wrote:

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>
> Cheers,
> Jon
>
> Jonathan Epstein DVM, MPH, PhD
>
> Vice President for Science and Outreach
>
> EcoHealth Alliance
> New York
>
> (
>
> On Jul 25, 2017 9:18 AM, "Katie Leahy" wrote:
>
> > ***Note: this email is best viewed in HTML***
> >
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Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

web: ecohealthalliance.org

Twitter: @epsteinjon

-

From: Nesreen Alhmoud
Sent: Monday, July 31, 2017 3:17 AM EDT
To: Katie Leahy ; kityrob ; ian.mendenhall joram.buza >; vkapur ; olival ; epstein >; Kading,Rebekah ; lelincdc ; l.urushadze ; tamar_kutateladze ; spwa >; abelwade ; c_demetria >; tigga.kingston ; cryanp >; dreeder >; gavin.smith >
CC: Stokes, Martha M CIV (US) >; Lancaster, Mary J CIV (US) ; Gamboa, Omar Maj USAF DTRA J3-7 (US) ; Sander, William E CTR (US) >; Caitlin Devaney
Subject: RE: GBA Products and Action Items

Dear Katie,

Thank you much for your e-mail and the provided documents.

I have successfully created an APAN account.

Regarding the name of the network, I prefer the following name: Global Bat Pathogen Disease Network (GBPDN).

For the next meeting, I vote for “Participatory Epidemiology Network for Animal and Public Health (PENAPH)” conference that will be held in Thailand next January.

My best regards,

Nisreen

الجمعية العلمية الملكية
Royal Scientific Society

Dr. Nesreen Alhmoud

Director of Bio-Safety and Bio-Security Center

P.O.Box: 1438 Amman 11941 Jordan
Website: www.rss.jo

Our Vision at The Royal Scientific Society is to be the local and regional reference point and knowledge leader for science and technology using scientific and engineering research to power economic development and social progress.

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>   c. Bat Alliance Trust Disease Network (BAT-DN)
>   d. Others??
>
> 3. We need nominations for co-chairs, seek your suggestions; we will plan to release nominees in one week from now for vote.

Katie Leahy
Program Manager | Global Systems Engineering
5881 Leesburg Pike, Suite 506
Baileys Crossroads, VA 22041

http://globalsyseng.com

From: Jon Epstein ecohealthalliance.org>
Sent: Thursday, July 27, 2017 8:42 PM EDT
To: Katie Leahy >
CC: abelwade l.urushadze >;
c_demetria ; Kading,Rebekah ; Lancaster,
Mary J CIV (US) >; spwa ; Stokes, Martha M CIV (US)
; gavin.smith >; tigga.kingston
>; Caitlin Devaney >; nisreen.hmoud
; Sander, William E CTR (US) joram.buza
; Gamboa, Omar Maj USAF DTRA J3-7 (US) >; vkapur
; lelincdc >; tamar kutateladze
; olival ecohealthalliance.org>; ian.mendenhall
; kityrob ; cryanp
; dreeder >
Subject: Re: GBA Products and Action Items

Hi Katie,
I propose meeting at the Prince Mahidol Award Conference (PMAC) in Bangkok, late January 2018. Primarily, I think November might be slightly early for our next meeting, given that we're working through governance and committee population. Also, PMAC is a big One Health meeting that at least three of us on the steering committee will already be attending, so there's some efficiency to it in terms of scheduling and expense, as well as having thematic relevance to our group.

Potential names:
1) Bat Ecology Research Network (BERN)

2) Bat Research Coordination Network (BRCN)

3) Global Alliance for Bat Research (GABR)

4) Research Alliance for Bat-borne Emerging Zoonoses (RABEZ)

Cheers,
Jon

Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
New York

On Jul 25, 2017 9:18 AM, "Katie Leahy" wrote:

> ***Note: this email is best viewed in HTML***
>
> Greetings, GBA Steering Committee!
>
> As promised we compiled a couple products and action items from our inaugural meeting on the 29th.
>
> The All Partners Access Network (the site we will use for document sharing and editing) is live and the Executive Summary from

our meeting, revised TORFTA, and TORFTA editing sheet have been uploaded. Here are the directions for access:

1. Go to www.apan.org
2. Click, “Create Account” (green button, upper right)
3. Use preferred work email and create password
4. Notify Will Sander once you have created your account; he will invite you to join the GBA SharePoint

For your ease, I have also attached the products that were hung on APAN:

1. An Executive Summary of the 29 June meeting for your files. This lists out key discussions, action items, and participants from the meeting.
2. Revised TORFTA (v14); **NOTE:** the plan for this document is to open a one week editing period for comments. If possible, edits and comments are due back NLT 31 July. After that, the official Version 1 of the GBA will be published.

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Katie Leahy

Program Manager | Global Systems Engineering

5881 Leesburg Pike, Suite 506

Baileys Crossroads, VA 22041

http://globalsyseng.com

From: Wade Abel
Sent: Tuesday, July 25, 2017 4:14 PM EDT
To: Katie Leahy
CC: kityrob ; ian.mendenhall
joram.buza >; vkapur ;
olival >; epstein
; Kading,Rebekah ; lelincdc
; l.urushadze >; tamar _kutateladze
; spwa ; c _demetria
>; tigga.kingston cryanp ;
dreeder >; gavin.smith ;
nisreen.hmoud Stokes, Martha M CIV (US) >; Lancaster,
Mary J CIV (US) ; Gamboa, Omar Maj USAF DTRA J3-7 (US)
; Sander, William E CTR (US) Caitlin Devaney

Subject: Re: GBA Products and Action Items

Dear Katie,

Thanks for your message. The system failed to create an APAN account for me, will try other way. However, I would like to response to the 2 points. My suggestions are:

a. Next meeting during International Congress on Pathogens at the Human and Animal Interface (ICOPHAI) 7-9 November 2017, Doha, Qatar https://icophai.org/
b. Network name: Global Alliance for Bat-borne Pathogens (GABP)

kind regards

On 25 July 2017 at 14:18, Katie Leahy wrote:

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>
> Greetings, GBA Steering Committee!
>
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>
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Katie Leahy

Program Manager | Global Systems Engineering

5881 Leesburg Pike, Suite 506

Baileys Crossroads, VA 22041

http://globalsyseng.com

--

Dr Abel WADE
Director of the National Veterinary Laboratory (LANAVET) annex inYaounde
Ministry of Livestock, Fisheries and Animal Industries (MINEPIA)
Yaounde-Cameroon

www.lanavet.com; www.minepia.org.cm

From: Caitlin Devaney
Sent: Tuesday, June 06, 2017 11:56 AM EDT
To: Lancaster, Mary J CIV (US) ; "Stokes, Martha M CIV (US)" ; Kevin Olival, PhD @ecohealthalliance.org>; Robert Kityo Gamboa, Omar Maj USAF DTRA J3-7 (US) ; Sander, William E CTR (US) ; Katie Leahy >; joram buza gavin.smith Ian MENDENHALL PhD Vivek Kapur >; Jon Epstein ecohealthalliance.org>; Kading,Rebekah ; mary dugan ; vklabcalendar

Subject: Re: GBA Steering Committee Planning Call
Attachment(s): "TORFTA_GBA_v7.docx","GBA Meeting Overview_29June2017.docx"

All,

This is a friendly reminder that we will be having the next planning call for the GBA Steering Committee tomorrow, Wednesday, 7 June at 0900 U.S. EST. The attached draft TORFTA and 29 June Fort Collins meeting agenda are attached for your reference (these were included on the Letter of Invitation emails that went out yesterday as well). Please review these documents, as we will be discussing them during the call.

Looking forward to speaking with you all tomorrow!

v/r,
Caitlin Devaney

From: caitlin.devaney
When: 9:00 AM - 10:00 AM June 7, 2017
Subject: GBA Steering Committee Planning Call
Location: Teleconference

All,

Please see below dial-in information for our next planning call scheduled for 7 June, at 0900 U.S. EST:

U.S. Dial-in: 1-703-552-8058

Singapore Dial-in: 65-3-1591097

Conference Code: 484877

(Alternative for Singapore callers) International Toll Free Dial-in: 800-492-2224

Call Agenda:

1. Brief Introductions
2. Review TORFTA feedback
    a. Discuss scope of the GBA steering committee membership
    b. Discuss organizational structure of the GBA steering committee
    c. Discuss roles and responsibilities of GBA steering committee membership
3. Discuss 29 June Fort Collins meeting
    a. Confirm attendance for 29 June meeting in Fort Collins
    b. Review meeting objectives
    c. Review meeting agenda
    d. Review proposed focus areas
4. Review action items (if any)

v/r,

Caitlin Devaney

Global Bat Alliance Meeting

Overview (objectives, agenda, and logistics)
29 June 2017

Meeting objectives (proposed)

1. Finalize GBA Terms of Reference for Trusted Agents (TORFTA)
2. Identify bat research focus areas and associated mentorship leads for each area
3. Prioritize research needs and gaps for each focus area and identify correlating researchers, institutions, other networks / alliances, and funding entities
4. Draft short and long-term timelines and workplans for each focus area
5. Determine steering committee convening schedule and Cohort II / III / IV training schedule

Focus areas (proposed)

- Virus / host relationship
- Commodity chain and trade routes
- Ecological change and effects
- Bat, livestock, and wildlife interactions

Note: these focus areas are not regionally based as previously discussed, in an effort to build towards the overarching objective of a multi-regional, multi-disciplinary network; they will be the subject of discussion during the 7 June virtual meeting and the 29 June GBA Meeting in Fort Collins

Logistics needs (proposed)

- Room for 25 with "U"-shaped set-up
- Projection capability
- Microphones (depending on #s)
- Catered lunch (working lunch w/ presentations)
- Name / organization table tents

Agenda

Time	Agenda Topic and Facilitator or Speaker	Expected Outcomes
0930 –	**Welcome and**	

1000	**Introductions**	
1000 – 1015	**Global Bat Alliance Overview** *Dr. Mary Lancaster (Africa Science Lead)* *Dr. Marty Stokes (SEA Science Lead, CBEP)*	• Review discussions leading up to this meeting • Discuss how this meeting is an opportunity to formalize the central / steering committee node for the distributed network • Emphasize that the steering committee shall focus on mentorship and connecting individuals and institutions across the globe
1015 – 1045	**Review Charter and Move to Agreement** *TBD*	• Vote to accept organizational document for steering committee • Unanimous (??) acceptance • We will advertise intent ahead of meeting • We will convene a meeting on 7 June to review and discuss the draft TORFTA
1045 – 1115	**Identify and discuss research focus areas** *TBD*	• Group will identify and discuss overarching focus areas and sub focus areas • Steering committee and invitees shall self nominate to groups and agree to serve as research mentors for the groups
1115 – 1230	**Breakout: Prioritize research needs and gaps** *TBD*	• Group will breakout into their research focus areas and begin identifying needs and gaps • Groups will then work to prioritize their lists
1230 – 1330	**Working Lunch** *TBD*	• Buffett • Convene back as a group, hold discussions about the overarching objectives of the alliance • Discuss One Health and Vector-based International meetings as an opportunity to re-convene semi-annually
1330 – 1400	**Breakout: Draft timelines and workplans** *TBD*	• Begin drafting short and long-term timelines and workplans for each focus area • Short-term milestones could include identifying key researchers and networks • Long-term milestones could include training events and focus area meetings
1400 – 1430	**Closing / review of actions** *TBD*	• Close-out meeting / 5min brief out for each group (2 slides) • Review action items and next steps

PROPOSED TERMS OF REFERENCE FOR TRUSTED AGENTS OF THE GLOBAL BAT ALLIANCE

1. BACKGROUND

The Global Bat Alliance (GBA) will serve as a platform to identify and connect interdisciplinary expertise to address challenges and threats posed by bat-associated pathogens of security concern. Specifically, the GBA shall convene a body of experts and researchers to: (1) share information, data, samples, and protocols; (2) coordinate research activities; (3) build training events and awareness-building workshops at all levels of decision-making authority; (4) develop community standards and best research practices; (5) create mentorship-based opportunities for students, trainees, and early-career researchers to convene, present, and share ideas; and (6) establish a community of international research leaders and champions.

Some of the world's most deadly emerging zoonotic diseases are found in bats, including Nipah, Hendra, and Marburg viruses. There are a number of factors which make bats unique disease reservoirs, including their social behavior and mutual grooming patterns, ability to travel long distances, nocturnal activity, species diversity, and long life span (10-20 years, compared with a rat's average life of two years).[1] These characteristics make bats very difficult to study within traditional controlled laboratory settings and create research challenges to understanding their roles in the global zoonotic disease ecology. The GBA will create opportunities for policy makers, researchers, funders, and students to identify research challenges, develop priority lists and associated action plans to target needs and gaps, and work at all levels to build awareness of bat-associated disease burden and transmission risks to improve the prevention, detection, diagnosis, and reporting of pathogens of security concern.[2]

2. GBA MISSION AND VISION

The GBA shall bring together scientists, policy makers, and medical/veterinary practitioners with interests in bat-related research involving pathogens of security concern. The network will build on community standards and best practices for research. The GBA will identify and share information on research funding opportunities offered by multiple institutions. Most importantly, the alliance will foster international relationships among collaborators, agencies, and organizations, which can produce long-term, sustainable partnerships that withstand changes in government and organization budgets, priorities, postures, and policies.

The Trusted Agents of the alliance with play a role in operationalizing the GBA, strengthening the linkages and reducing overlap in the global research effort on high-priority diseases of bats (especially

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[1] Hayman, David T.S., "As the bat flies," *Science* 02 Dec 2016: Vol. 354, Issue 6316, pp. 1099-1100 http://science.sciencemag.org/content/354/6316/1099

[2] Schountz, Tony, "Immunology of Bats and Their Viruses; Challenges and Opportunities," *Viruses,* 2014 Dec; 6(12): 4880-4901. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4276934/

zoonoses) to maximize the efficient use of expertise and resources and accelerate the coordinated development of disease surveillance and control methods.

3. OBJECTIVES

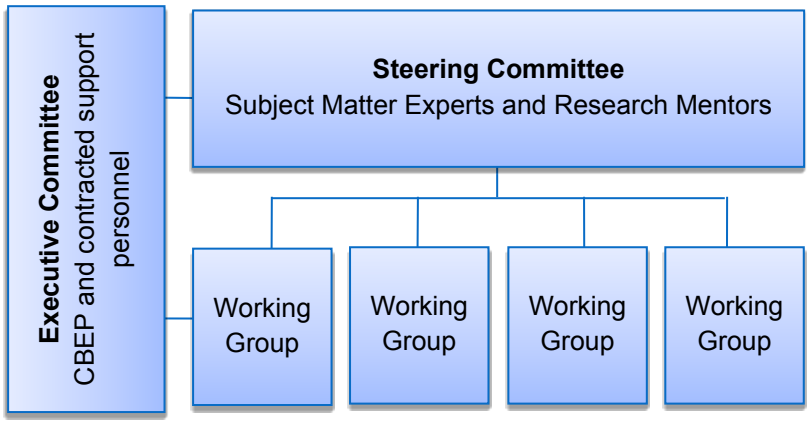
The objectives of the GBA are as follows:

- Facilitate interdisciplinary collaboration to identify research goals and needs for bat-associated disease research and disease threat reduction; and
- Unify CBEP regions to create a common action plan that yields collaborative projects that achieve the following end states: (1) better informed policy-makers; (2) better informed scientific community regarding funding targets and gaps in areas of research and development; and (3) better defined threat to global health security from bat-associated pathogens

4. APPROACH

The Terms of Reference for Trusted Agents (TORFTA) will convene subject matter experts to serve as mentors and function as independent, trusted advisors and honest brokers for research within the GBA. Trusted Agents will function within an organizational structure that consists of an Executive Committee, a Steering Committee, and four subject matter focused Working Groups.

4.1 The **Executive Committee (EC)** will be chaired by the CBEP Science Leads from Africa and Southeast Asia with organizational and administrative support from designated contractors for the program. The EC shall be responsible for developing GBA governance policies and guidelines, which could include coordinated research funding and approving invitations to serve on the Steering Committee and within the Working Groups. The EC and their team shall additionally be responsible for the following tasks (at a minimum):



- Establish broad objectives and goals for the GBA
- Organize and facilitate meetings for the GBA
- Provide secretarial support for all virtual and in-person meeting for the GBA
- Prepare materials on request
- Disseminate information including (but not limited to) newsletters, website links, press releases, meetings and conferences
- Coordinate with other funding agencies and organizations

4.2 The **Steering Committee (SC)** shall include scientific experts that shall act as the scientific coordinating body for global bat research, provide research gap analysis, and priority setting to the EC, as well as considering the scientific merit of proposals from the EC and assist with their implementation as per the terms of reference. To that end, the SC shall be responsible for the following items (at a minimum):

- Act as a scientific coordinating body for the GBA
- Consider the scientific merit of proposals from the EC
- Serve as subject matter experts and research mentors for implementation of accepted GBA-endorsed projects
- Propose research priorities
- Review and make recommendations on any matter involving an alteration in the mandate, terms of reference, membership, or structure of the GBA
- Review, discuss, and make recommendations for the logistics requirements of the GBA, sources and means of political and financial support, and its capability to function correctly in the future
- Define missions and submissions of the Working Groups, as well as identifying need for proposing establishment of new or closing-out existing WGs
- Supporting WGs in organizing gap analyses and research prioritization
- Promote interactions between WGs
- Assess and report progress of the WGs to other members of the SC and EC
- Develop and encourage exchange of protocols and best practices, and agree on standard operating procedures, good research practice, and roadmap to reach GBA goals (short and long-term)

4.2.1 Participate in semi-annual meetings. Meetings will normally take place twice annually in a place and at a time that is convenient for participants to a bat-relevant conference or meeting. The Chair may convene meetings at other times when they find support of at least two thirds of the members of the Steering Committee. These meetings can be virtual or in-person. The Secretary is responsible for ensuring that the agenda of the meeting is made available to the members in good time before the meeting.

4.2.2 Develop recommendations. Business will be conducted by careful and considered deliberation leading to recommendations to the GBA. Recommendations shall be decided by consensus where possible. Consensus means that after deliberation all members support a particular point of view. Where consensus is not achieved, recommendations shall be decided by simple majority vote of members voting on the question. In the case of a tied vote, the person acting as Chair shall be entitled to a second or deciding vote.

4.2.3 Attain consensus. A quorum is constituted by half of the number of individuals composing the Steering Committee rounded up when the number in the Steering Committee is uneven. The Steering Committee may decide by consensus or majority vote to ask parties who are not members of the Steering Committee to participate in a meeting so that they can provide relevant information, material, or knowledge. The Steering Committee may establish sub-committees consisting of 3 or more of its members and refer to them any matter in the Steering Committee's mandate. It may co-opt other GBA participants onto such committees.

4.3 The **Working Groups (WG)** shall serve to divide the GBA into multi-disciplinary, multi-national focus areas to meet the research challenges associated with bat-borne diseases. Members of the SC shall serve as research mentors and subject matter experts within each WG. The WGs will focus on the following focus areas (*please note, these focus areas are very much in draft form and will be the subject of discussion during the 7 June virtual meeting and the 29 June GBA Meeting in Fort Collins)*:

- Virus / host relationship
- Commodity chain and trade routes
- Ecological change and effects
- Bat, livestock, and wildlife interactions

5. GOVERNANCE AND MEMBERSHIP

5.1 Accountability

The overarching duty of the GBA is to develop multi-disciplinary and multi-national hypothesis driven research projects that meet the prioritized challenges defined by the Executive Committee under advice from the Steering Committee. Accountabilities of the GBA EC, SC, and Members include the following:

- Each member shall be familiar with the TORFTA and the mandate of the committees or WGs on which they serve
- Each member shall promote a culture of responsible practice for scientific research
- Each member shall work towards the short- and long-term goals of the GBA with a particular emphasis on the foci that fall within their WG
- Members of the SC are selected for their breadth of experience, insight and knowledge, integrity and character, and sound and independent judgment. Therefore, they are expected to bring these personal qualities to their role on the SC and apply impartial judgment to help the EC make informed and independent decisions

5.2 Conflicts of Interest

This terms of reference document adopts a modified National Academy of Sciences (NAS) definition of Conflict of Interest: a conflict of interest in research exists when the individual has interests in the outcome of the research that may lead to a personal, institutional, or financial advantage and that might therefore, in actuality or appearance compromise the integrity of the research."

No member of the Steering Committee may participate in a discussion where such participation would give rise to a potential conflict of interest. SC members must recuse themselves if such a conflict is perceived. The EC will review all situations where potential personal, institutional, or financial conflicts of interest are suspected.

SC members may leave their term of service on the SC if they wish to participate in a funding opportunity that would otherwise be perceived as a conflict of interest.

5.3 Selecting Committee Members

The SC and members of the WGs shall include members that reflect the multi-disciplinary and multi-national nature of the GBA. There are no term limits for members of the GBA, who are allowed to

participate at will in accordance with terms of the TORFTA. However, members of the SC follow other rules for selection:

- ***5.3.1*** ***Terms of service –*** *2 years, no term limit*
- ***5.3.2*** ***Eligibility*** *– representation from each CBEP region must be maintained*
- ***5.3.3*** ***Nomination process –*** *nominated at the end of even calendar years by peers (members of the GBA) at GBA research review meetings or electronically*
- ***5.3.4*** ***Selection process –*** *reviewed by members of the EC under advisement of the SC*

Members of the WGs will not follow any rules for selection other than representing CBEP regions. There will be no term limits, WG members are encouraged to contribute and participate indefinitely. Members shall be nominated and invited to participate by members of the EC and SC.

From: Caitlin Devaney >
Sent: Wednesday, June 07, 2017 2:53 PM EDT
To: Lancaster, Mary J CIV (US) ; "Stokes, Martha M CIV (US)" ; Kevin Olival, PhD ecohealthalliance.org>; Robert Kityo ; Gamboa, Omar Maj USAF DTRA J3-7 (US) Sander, William E CTR (US) ; Katie Leahy ; joram buza gavin.smith ; Ian MENDENHALL PhD ; Vivek Kapur Jon Epstein cohealthalliance.org>; Kading,Rebekah ; mary dugan >; vklabcalendar

Subject: Re: GBA Steering Committee Planning Call
Attachment(s): "GBA MEETING NOTES_7 JUNE.pdf"

All,

Attached please find notes and action items from this morning's planning call.

v/r,
Caitlin Devaney

From: Caitlin Devaney
Date: Tuesday, June 6, 2017 at 11:56 AM
To: "Lancaster, Mary J CIV (US)" , ""Stokes", "Kevin Olival, PhD" >, Robert Kityo , "Gamboa, Omar Maj USAF DTRA J3-7 (US)" >, "Sander, William E CTR (US)" >, Katie Leahy , joram buza >, "gavin.smith , Ian MENDENHALL PhD , Vivek Kapur , Jon Epstein ecohealthalliance.org>, "Rebekah.Kading >, mary dugan , "vklabcalendar "

Subject: Re: GBA Steering Committee Planning Call

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v/r,
Caitlin Devaney

From: caitlin.devaney
When: 9:00 AM - 10:00 AM June 7, 2017
Subject: GBA Steering Committee Planning Call
Location: Teleconference

All,

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U.S. Dial-in: 1-703-552-8058

Singapore Dial-in: 65-3-1591097

Conference Code: 484877

(Alternative for Singapore callers) International Toll Free Dial-in: 800-492-2224

Call Agenda:

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    b. Discuss organizational structure of the GBA steering committee

    c. Discuss roles and responsibilities of GBA steering committee membership

3. Discuss 29 June Fort Collins meeting

    a. Confirm attendance for 29 June meeting in Fort Collins

    b. Review meeting objectives

    c. Review meeting agenda

    d. Review proposed focus areas

4. Review action items (if any)

v/r,

Caitlin Devaney

Global Bat Alliance Steering Committee | Planning Meeting Notes
0900 US EST 7 JUNE 2017

ATTENDEES

- Dr. Marty Stokes (CBEP)
- Dr. Mary Lancaster (CBEP)
- MAJ Omar Gamboa (CBEP)
- Dr. Will Sander (CTR A&AS Booz Allen)
- Ms. Katie Leahy (Global Systems Engineering)
- Ms. Caitlin Devaney (Global Systems Engineering)
- Ms. Mary Dugan (Global Systems Engineering)
- Dr. Vivek Kapur (Penn State University)
- Dr. Jon Epstein (EcoHealth Alliance)
- Dr. Kevin Olival (EcoHealth Alliance)
- Dr. Joram Buza (NM-AIST)
- Dr. Rebekah Kading (Colorado State University)

ACTION ITEMS

Task	Responsible	Due Date
Send GBA research database to the group	Global Systems Engineering	14 JUNE
Add to GBA research database	ALL	Rolling; ~29 June meeting
Update TORFTA and send to the group	Global Systems Engineering	14 JUNE
CBEP to work with Dr. Kading on additional participants and logistics requirements	CBEP	Rolling

AGENDA

TORFTA feedback and discussion

- **Discussion was opened for comments and suggestions for TORFTA revisions**
  - The intent was to build toward consensus on a near-final document, so that the TORFTA can be finalized during the 29 June meeting in Fort Collins.
- **TORFTA concept and framework**
  - Trusted agents are individuals who act in the best interest, and as an extension, of the sponsor organization. In the case of the GBA steering committee, these trusted agents would become an extension of CBEP. They also deal with conflicts of interest with the intent to only better the organization.
  - The basic framework of the TORFTA consists of the steering committee and working groups, which report out to the executive committee. This hierarchy is very useful when large amounts of information are discussed / priorities within the alliance need to be established. The general structure has been proven to be effective in several other domestic and global alliances.
  - It will be important to first define the functions of the GBA, and the working groups, and to then build a complimentary and supportive organizational structure.
  - More information on the scope of the steering committee, and the steering committee selection process is needed.
    - Invitations to join the steering committee have been extended to individuals in PACOM, EUCOM, AFRICOM, CENTCOM, and the conservation field. In total 17 individuals are accounted for currently.
- **Resolution for potential conflict of interest issues**
  - The question of how subject matter experts with current / future work in the field can resolve any conflict of interest that could come with steering committee membership (advising, shaping, and mentoring while staying involved in research / fieldwork) was raised.
  - One of CBEP's biggest concerns is to ensure future projects and research are not precluded for steering committee members.

- Assigning mentors for each working group, who are not on the Steering Committee, could mitigate some of the conflict of interests.
- A system of checks and balances must be in place to account for possible overlap with facilitation of research.
- An alternative approach could be using a request for information/assessment which would draw interested parties together to form a research consortia. This way they can directly address the objectives, while still being able to award multiple lines of effort.
- It should be explicitly stated that the executive committee makes funding decisions, which is separate from the steering committee.
- Include definitions of funding selection criteria; and methods to support and relieve established researchers.
- Section 5.2 “Conflicts of Interest” must be clarified and strengthened in the TORFTA in order to highlight above discussion.

- **Roles and Responsibilities**
  - The last sentence of the TORFTA was discussed. It was noted that the steering committee will nominate members for the GBA, but that further clarification of rules and responsibilities of steering committee members must be defined. Mutual trust and shared philosophy is crucial in the membership process and for future growth and healthy agreements within the alliance.
  - Section 4.2 mentions the Chair position, a role that needs to be explicitly defined.
  - Section 4.3 regarding working groups needs to be built out further.

Discussion about the 29 June Fort Collins meeting

- The proposed GBA focus areas will be reviewed during the Fort Collins meeting.
  - Mentors for working groups will be identified, along with the structure of the working groups.
- All agreed that the proposed objectives and agenda for the meeting are satisfactory.
- The prioritization of the needs and gaps within research areas will be an ongoing process (it will take longer than the meeting itself).

From: Cryan, Paul
Sent: Thursday, August 24, 2017 12:38 PM EDT
To: Nesreen Alhmoud
CC: Katie Leahy ; Robert Kityo ; Ian Mendenhall Joram Buza Vivek Kapur >; Kevin Olival ecohealthalliance.org>; Jon Epstein @ecohealthalliance.org>; Kading,Rebekah >; Lela Urushadaze ; Lela Urushadaze ; Tamar Kutateladze >; Supaporn Wacharapluesadee >; Abel Wade ; Catalino Demetria ; Tigga Kingston >; DeeAnn Reeder ; Gavin Smith ; Lancaster, Mary J CIV (US) ; Stokes, Martha M CIV (US) ; Sander, William E CTR (US) ; Caitlin Devaney
Subject: Re: GBA Update and Request

Greetings,

Great to hear that we have such excellent steering committee co-chairs in place for the upcoming meeting in Thailand!

I prefer the BPERN name.

Best regards,
Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info
ORCID

On Thu, Aug 24, 2017 at 3:01 AM, Nesreen Alhmouc wrote:

> Dear Ms. Katie,
>
> Thank you for your e-mail.
>
> Regarding the name of the network, I will go for Option 1 *Bat-associated Pathogen and Ecology Research Network (BPERN).*
>
> Best,
>
> Nisreen

Dr. Nesreen Alhmoud

Director of Bio-Safety and Bio-Security Center

الجمعية العلمية الملكية
Royal Scientific Society

P.O.Box: 1438 Amman 11941 Jordan
Website: www.rss.jo

Our Vision at The Royal Scientific Society is to be the local and regional reference point and knowledge leader for science and technology using scientific and engineering research to power economic development and social progress.

From: Katie Leahy
Sent: Wednesday, August 23, 2017 3:18 AM
To: Robert Kityo; Ian Mendenhall; Joram Buza; Vivek Kapur; Kevin Olival; Jon Epstein; Rebekah Kading; Lela Urushadaze; Lela Urushadaze; Tamar Kutateladze; Supaporn Wacharapluesadee; Abel Wade; Catalino Demetria; Tigga Kingston; Paul Cryan; DeeAnn Reeder; Gavin Smith; Nesreen Alhmoud
Cc: Lancaster, Mary J CIV (US); Stokes, Martha M CIV (US); Sander, William E CTR (US); Caitlin Devaney
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All,

On behalf of Dr. Mary Lancaster and Dr. Marty Stokes, we would like to thank everyone, for your responses over the last couple weeks! Based on your feedback, we have a few announcements and one request:

Based on committee consensus, the group chose our next event to coincide with the Participatory Epidemiology Network for Animal and Public Health (PENAPH) on 10-12 January 2018, in Khon Kaen, Thailand. Details will be forthcoming, but please visit the hyperlink for further information (https://penaph.net/second-penaph-conference-participatory-approaches-in-animal-health-public-health-one-health-and-ecohealth/).

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V/r,

Katie Leahy

Program Manager | Global Systems Engineering

5881 Leesburg Pike, Suite 506

Baileys Crossroads, VA 22041

http://globalsyseng.com

From: Kingston, Tigga >
Sent: Tuesday, August 29, 2017 4:20 PM EDT
To: Cryan, Paul ; Nesreen Alhmoud >
CC: Katie Leahy >; Robert Kityo ; Ian Mendenhall Joram Buza ; Vivek Kapur ; Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Kading,Rebekah ; Lela Urushadaze ; Lela Urushadaze Tamar Kutateladze >; Supaporn Wacharapluesadee Abel Wade ; Catalino Demetria >; DeeAnn Reeder Gavin Smith >; Lancaster, Mary J CIV (US) >; Stokes, Martha M CIV (US) ; Sander, William E CTR (US) ; Caitlin Devaney >
Subject: RE: GBA Update and Request

BPERN gets my vote too. Looking forward to reconvening in January!
Tigga

Tigga Kingston, PhD
Co-Chair, Old World
IUCN SSC Bat Specialist Group

Associate Professor
Department of Biological Sciences
Texas Tech University
Lubbock, TX 79409-3131
USA

http://kingstonlab.org
http://seabcru.org

From: Cryan, Paul
Sent: Thursday, August 24, 2017 11:39 AM
To: Nesreen Alhmoud <
Cc: Katie Leahy ; Robert Kityo ; Ian Mendenhall ; Joram Buza >; Vivek Kapur ; Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Rebekah Kading ; Lela Urushadaze ; Lela Urushadaze >; Tamar Kutateladze >; Supaporn Wacharapluesadee ; Abel Wade >; Catalino Demetria ; Kingston, Tigga >; DeeAnn Reeder >; Gavin Smith Lancaster, Mary J CIV (US) ; Stokes, Martha M CIV (US) ; Sander, William E CTR (US) >; Caitlin Devaney >
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Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info
ORCID

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Nisreen

Dr. Nesreen Alhmoud

Director of Bio-Safety and Bio-Security Center

P.O.Box: 1438 Amman 11941
Jordan

Email:

Website: www.rss.jo

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Sent: Wednesday, August 23, 2017 3:18 AM
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Cc: Lancaster, Mary J CIV (US); Stokes, Martha M CIV (US); Sander, William E CTR (US); Caitlin Devaney
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V/r,

Katie Leahy
Program Manager | Global Systems Engineering
5881 Leesburg Pike, Suite 506
Baileys Crossroads, VA 22041

http://globalsyseng.com

From: DeeAnn Reeder
Sent: Monday, October 30, 2017 10:12 AM EDT
To: Katie Leahy <
CC: Robert Kityo ; Ian Mendenhall Joram Buza ; Vivek Kapur < >; Kevin Olival ecohealthalliance.org>; Jon Epstein ; Kading,Rebekah ; Lela Urushadaze ; Lela Urushadaze ; Tamar Kutateladze ; Supaporn Wacharapluesadee ; Abel Wade >; Catalino Demetria ; Tigga Kingston >; Paul Cryan ; Gavin Smith Nisreen Alhmoud ; Lancaster, Mary J CIV (US) ; Stokes, Martha M CIV (US) >; Sander, William E CTR (US) >; Caitlin Devaney >
Subject: Re: GBA Update and Request

Dear Katie et al.,

Can you please confirm that we are on for this conference? Will be be meeting the day before? For 1 or 2 days? I'm trying to work on my schedule for next year - and also noticed that early registration for this conference ends on Wednesday.

Looking forward to seeing everyone - DeeAnn

On Tue, Aug 22, 2017 at 8:17 PM, Katie Leahy< wrote:

> All,
>
> On behalf of Dr. Mary Lancaster and Dr. Marty Stokes, we would like to thank everyone, for your responses over the last couple weeks! Based on your feedback, we have a few announcements and one request:
>
> Based on committee consensus, the group chose our next event to coincide with the Participatory Epidemiology Network for Animal and Public Health (PENAPH) on 10-12 January 2018, in Khon Kaen, Thailand. Details will be forthcoming, but please visit the hyperlink for further information (https://penaph.net/second-penaph-conference-participatory-approaches-in-animal-health-public-health-one-health-and-ecohealth/).
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>
> V/r,

Katie Leahy

Program Manager | Global Systems Engineering

5881 Leesburg Pike, Suite 506

Baileys Crossroads, VA 22041

http://globalsyseng.com

--
DeeAnn M. Reeder, PhD
Presidential Professor
Department of Biology
Bucknell University
Lewisburg, PA 17837

From: Katie Leahy
Sent: Thursday, June 29, 2017 10:09 AM EDT
To: Sander, William E CTR (US) >
CC: kityob ; ian.mendenhall >; Prof. Joram Buza ; Vivek Kapur ; Kevin Olival, PhD ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; gavin.smith >; Kading,Rebekah >; lelincdc >; l.urushadze >; tamar _kutateladze ; spwa ; abelwade >; c demetria ; Kingston, Tigga < nisreen.hmoud ; cryanp dreeder ; Lancaster, Mary J CIV (US) ; Stokes, Martha M CIV (US) >; Gamboa, Omar Maj USAF DTRA J3-7 (US) Caitlin Devaney >
Subject: Re: Global Bat Alliance Steering Committee meeting - info

Hi, everyone. A quick reminder on behalf of Mary and Marty:

Our meeting this morning will be held in **Room 142**, in the University Center for the Arts. This is the **same building where the conference will be held**.

V/r,

Katie Leahy

Sent from my iPhone

On Jun 27, 2017, at 14:27, Sander, William E CTR (US) wrote:

> On behalf of Mary Lancaster and Marty Stokes, we're excited to convene the first in-person meeting of the Steering Committee for the Global Bat Alliance.
>
> As friendly reminders of what to expect:
>
> - Convene on Thursday, June 29th, in room 142 of the University Center for the Arts (same building as the conference)
> - Start at 9:30AM local time (room will be open by 9AM)
> - Working lunch (lunch provided) - vegetarian option included
> - Plan to end the meeting at 2:30PM local time
> - For those of you calling in, we will get that information to you within the next day.
>
> I have attached again our agenda as well as the Terms of Reference for Trusted Agents for your reference and review.
>
> If you have any questions, do not hesitate to reach out to any of us in the CC line. The number below is my cell phone.
>
> Best,
>
> Will Sander, DVM, MPH, DACVPM, PMP
> Veterinary Specialist
> Booz Allen Hamilton
> CTR A&AS Support Contractor
>
> <TORFTA_GBA_v10.docx>
>
> <GBA Meeting Overview_29June2017_v2.docx>

From: Wade Abel
Sent: Thursday, February 01, 2018 12:08 AM EST
To: Katie Leahy >
CC: Ian Mendenhall >; Joram Buza >; Vivek Kapur >; Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Kading,Rebekah ; Lela Urushadaze ; Tamar Kutateladze ; Supaporn Wacharapluesadee >; Catalino Demetria ; Tigga Kingston ; Paul Cryan ; DeeAnn Reeder >; Gavin Smith ; Nisreen Alhmoud Keti Sidamonidze ; Bounheuang, Kounnavong >; Stokes, Martha M CIV (US) >; mary.j.lancaster >; Newman, Carl I CIV DTRA J3-7 (US) ; christopher.r.lewis
Subject: Re: IMPORTANT: Transportation to Ambassador's Reception

Dear Katie.
Thank you for the clear information.

Have a nice day.
Wade

On 1 Feb 2018 12:03 pm, "Katie Leahy" wrote:

> All,
>
> There have been several inquiries. To be clear: CBEP **will not** be providing transportation to or from the Ambassador's reception this evening. You should have a hard copy of the invitation, please feel free to walk, cab, or uber to the residence address that is provided on your invitation. The reception runs from 1800-2000 and you are invited to arrive and leave at your discretion.
>
> V/r,
>
> Katie Leahy
>
> **Katie Leahy**
>
> *Program Manager* | Global Systems Engineering
>
> 6303 Little River Turnpike, Suite 208
>
> Alexandria, VA 22305
>
> http://globalsyseng.com
>
>

From: Robert Kityo
Sent: Monday, May 08, 2017 10:13 AM EDT
To: Leahy, Catharine (US)
CC: Lancaster, Mary J CIV (US) (
martha.m.stokes ; Sander, William E CTR (US)
(Joram Buza ; Vivek Kapur
; olival >; epstein
>; gavin.smith ; ian.mendenhall@
>; Devaney, Caitlin (US) Kading,Rebekah

Subject: Re: Meeting request: Global Bat Alliance Network (convened on behalf of CBEP)

Dear Katie,

Glad to receive yours. Thanks very much. Unfortunately i shall be in the field in a remote part of Uganda starting on the 14th-May-2017. Most of the day i shall not have access to connectivity, how ever please send the invitation to call in. If i happen to be at the hotel at that time, i will certainly join into the discussion. I will in the meantime look through the document that you attached.

Best regards

Kityo Robert M (PhD)
Makerere University
College of Natural Sciences
School of BioSciences
Department of Zoology, Entomology and Fisheries Sciences
P.O. Box 7062 Kampala

On Mon, May 8, 2017 at 4:32 PM, Leahy, Catharine (US)< wrote:

> All,
>
> On behalf of Dr. Mary Lancaster (Regional Science Manager, CBEP Africa) and Dr. Marty Stokes (Regional Science Manager, CBEP Southeast Asia) we request your participation in a virtual meeting to discuss the establishment and management of a Global Bat Alliance Network. This cross-regional and disease surveillance research network will serve as the platform to identify and connect interdisciplinary expertise to address an array of emerging challenges and threats associated with bat-borne diseases.
>
> This internal planning call is tentatively scheduled for 15 May 2017 at 0800 EST. Please reply to me at with your availability for this suggested date and time. I will provide call-in information and a more specific agenda for the call once we are able to confirm everyone's availability.
>
> Additionally, please find notes from a Global Bat Alliance Network planning call that took place on 9 February 2017 attached to this email, below my signature block.
>
> I am looking forward to hearing from you!
>
> v/r,
>
> Katie Leahy
>
> **Katie Leahy**
> Senior Analyst / Project Lead
> Global Security Programs
> Cubic Global Defense
> 5695 King Centre Drive
> Alexandria, VA 22315
>
> w: globalsecurity.cubic.com
>
>

From: Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)
Sent: Thursday, August 13, 2020 9:14 AM EDT
To: Kevin Olival ecohealthalliance.org>; Cara Brook >; Hon S Ip < >; Paul Cryan ; David Hayman >; epstein ecohealthalliance.org>; dreeder >; Hume Field ecohealthalliance.org>; Charles H Calisher Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) ; Wang Linfa ; Ralph S. Baric ; David S Blehert Kevin Castle Jeremy Coleman ; Peter Daszak >; wfrick ; Amy Gilbert >; William Karesh ; Christine Kreuder Johnson ; Kading,Rebekah ; Tigga Kingston ; Lorch, Jeffrey M Ian MENDENHALL PhD >; alisonpeel < ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; Jonathan D Reichard ; Jonathan M Sleeman ; Daniel Streicker

Subject: RE: Paper Proof - please review. "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPA...

Looks good to me, thanks Kevin.
Jon

_____
Jonathan S. Towner, PhD
Lead, Virus Host Ecology Team
Viral Special Pathogens Branch
Centers for Disease Control and Prevention
Mailstop H18-B

From: Kevin Olival < ecohealthalliance.org>
Sent: Wednesday, August 12, 2020 7:55 PM
To: Cara Brook ; Hon S Ip ; Paul Cryan >; David Hayman >; Jon Epstein ecohealthalliance.org>; dreeder Hume Field ecohealthalliance.org>; Charles H Calisher ; Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) ; Wang Linfa ; Ralph S. Baric >; David S Blehert ; Kevin Castle ; Jeremy Coleman ; Peter Daszak ecohealthalliance.org>; wfrick ; Amy Gilbert ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson Kading,Rebekah ; Tigga Kingston >; Lorch, Jeffrey M ; Ian MENDENHALL PhD ; alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina >; Jonathan D Reichard Jonathan M Sleeman >; Daniel Streicker < ; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)
Subject: Paper Proof - please review. "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPA...

Dear all,

The attached typeset proof of our paper just arrived, and I have two days to reply.*Acceptable corrections are limited to author name or affiliation errors, misleading scientific inaccuracies, and printer's errors.* Change requests beyond these items will not be accepted.

Please quickly double check your name and affiliation, and if you find any errors please let me know by COB tomorrow. If I don't hear back, I'll assume it is correct.

Our article currently has a provisional scheduled publication date of Sep 03, 2020. Please note that our paper will**remain under a strict press embargo** until 2 PM Eastern Time (US) on the date of publication, so please don't circulate or tweet! :)

Thanks!
Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance

520 Eighth Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

On Aug 7, 2020, at 9:09 AM, Kevin Olival ecohealthalliance.org> wrote:

Just wanted to send a quick update on our paper…. I'm honestly surprised at how long PLOS Pathogens is taking, but I guess the editorial process slowed down w COVID.

We send in edits on pre-proofs a couple of times over the last few weeks, and have been waiting for over a week for the typeset proofs to come in. Once those come back and we have a publication date, I'll let you all know ASAP.

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

From: Kevin Olival ecohealthalliance.org>
Sent: Sunday, June 28, 2020 7:59:53 AM
To: David Hayman ; Jon Epstein ecohealthalliance.org>; dreeder ; Hume Field ecohealthalliance.org>; Charles H Calisher ; Brian R. Amman ; Wang Linfa duke-nus.edu.sg>; Ralph S. Baric >; Blehert, David S Cara Brook ; Kevin Castle ; Coleman, Jeremy T Peter Daszak ecohealthalliance.org>; wfrick >; Gilbert, Amy T - APHIS >; Ip, Hon S ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah >; Tigga Kingston >; Lorch, Jeffrey M ; Ian MENDENHALL PhD < ; alisonpeel >; Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; Reichard, Jonathan D >; Sleeman, Jonathan M ; Daniel Streicker >; Jonathan S. Towner ; Cryan, Paul >
Subject: [EXTERNAL] Fwd: Editorial Acceptance of "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPATHOG...

Paper Accepted!! Thank you all for your patience, perseverance, and invaluable contributions. I haven't received the proofs yet, but will turn them around quickly when I do.

Cheers,
Kevin

Kevin J. Olival, PhD

Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org
EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

Begin forwarded message:

From: "PLOS Pathogens"
Subject: Editorial Acceptance of "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPATHOGENS-D-20-01177R1) - [EMID:902178ed8cb23641]
Date: June 26, 2020 at 4:39:55 PM EDT
To: "Kevin J. Olival" ecohealthalliance.org>
Reply-To: "PLOS Pathogens"

CC: "Paul M. Cryan" , "Brian R. Amman" , "Ralph S. Baric" "David S. Blehert" "Cara E. Brook" "Charles H. Calisher" "Kevin T. Castle" "Jeremy T. H. Coleman" , "Peter Daszak" ecohealthalliance.org, "Jonathan H. Epstein" ecohealthalliance.org, "Hume Field" ecohealthalliance.org, "Winifred F. Frick" "Amy T. Gilbert" "David T.S. Hayman" "Hon S. Ip' , "William B. Karesh" ecohealthalliance.org, "Christine Kreuder Johnson" , "Rebekah C. Kading" "Tigga Kingston" "Jeffrey M. Lorch" , "Ian H. Mendenhall" "Alison J. Peel" alisonpeel , "Kendra L. Phelps" "Raina K. Plowright" , "DeeAnn M. Reeder" dreeder , "Jonathan D. Reichard" , "Jonathan M. Sleeman' "Daniel G. Streicker" "Jonathan S. Towner" , "Lin-Fa Wang"

Dear Dr. Olival,
We are pleased to inform you that your manuscript 'Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats

Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats' has been provisionally accepted for publication in PLOS Pathogens.
Before your manuscript can be formally accepted you will need to complete some formatting changes, which you will receive in a follow up email. A member of our team will be in touch with a set of requests.
Please note that your manuscript will not be scheduled for publication until you have made the required changes, so a swift response is appreciated.
IMPORTANT: The editorial review process is now complete. PLOS will only permit corrections to spelling, formatting or significant scientific errors from this point onwards. Requests for major changes, or any which affect the scientific understanding of your work, will cause delays to the publication date of your manuscript.
Should you, your institution's press office or the journal office choose to press release your paper, you will automatically be opted out of early publication. We ask that you notify us now if you or your institution is planning to press release the article. All press must be co-ordinated with PLOS.
Thank you again for supporting Open Access publishing; we are looking forward to publishing your work in PLOS Pathogens.
Best regards,

Seema Lakdawala, PhD
Reviews Editor

PLOS Pathogens

Aaron Mitchell
Section Editor
PLOS Pathogens

Kasturi Haldar
Editor-in-Chief
PLOS Pathogens
orcid.org/0000-0001-5065-158X

Michael Malim
Editor-in-Chief
PLOS Pathogens
orcid.org/0000-0002-7699-2064

****

Reviewer Comments (if any, and for reference):

From: Kevin Castle
Sent: Wednesday, August 12, 2020 8:55 PM EDT
To: Kevin Olival ecohealthalliance.org>
CC: Cara Brook ; Hon S Ip ; Paul Cryan >; David Hayman >; epstein ecohealthalliance.org>; dreeder ; Hume Field ecohealthalliance.org>; Charles H Calisher Brian R. Amman ; Wang Linfa ; Ralph S. Baric David S Blehert ; Jeremy Coleman ; Peter Daszak ecohealthalliance.org>; wfrick >; Amy Gilbert ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah >; Tigga Kingston >; Lorch, Jeffrey M ; Ian MENDENHALL PhD >; alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; Jonathan D Reichard Jonathan M Sleeman ; Daniel Streicker ; Jonathan S. Towner
Subject: Re: Paper Proof - please review. "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPA...

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> **Kevin J. Olival, PhD**
> *Vice President for Research*
>
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> New York, NY 10018
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Date: June 26, 2020 at 4:39:55 PM EDT
To: "Kevin J. Olival" ecohealthalliance.org>
Reply-To: "PLOS Pathogens"

CC: "Paul M. Cryan" , "Brian R. Amman" "Ralph S. Baric" "David S. Blehert" "Cara E. Brook" "Charles H. Calisher" Kevin T. Castle" "Jeremy T. H. Coleman' , "Peter Daszak" ecohealthalliance.org, "Jonathan H. Epstein" ecohealthalliance.org, "Hume Field" ecohealthalliance.org, "Winifred F. Frick" "Amy T. Gilbert" , "David T.S. Hayman" , "Hon S. Ip" "William B. Karesh" ecohealthalliance.org, "Christine Kreuder Johnson" , "Rebekah C. Kading" , "Tigga Kingston" "Jeffrey M. Lorch" , "Ian H. Mendenhall" , "Alison J. Peel" "Kendra L. Phelps" "Raina K. Plowright" , "DeeAnn M. Reeder" , "Jonathan D. Reichard" , "Jonathan M. Sleeman" "Daniel G. Streicker" "Jonathan S. Towner" , "Lin-Fa Wang"

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Best regards,

Seema Lakdawala, PhD
Reviews Editor
PLOS Pathogens

Aaron Mitchell

Section Editor
PLOS Pathogens

Kasturi Haldar
Editor-in-Chief
PLOS Pathogens
orcid.org/0000-0001-5065-158X

Michael Malim
Editor-in-Chief
PLOS Pathogens
orcid.org/0000-0002-7699-2064

****

Reviewer Comments (if any, and for reference):

--
Kevin T. Castle, DVM, MS
Wildlife Veterinary Consulting, LLC

From: DeeAnn Reeder
Sent: Wednesday, August 12, 2020 9:06 PM EDT
To: Kevin Castle
CC: Kevin Olival ecohealthalliance.org>; Cara Brook ; Hon S Ip < >; Paul Cryan ; David Hayman >; epstein ecohealthalliance.org>; Hume Field ecohealthalliance.org>; Charles H Calisher ; Brian R. Amman ; Wang Linfa ; Ralph S. Baric ; David S Blehert ; Jeremy Coleman ; Peter Daszak ecohealthalliance.org>; wfrick ; Amy Gilbert ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson >; Kading,Rebekah >; Tigga Kingston ; Lorch, Jeffrey M Ian MENDENHALL PhD alisonpeel Kendra Phelps ecohealthalliance.org>; Plowright, Raina < ; Jonathan D Reichard >; Jonathan M Sleeman ; Daniel Streicker >; Jonathan S. Towner >
Subject: Re: Paper Proof - please review. "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" (PPA...

Me too! - DeeAnn

On Wed, Aug 12, 2020 at 8:56 PM Kevin Castle > wrote:

> Thanks Kevin. My info is correct.
>
> Kevin
>
> On Wed, Aug 12, 2020 at 5:55 PM Kevin Olival ecohealthalliance.org> wrote:
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> > Dear all,
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> > Thanks!
> > Kevin
> >
> > **Kevin J. Olival, PhD**
> > *Vice President for Research*
> >
> > EcoHealth Alliance
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From: Kevin Olival ecohealthalliance.org>
Sent: Sunday, June 28, 2020 7:59:53 AM
To: David Hayman Jon Epstein ecohealthalliance.org>; dreeder < ; Hume Field ecohealthalliance.org>; Charles H Calisher >; Brian R. Amman >; Wang Linfa >; Ralph S. Baric >; Blehert, David S < >; Cara Brook >; Kevin Castle ; Coleman, Jeremy T ; Peter Daszak ecohealthalliance.org>; wfrick >; Gilbert, Amy T - APHIS ; Ip, Hon S >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson >; Kading,Rebekah >; Tigga Kingston >; Lorch, Jeffrey M >; Ian MENDENHALL PhD >; alisonpeel >; Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; Reichard, Jonathan D ; Sleeman, Jonathan M ; Daniel Streicker Jonathan S. Towner >; Cryan, Paul >
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Date: June 26, 2020 at 4:39:55 PM EDT
To: "Kevin J. Olival" ecohealthalliance.org>
Reply-To: "PLOS Pathogens"

CC: "Paul M. Cryan" "Brian R. Amman" , "Ralph S. Baric" "David S. Blehert" "Cara E. Brook" , "Charles H. Calisher" , "Kevin T. Castle" , "Jeremy T. H. Coleman" , "Peter Daszak" ecohealthalliance.org, "Jonathan H. Epstein" ecohealthalliance.org, "Hume Field" ecohealthalliance.org, "Winifred F. Frick" "Amy T. Gilbert" v, "David T.S. Hayman" , "Hon S. Ip" "William B. Karesh" ecohealthalliance.org, "Christine Kreuder Johnson" , "Rebekah C. Kading" , "Tigga Kingston" "Jeffrey M. Lorch" , "Ian H. Mendenhall" , "Alison J. Peel" "Kendra L. Phelps" "Raina K. Plowright" , "DeeAnn M. Reeder" , "Jonathan D. Reichard" "Jonathan M. Sleeman" , "Daniel G. Streicker" "Jonathan S. Towner" "Lin-Fa Wang"

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Reviewer Comments (if any, and for reference):

--
Kevin T. Castle, DVM, MS
Wildlife Veterinary Consulting, LLC

--
DeeAnn M. Reeder, PhD
Professor
Department of Biology
Bucknell University
Lewisburg, PA 17837

http://deeannreeder.scholar.bucknell.edu

From: Ian Mendenhall
Sent: Wednesday, August 12, 2020 9:37 PM EDT
To: Kevin Olival ecohealthalliance.org>; Cara Brook ; Hon S Ip ; Paul Cryan >; David Hayman epstein ecohealthalliance.org>; dreeder >; Hume Field ecohealthalliance.org>; Charles H Calisher ; Brian R. Amman Wang Linfa ; Ralph S. Baric ; David S Blehert ; Kevin Castle >; Jeremy Coleman ; Peter Daszak ecohealthalliance.org>; wfrick ; Amy Gilbert >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson >; Kading,Rebekah Tigga Kingston ; Lorch, Jeffrey M ; alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; Jonathan D Reichard Jonathan M Sleeman ; Daniel Streicker Jonathan S. Towner
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Mine is also correct. Thanks much.

Ian H MENDENHALL, Ph.D. | Principal Research Scientist | **Laboratory of Virus Evolution** | Emerging Infectious Disease | Duke-NUS Medical School | 8 College Road, Singapore 169857 | Email:

From: Kevin Olival ecohealthalliance.org>
Date: Thursday, 13 August 2020 at 7:56 AM
To: Cara Brook , Hon S Ip Paul Cryan , David Hayman , Jon Epstein ecohealthalliance.org>, "dreede Hume Field ecohealthalliance.org>, Charles H Calisher "Brian R. Amman" >, Wang Linfa , "Ralph S. Baric" , David S Blehert , Kevin Castle >, Jeremy Coleman >, Peter Daszak ecohealthalliance.org>, "wfrick Amy Gilbert >, William Karesh ecohealthalliance.org>, Christine Kreuder Johnson , "Kading,Rebekah" , Tigga Kingston >, "Lorch, Jeffrey M" , Ian Mendenhall "alisonpeel " , Kendra Phelps ecohealthalliance.org>, "Plowright, Raina" >, Jonathan D Reichard >, Jonathan M Sleeman >, Daniel Streicker , "Jonathan S. Towner"
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orcid.org/0000-0001-5065-158X

Michael Malim
Editor-in-Chief
PLOS Pathogens
orcid.org/0000-0002-7699-2064

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Reviewer Comments (if any, and for reference):

From: calisher
Sent: Wednesday, August 12, 2020 10:22 PM EDT
To: Kevin Olival ecohealthalliance.org>; Cara Brook ; Hon S Ip ; Paul Cryan ; David Hayman ; epstein ecohealthalliance.org>; dreeder ; Hume Field ecohealthalliance.org>; Brian R. Amman ; Wang Linfa ; Ralph S. Baric < ; David S Blehert ; Kevin Castle >; Jeremy Coleman ; Peter Daszak ecohealthalliance.org>; wfrick >; Amy Gilbert ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson Kading,Rebekah >; Tigga Kingston ; Lorch, Jeffrey M ; Ian MENDENHALL PhD alisonpeel >; Kendra Phelps ecohealthalliance.org>; Plowright, Raina >; Jonathan D Reichard Jonathan M Sleeman >; Daniel Streicker >; Jonathan S. Towner
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Okay by me. Thanks for all your hard work.

Charlie

From: Kevin Olival ecohealthalliance.org>
Sent: Wednesday, August 12, 2020 5:55 PM
To: Cara Brook >; Hon S Ip >; Paul Cryan ; David Hayman ; Jon Epstein ecohealthalliance.org>; dreeder Hume Field ecohealthalliance.org>; Charles H Calisher Brian R. Amman ; Wang Linfa ; Ralph S. Baric ; David S Blehert >; Kevin Castle ; Jeremy Coleman ; Peter Daszak ecohealthalliance.org>; wfrick Amy Gilbert William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah Tigga Kingston ; Lorch, Jeffrey M >; Ian MENDENHALL PhD alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina >; Jonathan D Reichard ; Jonathan M Sleeman ; Daniel Streicker ; Jonathan S. Towner >
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Thanks!
Kevin

From: Dr. Melinda Rostal ecohealthalliance.org>
Sent: Tuesday, August 18, 2020 10:29 AM EDT
To: Dr. Kevin Olival ecohealthalliance.org>
CC: Kading,Rebekah ; Tigga Kingston < ; Rodrigo Medellin >; Billy Karesh ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Isabella Mandl <
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure
Attachment(s): "Infographic and acknowledgement.docx"

Dear Tigga and Rodrigo,
Attached is the figure with the acknowledgment. The WHSG would prefer not to include logos on the figure if possible as it is positioned in the middle of our text. However, I want to ensure you are satisfied with it. So if you have any concerns about the acknowledgement, please let me know by Thursday Aug 20.

Thanks very much!

And thanks again to you and Rebekah for letting us modify your great figure:)

Best,

Mindy

Melinda Rostal DVM, MPH, PhD
Principal Scientist, Vector-Borne Diseases

Rift Valley Fever Virus Project Manager

EcoHealth Alliance
520 Eighth Ave, Ste. 1200
New York, NY 10018

www.ecohealthalliance.org

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EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

On Aug 12, 2020, at 2:49 PM, Kevin Olival ecohealthalliance.org> wrote:

Looks wonderful, and thanks all for adapting this for a wider distribution.

Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

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On Aug 11, 2020, at 9:47 AM, Kading,Rebekah wrote:

Hi Mindy, Billy, Kevin, and Kendra -

I hope your week has gotten off to a good start!

I'm attaching a draft infographic for your review. I've modified the current BSG MAP infographic per your suggestions for a wildlife version. I can also add a logo, QR, and/or website at the bottom if you'd like. Not sure of exactly the best way to portray environmental samples...I was assuming this will comprise activities like passive fecal sample collections...so please let me know if this captures what you had in mind or if there is something else you're envisioning and I can revise accordingly! (BioRender does have an amusing variety of poo icons, but I was trying to keep it classy and professional.) ��

Take care, and I'll look forward to your feedback.

Best,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Dr. Melinda Rostal ecohealthalliance.org>
Sent: Friday, August 7, 2020 2:16 PM
To: Kading,Rebekah
Cc: Kingston, Tigga Rodrigo Medellin ; Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Isabella Mandl
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

That's great Rebekah!

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<IUCN infographic wildlife version.png>

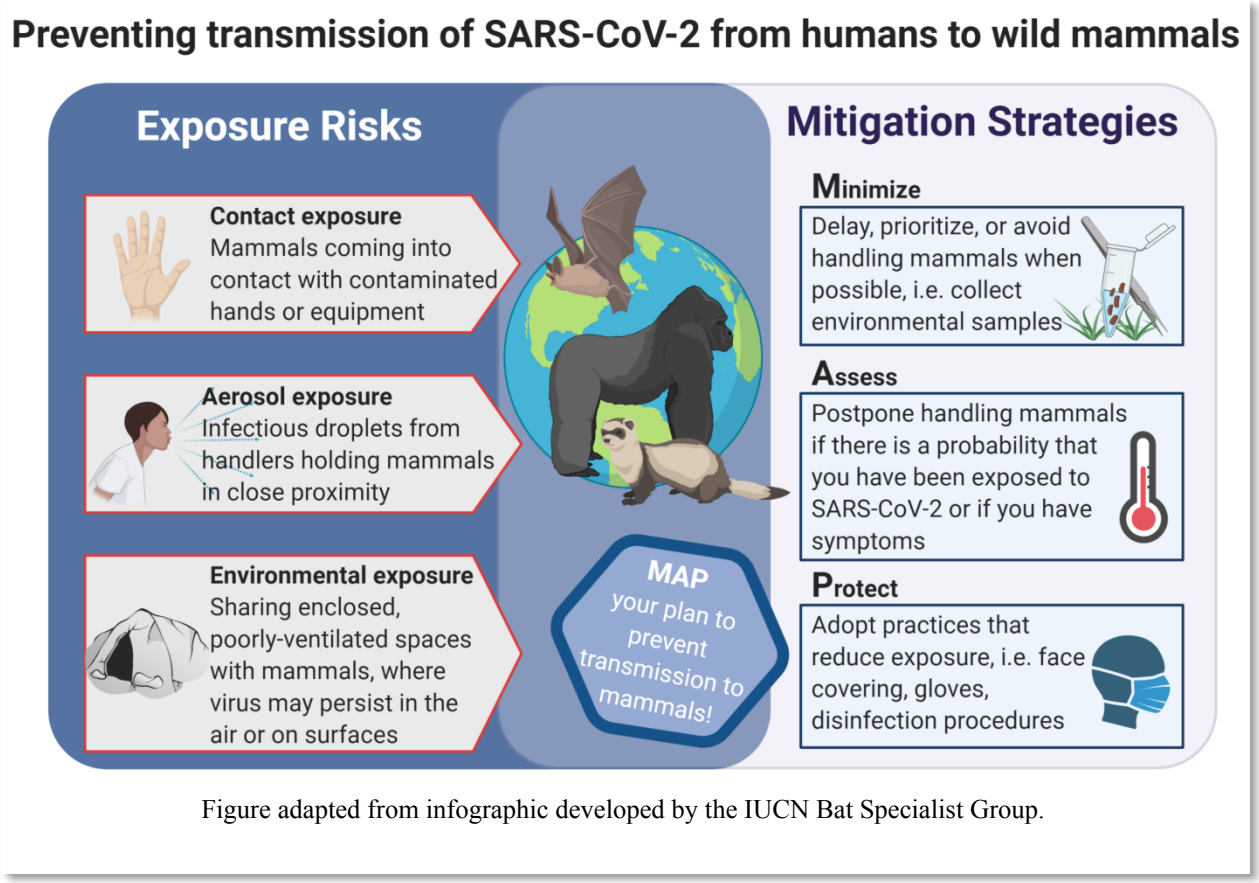

Figure adapted from infographic developed by the IUCN Bat Specialist Group.

From: Dr. Melinda Rostal ecohealthalliance.org>
Sent: Tuesday, August 11, 2020 11:54 PM EDT
To: Kading,Rebekah >
CC: Kingston, Tigga >; Rodrigo Medellin >; Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Isabella Mandl
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Dear Rebekah,

This looks awesome!! I shared it this evening with our small team that is preparing the guidelines for the rest of the specialist group to review and they like it very much (that's a great ferret:)! We are going to share the guidelines tomorrow with a larger team in the specialist group for the final review so this is perfect timing.

I will also find out about branding from the WHSG and will get back to you on that. I also want to make sure we also give credit your specialist group. Tigga and Rodrigo, as I mentioned we will include a statement that this is modified from the BSG's figure. Please advise on any other branding requirements.

Thanks very much!!

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<IUCN infographic wildlife version.png>

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Sent: Wednesday, August 12, 2020 2:49 PM EDT
To: Kading,Rebekah
CC: Mindy Rostal ecohealthalliance.org>; Tigga Kingston Medellin >; William Karesh ecohealthalliance.org>; Kendra Phelps ; Isabella Mandl >
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Looks wonderful, and thanks all for adapting this for a wider distribution.

Kevin

Kevin J. Olival, PhD
Vice President for Research

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Hi Rebekah and all.

Thanks again for the graphic.

OIE is distributing our joint WHSG/OIE guidelines and also translating it to French and Spanish as they normally do. They would like to change the language in the graphic also but need either the editable file or at least the background images on which they can overlay the French and Spanish. Are either of those something you could provide?

Thanks,

Billy

William B. Karesh, D.V.M
Executive Vice President for Health and Policy

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www.ecohealthalliance.org

President, OIE Working Group on Wildlife

Co-chair, IUCN Species Survival Commission - Wildlife Health Specialist Group

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EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

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Hi everyone -

So sorry for the delay! I'm attaching the Infographic -- a pdf version with clickable links and a png version which may be easier for social media postings. Just let me know if you have any final suggestions. We are very happy to collaborate with you on aligning the messaging coming from our working groups on this issue - thank you again very much for reaching out about this!

Kind regards,
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Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

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Sent: Tuesday, August 18, 2020 8:29 AM
To: Dr. Kevin Olival ecohealthalliance.org>
Cc: Kading,Rebekah >; Tigga Kingston >; Rodrigo Medellin ; Billy Karesh ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Isabella Mandl
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Dear Tigga and Rodrigo,
Attached is the figure with the acknowledgment. The WHSG would prefer not to include logos on the figure if possible as it is positioned in the middle of our text. However, I want to ensure you are satisfied with it. So if you have any concerns about the acknowledgement, please let me know by Thursday Aug 20.

Thanks very much!

And thanks again to you and Rebekah for letting us modify your great figure:)

Best,

Mindy

Melinda Rostal DVM, MPH, PhD
Principal Scientist, Vector-Borne Diseases

Rift Valley Fever Virus Project Manager

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New York, NY 10018

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Vice President for Research

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On Aug 11, 2020, at 9:47 AM, Kading,Rebekah < wrote:

Hi Mindy, Billy, Kevin, and Kendra -

I hope your week has gotten off to a good start!

I'm attaching a draft infographic for your review. I've modified the current BSG MAP infographic per your suggestions for a wildlife version. I can also add a logo, QR, and/or website at the bottom if you'd like. Not sure of exactly the best way to portray environmental samples...I was assuming this will comprise activities like passive fecal sample collections...so please let me know if this captures what you had in mind or if there is something else you're envisioning and I can revise accordingly! (BioRender does have an amusing variety of poo icons, but I was trying to keep it classy and professional.) ��

Take care, and I'll look forward to your feedback.

Best,
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human-to-bat transmission of SARS-CoV-2 Figure

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<IUCN infographic wildlife version.png>

<IUCN infographic wildlife version_cc.pdf><IUCN infographic wildlife version_cc.png>

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To: Kingston, Tigga
CC: Rodrigo Medellin >; Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Kading,Rebekah ; Isabella Mandl
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CC: Dr. Melinda Rostal ecohealthalliance.org>; Kevin Olival ecohealthalliance.org>; Tigga.Kingston ; Rodrigo Medellin ; Kendra Phelps ecohealthalliance.org ; Isabella Mandl

Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Thanks Rebekah and all. We will share final version and posting links soon.

All the Best,

Billy

William B. Karesh, D.V.M
Executive Vice President for Health and Policy

EcoHealth Alliance
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New York, NY 10018 USA

www.ecohealthalliance.org

President, OIE Working Group on Wildlife

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Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org
EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

On Aug 11, 2020, at 9:47 AM, Kading,Rebekah > wrote:

Hi Mindy, Billy, Kevin, and Kendra -

I hope your week has gotten off to a good start!

I'm attaching a draft infographic for your review. I've modified the current BSG MAP infographic per your suggestions for a wildlife version. I can also add a logo, QR, and/or website at the bottom if you'd like. Not sure of exactly the best way to portray environmental samples...I was assuming this will comprise activities like passive fecal sample collections...so please let me know if this captures what you had in mind or if there is something else you're envisioning and I can revise accordingly! (BioRender does have an amusing variety of poo icons, but I was trying to keep it classy and professional.) ��

Take care, and I'll look forward to your feedback.

Best,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

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Sent: Friday, August 7, 2020 2:16 PM
To: Kading,Rebekah >
Cc: Kingston, Tigga >; Rodrigo Medellin >; Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Isabella Mandl
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

That's great Rebekah!

Thanks! I'm happy to chat more with you about it, if that's helpful:)

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To: Kading,Rebekah
CC: Dr. Kevin Olival ecohealthalliance.org>; Tigga Kingston ; Rodrigo Medellin < >;
Billy Karesh ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Isabella Mandl
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Perfect Rebekah!

This is awesome:).

Thanks everyone for sharing your great work! I double check our final pdf and your links were working for me so I think it's all good. The WHSG guidelines should be posted online shortly:)

It has been great working with you!

Mindy

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On Aug 20, 2020, at 10:43 AM, Kading,Rebekah wrote:

Hi everyone -

So sorry for the delay! I'm attaching the Infographic -- a pdf version with clickable links and a png version which may be easier for social media postings. Just let me know if you have any final suggestions. We are very happy to collaborate with you on aligning the messaging coming from our working groups on this issue - thank you again very much for reaching out about this!

Kind regards,
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Cc: Kading,Rebekah ; Tigga Kingston >; Rodrigo Medellin
>; Billy Karesh ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Isabella Mandl
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Dear Tigga and Rodrigo,
Attached is the figure with the acknowledgment. The WHSG would prefer not to include logos on the figure if possible as it is positioned in the middle of our text. However, I want to ensure you are satisfied with it. So if you have any concerns about the acknowledgement, please let me know by Thursday Aug 20.

Thanks very much!

And thanks again to you and Rebekah for letting us modify your great figure:)

Best,

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On Aug 12, 2020, at 2:49 PM, Kevin Olival ecohealthalliance.org> wrote:

Looks wonderful, and thanks all for adapting this for a wider distribution.

Kevin

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Kind regards,

Mindy

<PastedGraphic-3.png>

Melinda Rostal DVM, MPH, PhD
Principal Scientist, Vector-Borne Diseases

Rift Valley Fever Virus Project Manager

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520 Eighth Ave, Ste. 1200
New York, NY 10018

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EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

From: Rodrigo Medellin >
Sent: Tuesday, August 04, 2020 5:14 PM EDT
To: Kingston, Tigga
CC: Melinda Rostal ecohealthalliance.org>; Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Kading,Rebekah ; Isabella Mandl >
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Hi everyone

Thank you Tigga for copying me with the good email address. Mindy good talking to you again. I fully concur with Tigga about being mindful of the brains behind the infographic, and of course about any changes. If at all possible Mindy we would rather have it presented with due credits verbatim. Multiple version will be confusing, regardless of whether the different versions clash with each other. Stay safe.

--

Dr. Rodrigo A. Medellin
Instituto de Ecología, UNAM
Ap. Postal 70-275
04510 Ciudad Universitaria, D. F.
MEXICO

DIRECCION FISICA (STREET ADDRESS):

Dr. Rodrigo A. Medellín
Instituto de Ecologia, UNAM
Circuito Exterior s/n junto al Jardín Botánico Exterior
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https://www.facebook.com/rodrigo.a.medellin
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https://twitter.com/rodrigomedellin

Check out our YouTube channel with dozens of cool, short videos on bats:https://www.youtube.com/user/RMedellinbats
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On Tue, Aug 4, 2020 at 9:22 AM Kingston, Tigga > wrote:

> Dear Mindy
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> The infographic was constructed in BioRender by Dr Rebekah Kading, so they would probably need to be manipulated in that environment. I've copied Rebekah and Dr Bella Mandl – who is also leading our graphics – on this email.
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> Do you have a clearer idea of how you would use the infographic?
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From: Melinda Rostal ecohealthalliance.org>
Sent: Monday, August 3, 2020 8:41 PM
To: Kingston, Tigga >; Rodrigo A. Medellín
Cc: Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>
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I hope to hear from you soon about whether the Wildlife Health Specialist Group can use or modify your infographic (with the appropriate credit).

Best,

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Sent from my iPhone

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From: Kingston, Tigga >
Sent: Friday, August 07, 2020 12:04 PM EDT
To: Dr. Melinda Rostal ecohealthalliance.org>; Rodrigo Medellin
CC: Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Kading,Rebekah ; Isabella Mandl

Subject: RE: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Dear Melinda
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Tigga

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Sent: Friday, August 7, 2020 10:39 AM
To: Rodrigo Medellin >
Cc: Kingston, Tigga ; Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Kading,Rebekah ; Isabella Mandl
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Principal Scientist, Vector-Borne Diseases

Rift Valley Fever Virus Project Manager

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From: Dr. Melinda Rostal ecohealthalliance.org>
Sent: Tuesday, August 04, 2020 5:20 PM EDT
To: Rodrigo Medellin >
CC: Kingston, Tigga ; Billy Karesh @ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Kading,Rebekah ; Isabella Mandl
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Thank you Rodrigo and Tigga for your thoughtful responses.

I am going to take your response back to our group. We will see if we can make it work without changes and if not come back to you with as few changes as we think would be necessary (e.g. changing “bats” to “mammals”, etc.) and see if you think the changes are minimal enough that it still provides the same strong message. We do like your message and that was part of the reason why we wanted to use the figure:)

Kind regards,

Mindy

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Principal Scientist, Vector-Borne Diseases

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To: Kingston, Tigga ; Rodrigo A. Medellín >
Cc: Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>

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> <PastedGraphic-3.png>
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Rift Valley Fever Virus Project Manager

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460 West 34th Street – 17th floor
New York, NY 10001

From: William B. Karesh ecohealthalliance.org>
Sent: Tuesday, August 25, 2020 12:46 PM EDT
To: Kading,Rebekah
CC: Dr. Melinda Rostal ecohealthalliance.org>; Kevin Olival ecohealthalliance.org>; Tigga.Kingston >; Rodrigo Medellin >; Kendra Phelps ecohealthalliance.org ; Isabella Mandl

Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Thanks !! I'll keep you posted.

BK

William B. Karesh, D.V.M
Executive Vice President for Health and Policy

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018 USA

www.ecohealthalliance.org

President, OIE Working Group on Wildlife

Co-chair, IUCN Species Survival Commission - Wildlife Health Specialist Group

EPT Partners Liaison, USAID Emerging Pandemic Threats - PREDICT-2 Program

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On Aug 25, 2020, at 12:35 PM, Kading,Rebekah wrote:

Hi Billy,

The pdf version should be editable, so they should be able to work directly on that and then re-save as an image file. As an alternative, if anyone in your working group or OIE has a BioRender license, I can share the infographic file directly with that person through BioRender to edit. Third option - I'm attaching a translation sheet that could be used as a template. It still has the bat infographic language on it, but if this is updated with the French and Spanish translations for the wildlife infographic, feel free to send those translations back to me and I'd be happy to update the infographic.

Hope that helps, and just let me know how you'd like to proceed.

Best regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: William B. Karesh ecohealthalliance.org>
Sent: Tuesday, August 25, 2020 9:22 AM
To: Kading,Rebekah >
Cc: Dr. Melinda Rosta ecohealthalliance.org>; Kevin Olival ecohealthalliance.org>; Tigga.Kingstor ; Rodrigo Medellin >; Kendra Phelps cohealthalliance.org Isabella Mandl

Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Hi Rebekah and all.

Thanks again for the graphic.

OIE is distributing our joint WHSG/OIE guidelines and also translating it to French and Spanish as they normally do. They would like to change the language in the graphic also but need either the editable file or at least the background images on which they can overlay the French and Spanish. Are either of those something you could provide?

Thanks,

Billy

William B. Karesh, D.V.M
Executive Vice President for Health and Policy

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On Aug 20, 2020, at 10:43 AM, Kading,Rebekah < wrote:

Hi everyone -

So sorry for the delay! I'm attaching the Infographic -- a pdf version with clickable links and a png version which may be easier for social media postings. Just let me know if you have any final suggestions. We are very happy to collaborate with you on aligning the messaging coming from our working groups on this issue - thank you again very much for reaching out about this!

Kind regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Dr. Melinda Rostal ecohealthalliance.org>
Sent: Tuesday, August 18, 2020 8:29 AM
To: Dr. Kevin Olival ecohealthalliance.org>
Cc: Kading,Rebekah >; Tigga Kingston ; Rodrigo Medellin ; Billy Karesh ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Isabella Mandl
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Dear Tigga and Rodrigo,
Attached is the figure with the acknowledgment. The WHSG would prefer not to include logos on the figure if possible as it is positioned in the middle of our text. However, I want to ensure you are satisfied with it. So if you have any concerns about the acknowledgement, please let me know by Thursday Aug 20.

Thanks very much!

And thanks again to you and Rebekah for letting us modify your great figure:)

Best,

Mindy

Melinda Rostal DVM, MPH, PhD
Principal Scientist, Vector-Borne Diseases

Rift Valley Fever Virus Project Manager

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> On Aug 12, 2020, at 2:49 PM, Kevin Olival ecohealthalliance.org> wrote:
>
> Looks wonderful, and thanks all for adapting this for a wider distribution.
>
> Kevin
>
> **Kevin J. Olival, PhD**
> *Vice President for Research*
>
> EcoHealth Alliance
> 520 Eighth Avenue, Suite 1201
> New York, NY 10018
>
> www.ecohealthalliance.org
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>
> > On Aug 11, 2020, at 9:47 AM, Kading,Rebekah wrote:
> >
> > Hi Mindy, Billy, Kevin, and Kendra -
> >
> > I hope your week has gotten off to a good start!
> >
> > I'm attaching a draft infographic for your review. I've modified the current BSG MAP infographic per your suggestions for a wildlife version. I can also add a logo, QR, and/or website at the bottom if you'd like. Not sure of exactly the best way to portray environmental samples...I was assuming this will comprise activities like passive fecal sample collections...so please let me know if this captures what you had in mind or if there is something else you're envisioning and I can revise accordingly! (BioRender does have an amusing variety of poo icons, but I was trying to keep it classy and professional.) ��
> >
> > Take care, and I'll look forward to your feedback.
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> > Best,
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> > **Rebekah C. Kading, PhD**
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> > Department of Microbiology Immunology and Pathology
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From: Dr. Melinda Rostal ecohealthalliance.org>
Sent: Friday, August 7, 2020 2:16 PM
To: Kading,Rebekah
Cc: Kingston, Tigga >; Rodrigo Medellin Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Isabella Mandl
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

That's great Rebekah!

Thanks! I'm happy to chat more with you about it, if that's helpful:)

~ Mindy

Melinda Rostal DVM, MPH, PhD
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On Aug 7, 2020, at 3:22 PM, Kading,Rebekah < wrote:

Hi everyone,

Just chiming in to say thank you for the discussion and interest in the Infographic! I'm so glad it has been a good communication tool - the suggested modifications would be very easy to make.

Kind regards,
Rebekah

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> **Critically, we would need to review and sanction any changes because we don't want any messages to conflict with our own.** It would be confusing to have essentially the same graphic circulating saying different things. Our messaging is organized around the MAP concept so we don't want that disrupted, for example.
>
> Do you have a clearer idea of how you would use the infographic?
>
> Caveats aside, happy to work with you of course!!
>
> Best wishes
> Tigga
>
> P.S. I copied Rodrigo with his current email.
>
> ---
>
> **From:** Melinda Rostal ecohealthalliance.org>
> **Sent:** Monday, August 3, 2020 8:41 PM
> **To:** Kingston, Tigga ; Rodrigo A. Medellín
> **Cc:** Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>
> **Subject:** Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure
>
> Dear Tigga,
> I just wanted to let you know that I've sent this to 2 email addresses for Rodrigo and it seems they have bounced back. I am not sure if he has seen my request.
>
> I hope to hear from you soon about whether the Wildlife Health Specialist Group can use or modify your infographic (with the appropriate credit).
>
> Best,
> Mindy
>
> Sent from my iPhone
>
> On Jul 29, 2020, at 3:11 PM, Dr. Melinda Rostal ecohealthalliance.org> wrote:

Dear Rodrigo and Tigga,

Rodrigo, it's been several years since we have spoken and I hope you are well.
I hope you are both managing to stay safe during the pandemic.

I have been working with Billy Karesh, some folks from the Wildlife Health Specialist Group and the OIE to come up with some recommendations for working with free-living, wild mammals during the pandemic. We thought that the documents that the Bat Specialist Group wrote were great and we certainly refer anyone working with bats to review your guidelines as well.

We really liked the figure you used (pasted below) and were wondering if we could reproduce it and/or modify it slightly in our document. We would certainly credit your group with creating it.

If it is ok to modify it, would it be possible to get a powerpoint slide or photoshop document to allow for easy modification?

I look forward to hearing from you and we would be happy to promote your work.

Kind regards,

Mindy

<PastedGraphic-3.png>

Melinda Rostal DVM, MPH, PhD
Principal Scientist, Vector-Borne Diseases

Rift Valley Fever Virus Project Manager

EcoHealth Alliance
520 Eighth Ave, Ste. 1200
New York, NY 10018

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.
EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

<IUCN infographic wildlife version.png>

<IUCN infographic wildlife version_cc.pdf><IUCN infographic wildlife version_cc.png>

<IUCN BSG MAP TRANSLATION SHEET.docx><IUCN infographic wildlife version_cc.pdf>

From: Kendra Phelps ecohealthalliance.org>
Sent: Tuesday, August 11, 2020 4:49 PM EDT
To: Kading,Rebekah
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Hi Rebekah,

Wow, that is amazing! The environmental sampling icons are perfect!

I was checking into BioRender today to make a schematic for a publication, do you use the free version?

Cheers,
Kendra

P.S. Fingers and toes crossed for Anna's interview with EHA this Friday:)

Kendra Phelps, PhD
Research Scientist

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200
New York, NY 10018

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

> On Aug 11, 2020, at 3:47 PM, Kading,Rebekah > wrote:
>
> Hi Mindy, Billy, Kevin, and Kendra -
>
> I hope your week has gotten off to a good start!
>
> I'm attaching a draft infographic for your review. I've modified the current BSG MAP infographic per your suggestions for a wildlife version. I can also add a logo, QR, and/or website at the bottom if you'd like. Not sure of exactly the best way to portray environmental samples...I was assuming this will comprise activities like passive fecal sample collections...so please let me know if this captures what you had in mind or if there is something else you're envisioning and I can revise accordingly! (BioRender does have an amusing variety of poo icons, but I was trying to keep it classy and professional.) ��
>
> Take care, and I'll look forward to your feedback.
>
> Best,
> Rebekah
>
> **Rebekah C. Kading, PhD**
> Assistant Professor
> Department of Microbiology Immunology and Pathology
> Colorado State University

From: Dr. Melinda Rostal ecohealthalliance.org>
Sent: Friday, August 7, 2020 2:16 PM
To: Kading,Rebekah
Cc: Kingston, Tigga ; Rodrigo Medellin ; Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Isabella Mandl >
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

That's great Rebekah!

Thanks! I'm happy to chat more with you about it, if that's helpful:)

~ Mindy

Melinda Rostal DVM, MPH, PhD
Principal Scientist, Vector-Borne Diseases

Rift Valley Fever Virus Project Manager

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New York, NY 10001

On Aug 7, 2020, at 3:22 PM, Kading,Rebekah < > wrote:

Hi everyone,

Just chiming in to say thank you for the discussion and interest in the Infographic! I'm so glad it has been a good communication tool - the suggested modifications would be very easy to make.

Kind regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kingston, Tigga >
Sent: Friday, August 7, 2020 10:04 AM
To: Dr. Melinda Rostal ecohealthalliance.org>; Rodrigo Medellin
Cc: Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Kading,Rebekah < >; Isabella Mandl

Subject: RE: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Dear Melinda
That sounds appropriate to me. Our group meets early on Tuesday morning, so I'd like to run this by them then for final agreement, if that's OK, but I don't imagine any objections.

Best
Tigga

From: Dr. Melinda Rostal ecohealthalliance.org>
Sent: Friday, August 7, 2020 10:39 AM
To: Rodrigo Medellin
Cc: Kingston, Tigga Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Kading,Rebekah >; Isabella Mandl < >
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Dear Rodrigo and Tigga,

I spoke to my colleagues and we would propose to change "bats" to either "mammals" or "wild mammals", change the graphic in the center to include a smaller version of the bat that is there as well as an ape and a mustelid, change the example in the Minimize box from "i.e. implement acoustic surveys" to "i.e. collect environmental samples", and change the figure of the bat calling to a figure of collecting an environmental sample.

The risks and mitigation strategies are really nicely laid out as you originally made it so we wouldn't need to change that or the rest of the text/figures. We support your MAP plan.

Do you think that would be acceptable? We think it remains very consistent with your message.

If yes, what is the best way to proceed with the modification?

Kind regards,

Mindy

Melinda Rostal DVM, MPH, PhD
Principal Scientist, Vector-Borne Diseases

Rift Valley Fever Virus Project Manager

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On Aug 4, 2020, at 5:14 PM, Rodrigo Medellin wrote:

Hi everyone

Thank you Tigga for copying me with the good email address. Mindy good talking to you again. I fully concur with Tigga about being mindful of the brains behind the infographic, and of course about any changes. If at all possible Mindy we would rather have it presented with due credits verbatim. Multiple version will be confusing, regardless of whether the different versions clash with each other. Stay safe.

--

Dr. Rodrigo A. Medellin
Instituto de Ecología, UNAM
Ap. Postal 70-275
04510 Ciudad Universitaria, D. F.
MEXICO

DIRECCION FISICA (STREET ADDRESS):

Dr. Rodrigo A. Medellín
Instituto de Ecologia, UNAM
Circuito Exterior s/n junto al Jardín Botánico Exterior
04510 Ciudad Universitaria, D. F.
MEXICO

https://www.facebook.com/rodrigo.a.medellin
https://www.instagram.com/rodrigomedellin1223/
https://twitter.com/rodrigomedellin

Check out our YouTube channel with dozens of cool, short videos on bats:https://www.youtube.com/user/RMedellinbats
http://web.ecologia.unam.mx/medellin/

On Tue, Aug 4, 2020 at 9:22 AM Kingston, Tigga wrote:

> Dear Mindy
>
> The infographic was constructed in BioRender by Dr Rebekah Kading, so they would probably need to be manipulated in that environment. I've copied Rebekah and Dr Bella Mandl – who is also leading our graphics – on this email.
>
> They have also worked up infographics for rehabbers and cavers and the original is now in a number of languages. Rebekah is a whizz at adapting the base design, but we of course need to be mindful of her time.
>
> **Critically, we would need to review and sanction any changes because we don't want any messages to conflict with our own.** It would be confusing to have essentially the same graphic circulating saying different things. Our messaging is organized around the MAP concept so we don't want that disrupted, for example.
>
> Do you have a clearer idea of how you would use the infographic?

Caveats aside, happy to work with you of course!!

Best wishes
Tigga

P.S. I copied Rodrigo with his current email.

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Sent: Monday, August 3, 2020 8:41 PM
To: Kingston, Tigga ; Rodrigo A. Medellín

Cc: Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

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I hope to hear from you soon about whether the Wildlife Health Specialist Group can use or modify your infographic (with the appropriate credit).

Best,
Mindy

Sent from my iPhone

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>
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> I hope you are both managing to stay safe during the pandemic.
>
> I have been working with Billy Karesh, some folks from the Wildlife Health Specialist Group and the OIE to come up with some recommendations for working with free-living, wild mammals during the pandemic. We thought that the documents that the Bat Specialist Group wrote were great and we certainly refer anyone working with bats to review your guidelines as well.
>
> We really liked the figure you used (pasted below) and were wondering if we could reproduce it and/or modify it slightly in our document. We would certainly credit your group with creating it.
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>
> I look forward to hearing from you and we would be happy to promote your work.
>
> Kind regards,
>
> Mindy
>
> <PastedGraphic-3.png>
> **Melinda Rostal DVM, MPH, PhD**
> *Principal Scientist, Vector-Borne Diseases*
>
> *Rift Valley Fever Virus Project Manager*
>
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)
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New York, NY 10001

<IUCN infographic wildlife version.png>

From: Tamar Kutateladze
Sent: Wednesday, February 14, 2018 3:02 AM EST
To: Katie Leahy ; lance.r.brooks ; Newman, Carl I CIV DTRA J3-7 (US) Lancaster, Mary J CIV (US) ; christopher.r.lewis >; Kading,Rebekah ; DeeAnn Reeder ; Cryan, Paul ; Vivek Kapur ; Gavin James Smith >; abelwade >; Ian Mendenhall ; Keti Sidamonidze ; Lela Urushadze ; c_demetria ; Jon Epstein ecohealthalliance.org>; cryan.paul ; Kingston, Tigga >
CC: Stokes, Martha M CIV (US) >; Simmi Ghai ; S Wacharapluesadee
Subject: Re: RE: Afternoon Session

Dear Katie,

We kindly ask you to send the final slides also to us.

Yours sincerely,

Tamar

Tamar Kutateladze,

MD, PhD.Department of Virology, MolecularBiology and Genome Research,

R. Lugar Center for Public Health Research
National Center for Disease Control & Public Health

Phone:

On Tuesday, February 13, 2018, 6:59:07 PM GMT+4, Kingston, Tigga < wrote:

Katie

Could you share (or share again) the final slides we put together for the afternoon session – these were the ones we presented to the group. Possibly they were sent out before, but I can't find them.

Thank you

Tigga

From: Cryan, Paul
Sent: Wednesday, January 10, 2018 2:12 PM EST
To: DeeAnn Reeder >
CC: Jon Epstein ecohealthalliance.org>; Katie Leahy
lance.r.brooks >; carl.i.newman. >;
christopher.r.lewis ; mary.j.lancaster
; BounheuangK ; Kading,Rebekah
vkapur ; olival
ecohealthalliance.org>; ian.mendenhall
l.urushadze ; gavin.smith ;
abelwade >; c_ demetria >;
spwa >; kityrob >; tamar_kutateladze
>; nisreen.hmoud >; joram.buza
>; Tigga Kingston >; Keti Sidamonidze <
martha.m.stokes.civ >; Megan Hudson >
Subject: Re: Reception at U.S. Embassy (Context)

Hi Katie,

I too received the invitation and will gratefully accept.

All the best,
Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info
ORCID

On Wed, Jan 10, 2018 at 10:07 AM, DeeAnn Reeder< > wrote:

> Me too, and I have responded directly to the invitation email.
>
> Looking forward to seeing everyone - DeeAnn
>
> On Wed, Jan 10, 2018 at 11:32 AM, Jon Epstein ecohealthalliance.org > wrote:
>
> > Katie,
> > Thank you for the background and the invitation. I'll plan on attending as well.
> >
> > Cheers,
> > Jon
> >
> > Jonathan Epstein DVM, MPH, PhD
> >
> > Vice President for Science and Outreach
> >
> > EcoHealth Alliance
> > New York
> >
> > On Jan 10, 2018 12:07 PM, "Katie Leahy" > wrote:
> >
> > > All,
> > >
> > > You likely received an invitation from “Protocol Bangkok” inviting you to a Prince Mahidol Award Reception at the U.S. Ambassador’s residence on Thursday, February 1 from 1800 – 2000.
> > >
> > > Here is a bit of context about the event: this year, the United States became the first country to receive awards in all categories of the Prince Mahidol Awards, which are awarded annually under patronage of the Thai Royal Family to individuals and organizations that have made

outstanding contributions to medicine and public health. Historically, winners have been forerunners to Nobel prizes. This year's American awardees include the Human Genome Project and a team of researchers who developed a vaccine against Haemophilus influenza.

The U.S. Ambassador is not only proud of this historic American accomplishment, but would also like to use the opportunity to highlight the U.S. Government's long history of military and civilian cooperation on health issues in Thailand and the greater region. The 60-year history of U.S. – Thai health cooperation is one of the lesser told success stories of the long-standing relationship with a close regional ally; and further, an alignment with the 200-year anniversary of U.S. – Thai friendship, which also occurs in 2018.

CBEP is very much a contributor to U.S.-Thai military and civilian cooperation and accomplishment on health issues; therefore, Dr. Stokes and her colleagues are co-sponsoring the celebration at the Ambassador's residence and provided your names as their guests to the event. On behalf of her and the CBEP delegation, we very much hope you will attend.

Please let me know **if you did not receive an invitation**. Please also let me know if you have any questions. Otherwise, please follow the instructions in your invitation for favorable response.

Thank you!

V/r,

Katie Leahy

Katie Leahy

Program Manager | Global Systems Engineering

http://globalsyseng.com

--
DeeAnn M. Reeder, PhD
Presidential Professor
Department of Biology
Bucknell University
Lewisburg, PA 17837

From: Wade Abel >
Sent: Thursday, January 11, 2018 12:40 AM EST
To: Katie Leahy >
CC: lance.r.brooks ; Newman, Carl I CIV DTRA J3-7 (US) ; christopher.r.lewis >; mary.j.lancaster ; BounheuangK ; cryanp Kading,Rebekah ; vkapur >; olival ecohealthalliance.org>; epstein ecohealthalliance.org>; ian.mendenhall >; l.urushadze < ; gavin.smith >; c demetria ; spwa ; kityrob ; tamar_kutateladze >; nisreen.hmoud >; joram.buza ; Tigga Kingston ; DeeAnn Reeder Keti Sidamonidze ; martha.m.stokes.civ Megan Hudson
Subject: Re: Reception at U.S. Embassy (Context)

Dear Katie,

I have confirmed my participation. Thanks for the clarification.

Best regards and Happy New Year

On 10 January 2018 at 12:07, Katie Leahy< > wrote:

> All,
>
> You likely received an invitation from "Protocol Bangkok" inviting you to a Prince Mahidol Award Reception at the U.S. Ambassador's residence on Thursday, February 1 from 1800 – 2000.
>
> Here is a bit of context about the event: this year, the United States became the first country to receive awards in all categories of the Prince Mahidol Awards, which are awarded annually under patronage of the Thai Royal Family to individuals and organizations that have made outstanding contributions to medicine and public health. Historically, winners have been forerunners to Nobel prizes. This year's American awardees include the Human Genome Project and a team of researchers who developed a vaccine against Haemophilus influenza.
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>
> Please let me know **if you did not receive an invitation**. Please also let me know if you have any questions. Otherwise, please follow the instructions in your invitation for favorable response.
>
> Thank you!
>
> V/r,
>
> Katie Leahy

From: Keti Sidamonidze >
Sent: Thursday, January 11, 2018 6:27 AM EST
To: Katie Leahy
CC: lance.r.brooks ; Newman, Carl I CIV DTRA J3-7 (US) ; christopher.r.lewis >; mary.j.lancaster ; BounheuangK ; cryanp >; Kading,Rebekah ; vkapur ; oliva ecohealthalliance.org>; epstein@ ecohealthalliance.org>; ian.mendenhall l.urushadze ; gavin.smith abelwade >; c_ demetria spwa ; kityrob ; tamar_kutateladze ; nisreen.hmoud ; joram.buza Tigga Kingston ; DeeAnn Reeder ; martha.m.stokes < Megan Hudson
Subject: Re: Reception at U.S. Embassy (Context)

Dear Katie,
I do confirm reception of the invitation and looking forward to attend.
Best,
- Keti

On Wed, Jan 10, 2018 at 3:07 PM, Katie Leahy< > wrote:

> All,
>
> You likely received an invitation from "Protocol Bangkok" inviting you to a Prince Mahidol Award Reception at the U.S. Ambassador's residence on Thursday, February 1 from 1800 – 2000.
>
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>
> Thank you!
>
> V/r,
>
> Katie Leahy

From: Kevin Olival, PhD ecohealthalliance.org>
Sent: Wednesday, January 10, 2018 5:22 PM EST
To: Katie Leahy >
CC: Lance R CIV DTRA J3-7 (US) Brooks ; Newman, Carl I CIV DTRA J3-7 (US) ; christopher.r.lewis >; Mary J. Lancaster Ph.D. >; BounheuangK >; Paul Cryan Kading,Rebekah Vivek Kapur Jon Epstein ecohealthalliance.org>; Ian MENDENHALL PhD ; l.urushadze >; gavin.smith ; abelwade >; c_demetria >; Supaporn Wacharapluesadee ; kityrob ; tamar kutateladze ; Nisreen AL-Hmoud ; joram.buza ; Tigga Kingston ; DeeAnn Reeder >; Keti Sidamonidze >; Martha M CIV Stokes >; Megan Hudson >
Subject: Re: Reception at U.S. Embassy (Context)

Katie,

I have RSVP'd to the invitation from the Ambassador. Thank you all for facilitating this, I look forward to the event.

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research
USAID PREDICT-2 Modeling & Analytics Coordinator

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

www.ecohealthalliance.org

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>
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>
> Thank you!
>
> V/r,
>
> Katie Leahy

From: Aleksei Chmura ecohealthalliance.org>
Sent: Tuesday, September 01, 2020 4:00 PM EDT
To: Kading,Rebekah
CC: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Re: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

Dear Rebekah,

Thank you very much for sending us your enthusiastic and detailed comments about Anna!

These will be a great help for our hiring committee.

Cheers,

-Aleksei

On Sep 1, 2020, at 15:57, Kading,Rebekah > wrote:

Dear Aleksei, Peter, and Hongying,

I enthusiastically recommend Dr. Anna Fagre for the Research Scientist and Project Manager position at EcoHealth Alliance.

To speak to Anna's **research experience and capability**: I've known Anna since I joined the CSU faculty in 2016, when she arranged to a rotation as part of her microbiology residency. Anna formally joined my laboratory as a PhD student in July 2017. Her dissertation is focused on the role of bats as reservoirs of emerging arboviruses, and she has made significant progress on both *in vitro* and *in vivo* studies involving bat-associated orbiviruses. The primary emphasis of these studies is on characterization of Bukakata orbivirus, a novel virus that I isolated from a fruit bat in Uganda in 2013. Bukakata orbivirus is putatively tick-borne, based on the phylogenetic analyses we have conducted. To study this virus in the broader context of other orbiviruses that have been isolated from naturally-infected bats, we acquired all three of the remaining bat-associated orbiviruses from the CDC reference collection as well as Chobar Gorge virus, a tick-borne orbivirus to which Bukakata appears to be closely related. Anna's molecular and phylogenetic characterization of Bukakata and other bat-associated orbiviruses was published in a special collection on bat viruses, in the journal Viruses (PMID: 30832334) along with a comprehensive review of the potential for bats to serve as reservoirs for arboviruses (PMID: 30832426). Since the time these papers were completed, Anna has also put significant effort into investigating the use of subgenomic RNA derived from the 3'UTR of flaviviruses to look for evidence of past infection in archived tissue samples. Because of the complex hairpin structure of the viral RNA in the 3'UTR, it is protected from RNA degradation by the exonuclease XRN1, so we hypothesized that we would find residual viral RNA that could be amplified and sequenced. After optimizing this methodology, Anna screened all of our remaining bat tissue samples from Uganda, going back 10 years, and discovered that 4 bats between 2009 – 2013 had been infected with Zika virus. Moreover, this Zika virus sequence was most similar to the Asian lineage, suggesting either diversification of Zika virus strains prior to the virus expanding into Asian in the ~1960s or spillback into Africa of the epidemic strain much earlier than we have appreciated. This manuscript is currently in review. All in all, Anna's work in my lab has been top-notch. She is meticulous and hard-working and has an excellent grasp of the molecular methodologies and big picture of how they can be applied innovatively in an ecological context. In each of these projects, she has done an excellent job leading, and taken initiatives beyond the original study scope that have made the work much stronger in the end. Her **background in veterinary medicine** has also added valuable perspective, and been very much in-demand as she has helped other laboratories on campus during this pandemic with *in vivo*studies involving SARS-CoV-2.

Other key attributes relevant to the current opportunity:

Anna is highly **collaborative,** personable, and very proactive in seeking these collaborations. This year she has re-connected with a former CSU graduate school colleague who is now in Bangladesh, and has been actively developing some research ideas and using her own funding to generate preliminary data. She also joined the VERENA consortium and has been working on a review paper with collaborators in that group. She works very well with others, as a leader of diverse teams as well as a contributing member. She has had the opportunity to contribute to a number of **international projects** both as part of my lab and during her previous experience, and is very adaptable, capable, and enthusiastic about working internationally. Over the past year she has been an invaluable member of an global initiative led by the CSU Office of the Vice President for Research, and has earned the respect of the highest CSU leadership for her contributions to this team.

Anna has been successful at **securing extramural funding**, of her own initiative. Since joining my lab, she has been awarded three highly-competitive fellowships and grants: An NIH TL1 fellowship through the Colorado Clinical and Translational Science Institute, a spot on the NIH T32 award to CSU, and the 2019 Robert E. Shope International Fellowship in Infectious Diseases through ASTMH/ACAV.

Anna is an excellent writer and **science communicator**, and also publishes frequently on blogs and other social media platforms in addition to her prolific peer-reviewed publications. She is the literature watchdog of the lab, and somehow seems to know about every relevant paper or report that is published within a half hour of it hitting the press. Anna has

excellent soft skills when interacting with other professionals. She was featured in a documentary video made by CSU, and had a very natural presence and ability to clearly explain her research and general principles of disease ecology in lay terms.

In conclusion, I give Anna my highest recommendation and think she would be a fantastic addition to your team. Anna is extremely proactive, self-motivated, skilled, and has brought a wonderful energy and work ethic to my laboratory. She is an up-and-coming leader in the field, and I am thrilled to have her as part of my team. This turned out to be not-so-brief a recommendation, but I hope was a useful assessment! If you have any questions or if I can be of any additional assistance, please do not hesitate to contact me.

Best regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Aleksei Chmura ecohealthalliance.org>
Sent: Sunday, August 30, 2020 10:25 PM
To: Kading,Rebekah
Cc: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Re: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

Dear Rebekah,

Thanks for your quick reply and it is good to read your enthusiasm about Anna! An informal, brief, and detailed email reply-to-all will be splendid - any time this week.

Much appreciated!

-Aleksei

On Aug 31, 2020, at 00:15, Kading,Rebekah > wrote:

Hi Aleksei,

This is wonderful news!! I'm thrilled for Anna. She really is a shining star and I will be sad to see her go when that time comes, but I know she has an amazing future ahead of her and its been exciting to see her career blossom already. I'd be happy to put my thoughts into a letter of recommendation this week if that's what you prefer? Otherwise Tuesday and Friday are my most open days this week for a phone call; I could talk Tuesday anytime between 1-5 Eastern time or Friday is wide open.

Best regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Aleksei Chmura ecohealthalliance.org>
Sent: Sunday, August 30, 2020 4:26 PM
To: Kading,Rebekah
Cc: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

Dear Dr. Kading,

We just interviewed Anna Fagre for a position here at EcoHealth Alliance as a Research Scientist and Project Manager. Our hiring committee thought she was terrific with the right background and attitude for our team. Anna listed you as a reference. If you would be willing to send some comments about Anna, that would be terrific!

I have attached our position advertisement, so you may know more about the position - though based on her skillset, the specifics would evolve a bit. This position would focus primarily on our emerging infectious disease projects based in Southeast Asia including our recently awarded, NIAID funded EID-SEARCH program:

- https://www.ecohealthalliance.org/program/south-east-asia-research-collaboration-hub

I look forward to your reply and should a phone call be more convenient, we could do that as well.

On behalf of our whole committee, I sincerely appreciate your time.

-Aleksei

Aleksei Chmura, PhD
Chief of Staff

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-4182

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

From: Aleksei Chmura ecohealthalliance.org>
Sent: Monday, August 31, 2020 12:25 AM EDT
To: Kading,Rebekah
CC: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Re: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

Dear Rebekah,

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Best regards,
Rebekah

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Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Aleksei Chmura ecohealthalliance.org>
Sent: Sunday, August 30, 2020 4:26 PM
To: Kading,Rebekah >
Cc: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

Dear Dr. Kading,

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- https://www.ecohealthalliance.org/program/south-east-asia-research-collaboration-hub

I look forward to your reply and should a phone call be more convenient, we could do that as well.

On behalf of our whole committee, I sincerely appreciate your time.

-Aleksei

Aleksei Chmura, PhD
Chief of Staff

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-4182

)
www.ecohealthalliance.org

From: Kingston, Tigga >
Sent: Wednesday, September 12, 2018 5:47 PM EDT
To: Megan Hudson ; cryanp epstein >; Kading,Rebekah ; vkapur >; olival ecohealthalliance.org>; raina.plowright >; c_demetria >
CC: Stokes, Martha M CIV (US) >; Katie Leahy < >; Aleman, Nicki D CTR DTRA PARTNERSHIP AND INSP (US) ; Becker, Stephen M CTR DTRA J3-7 (US)
Subject: RE: Reminder: BOHRN November IMED Meeting Invitation

Good Afternoon Megan
I am able to attend.
Tigga

From: Megan Hudson >
Sent: Monday, September 10, 2018 8:45 AM
To: cryanp ; ecohealthalliance.org; rebekah.kading ; vkapur Kingston, Tigga >; ecohealthalliance.org; raina.plowright ; c_demetria
Cc: Stokes, Martha M CIV (US) ; Katie Leahy >; Aleman, Nicki D CTR DTRA PARTNERSHIP AND INSP (US) ; Becker, Stephen M CTR DTRA J3-7 (US)

Subject: Reminder: BOHRN November IMED Meeting Invitation

All,

As a reminder, please respond NLT **14 September** if you are able to attend the BOHRN/IMED Meeting in Vienna on 8-12 November 2018. The BOHRN meeting will be held 8-9 November.

We are looking for nominations to grow the BOHRN network, please send any nominations of subject matter experts or other participants who would be beneficial to this discussion **no later than Today, 10 September 2018**.

IMED will take place 9 – 12 November at the Hilton Vienna. The 2018 IMED will focus on innovation and changes in political and societal responses to outbreaks. The theme of IMED aligns with our overall BOHRN objectives and we encourage all BOHRN members to stay and participant in the conference.

We need you to confirm your attendance to BOHRN and IMED NLT 14 September.

v/r,

Megan

Megan Hudson
Task Lead | Global Systems Engineering

http://globalsyseng.com

Travel instructions:
Please contact Nicki Aleman **NLT 14 September 2018** if you intend to travel; you will likely need to provide her with your passport information, to and from destinations, and travel dates. CBEP's logistics support coordinators will work with you to secure plane reservations. Please note that they try to work with your preferences, but must remain within the boundaries of the Department of Defense regulations for travel.

From: Megan Hudson
Date: Thursday, September 6, 2018 at 10:54
To: "cryanp " , "epstein " >, "rebekah.kading " , "vkapur " , "tigga.kingston " , "olival " "dreeder " , "raina.plowright " >, "ian.mendenhall , "c_demetria "

Cc: "Stokes, Martha M CIV (US)" >, Katie Leahy ,
"Aleman, Nicki D CTR DTRA PARTNERSHIP AND INSP (US)" >, "Becker, Stephen M CTR DTRA J3-7 (US)"
Subject: BOHRN November IMED Meeting Invitation

All,

On behalf of Dr. Marty Stokes you are receiving this email, as part of a save the date to attend our BOHRN Steering Committee meeting and International Meeting on Emerging Diseases and Surveillance (IMED) 8 – 12 November 2018 in Vienna, Austria.

Our meeting will take place on 8 – 9 November (hotel/meeting location TBD). The BOHRN steering committee meeting will aim to meet the objectives the group identified in Saskatoon. The following objectives were suggested based on your survey responses:

1. Prioritizes funding needs based on working groups' characterization of gaps and needs, to help organize and develop funding initiatives; and
2. Analyze progress of action plans and their yields establishing collaborate and sustainable projects

To facilitate these objectives, we will be asking each working group to present their progress. The progress updates for each working group are imperative to the outcomes for this meeting.

As discussed during the June BOHRN meeting, an objective of this meeting is to develop our outreach and populate working groups. Please send any nominations of subject matter experts or other participants who would be beneficial to this discussion **no later than 10 September 2018**.

IMED will take place 9 – 12 November at the Hilton Vienna. The 2018 IMED will focus on innovation and changes in political and societal responses to outbreaks. The theme of IMED aligns with our overall BOHRN objectives and we encourage all BOHRN members to stay and participant in the conference. **Therefore, we need you to confirm your attendance to BOHRN and IMED NLT 14 September.**

v/r,

Megan

Megan Hudson
Task Lead | Global Systems Engineering

http://globalsyseng.com

Travel instructions:
Please contact Nicki Aleman **NLT 14 September 2018** if you intend to travel; you will likely need to provide her with your passport information, to and from destinations, and travel dates. CBEP's logistics support coordinators will work with you to secure plane reservations. Please note that they try to work with your preferences, but must remain within the boundaries of the Department of Defense regulations for travel.

From: Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) >
Sent: Tuesday, June 02, 2020 3:26 PM EDT
To: Grant, Evan H >; Gilbert, Amy T - APHIS >; Kevin Castle >; Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) ; epstein ecohealthalliance.org>; dreeder >; Daniel Streicker ; kate.e.jones ; Kading,Rebekah ; Plowright, Raina >; wfrick a.peel ; Christine Kreuder Johnson

Subject: RE: SARS expert judgement - final report on the risk assessment

Nice report! It was a really interesting and informative process. Many thanks for including me.
Best wishes,
Jon

_____
Jonathan S. Towner, PhD
Lead, Virus Host Ecology Team
Viral Special Pathogens Branch
Centers for Disease Control and Prevention

From: Grant, Evan H >
Sent: Tuesday, June 2, 2020 1:39 PM
To: Gilbert, Amy T - APHIS ; Kevin Castle >; Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) ; Jon Epstein ecohealthalliance.org>; dreeder Daniel Streicker >; kate.e.jones ; Kading,Rebekah < >; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) >; Plowright, Raina ; wfrick ; a.peel ; Christine Kreuder Johnson
Subject: SARS expert judgement - final report on the risk assessment

SARS-bat Experts,
Thanks again for lending your expertise to this risk assessment. I attach here the report from this work.
Kindest regards,
Evan and Mike

From: Kevin Castle
Sent: Tuesday, June 02, 2020 9:01 PM EDT
To: Grant, Evan H >
CC: Gilbert, Amy T - APHIS >; Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) epstein ecohealthalliance.org>; dreeder ; Daniel Streicker >; kate.e.jones ; Kading,Rebekah ; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) ; Plowright, Raina ; wfrick ; a.peel ; Christine Kreuder Johnson
Subject: Re: SARS expert judgement - final report on the risk assessment

Thank you Evan and Mike,
You herded us cats in no time!
Kevin

On Tue, Jun 2, 2020 at 11:39 AM Grant, Evan H wrote:

> SARS-bat Experts,
>
> Thanks again for lending your expertise to this risk assessment. I attach here the report from this work.
>
> Kindest regards,
>
> Evan and Mike

--
Kevin T. Castle, DVM, MS
Wildlife Veterinary Consulting, LLC

From: DeeAnn Reeder >
Sent: Tuesday, June 02, 2020 5:27 PM EDT
To: Kading,Rebekah <
CC: Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) >; Grant, Evan H ; Gilbert, Amy T - APHIS >; Kevin Castle ; Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) ; epstein ecohealthalliance.org>; Daniel Streicker ; kate.e.jones >; Plowright, Raina ; wfrick < >; a.peel Christine Kreuder Johnson >
Subject: Re: SARS expert judgement - final report on the risk assessment

Agreed! This was a herculean yet critically important document!

Cheers - DeeAnn

On Tue, Jun 2, 2020 at 5:25 PM Kading,Rebekah > wrote:

> Thank you very much, Evan and Mike, and congratulations on completing such a tremendous amount of work! It was a pleasure to be involved in this process, and have such thorough and insightful discussions with all of you. I learned a lot, and look forward to future interactions.
> Kind regards,
> Rebekah
>
> **Rebekah C. Kading, PhD**
> Assistant Professor
> Department of Microbiology Immunology and Pathology
> Colorado State University

From: Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)
Sent: Tuesday, June 2, 2020 1:26 PM
To: Grant, Evan H ; Gilbert, Amy T - APHIS >; Kevin Castle >; Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) >; epstein ecohealthalliance.org>; dreeder ; Daniel Streicker >; kate.e.jones ; Kading,Rebekah ; Plowright, Raina wfrick ; a.peel Christine Kreuder Johnson >
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_____

Jonathan S. Towner, PhD

Lead, Virus Host Ecology Team

Viral Special Pathogens Branch

Centers for Disease Control and Prevention

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Subject: SARS expert judgement - final report on the risk assessment

SARS-bat Experts,

Thanks again for lending your expertise to this risk assessment. I attach here the report from this work.

Kindest regards,

Evan and Mike

--
DeeAnn M. Reeder, PhD
Professor
Department of Biology
Bucknell University
Lewisburg, PA 17837

From: Alison Peel >
Sent: Tuesday, June 02, 2020 9:07 PM EDT
To: Kevin Castle
CC: Grant, Evan H ; Gilbert, Amy T - APHIS >; Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) ; epstein ecohealthalliance.org>; dreeder >; Daniel Streicker < ; kate.e.jones ; Kading,Rebekah Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) >; Plowright, Raina >; wfrick >; Christine Kreuder Johnson >
Subject: Re: SARS expert judgement - final report on the risk assessment

Many thanks and Congratulations from down under too! The report represents an enormously valuable contribution.
Alison

On Wed, 3 Jun 2020 at 11:02, Kevin Castle > wrote:

> Thank you Evan and Mike,
> You herded us cats in no time!
> Kevin
>
> On Tue, Jun 2, 2020 at 11:39 AM Grant, Evan H > wrote:
>
>> SARS-bat Experts,
>>
>> Thanks again for lending your expertise to this risk assessment. I attach here the report from this work.
>>
>> Kindest regards,
>>
>> Evan and Mike
>
> --
> Kevin T. Castle, DVM, MS
> Wildlife Veterinary Consulting, LLC

From: Kingston, Tigga
Sent: Wednesday, April 15, 2020 9:52 AM EDT
To: Cryan, Paul ; Kading,Rebekah
CC: olival ecohealthalliance.org>
Subject: RE: SARS-CoV-2 spillback risk to North American bats

Hi Paul
Very interested to see the MS. Rebekah and I have been working on something that arose out of BOHRN that would be very complementary and might be worth trying to coordinate dissemination in some way. We are meeting today and will take stock of where we are at.

I just started an email to you and Kevin about the state of affairs as we Rodrigo and I are getting quite a bit of push-back on the IUCN BSG recommendation to suspend field studies while further data are gathered (primarily from western scientists with access to PPE). It would be good to hear what those committees are finding sooner rather than later.

Best wishes
Tigga

From: Cryan, Paul
Sent: Tuesday, April 14, 2020 2:16 PM
To: Kingston, Tigga < >
Cc: ecohealthalliance.org
Subject: SARS-CoV-2 spillback risk to North American bats

Hi Tigga,

Sorry for the silence since my call for help about the risks of humans potentially infecting bats in North America with the SARS-CoV-2 virus. Thanks for your patience and willingness to get involved in what we're hoping can be another disease response where scientists coming at disparate aspects of bats and pathogens can help each other. Those of us in the bat research world that focused most of our past efforts in the U.S. on conservation and management of bat populations can certainly use your expertise and help adjusting to the new situation.

A lot happened during my silence. Another group in USGS has been working at the behest of decision makers across federal and state natural resource management agencies to pull off a formal risk assessment by querying a subset of the experts we've reached out to. You lucked out and were not chosen for that exercise (yet), but we will keep you posted on the outcomes of that rapid assessment.

The other thing keeping me silent over the past couple of weeks is a short manuscript (currently 5 pages single spaced) that Kevin Olival and I drafted to articulate the potential risks of humans infecting North American temperate-zone bats with SARS-CoV-2, potentially relevant patterns we observed in bat-CoV distributions at a global scale, and the likely benefits of disease and bat researchers working together to draw on the strengths of our various disciplines. We hope to have a draft to circulate by tomorrow and would appreciate input and feedback from any of you willing to read it and help us stress test the concepts and assertions therein. Please let me know if you are interested.

Thanks again for your help and patience.

All the best,
Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Wang Linfa
Sent: Tuesday, June 16, 2020 1:22 AM EDT
To: Kevin Olival ecohealthalliance.org>; DeeAnn Reeder >; Hume Field ecohealthalliance.org>; Charles H Calisher >; Brian R. Amman ; Ralph S. Baric ; David S Blehert ; Cara Brook ; Kevin Castle ; Jeremy Coleman ; Peter Daszak ecohealthalliance.org>; epstein ecohealthalliance.org>; Winifred F Frick, Ph.D. < ; Gilbert, Amy T - APHIS >; David Hayman Hon S Ip ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson < >; Kading,Rebekah >; Tigga Kingston ; Lorch, Jeffrey M ; Ian Mendenhall >; alisonpee ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina >; Jonathan D Reichard ; Jonathan M Sleeman ; Daniel Streicker ; Jonathan S. Towner
CC: Paul Cryan
Subject: RE: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Thanks Kevin and Paul for doing a great job so quickly.

I guess the CNN documentary yesterday also made this a hot (hotter) topic now and the editor may want to have “a ride on the bat wings” to get it out asap!

Fingers crossed.

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,

From: Kevin Olival ecohealthalliance.org>
Sent: Tuesday, 16 June 2020 1:19 PM
To: DeeAnn Reeder ; Hume Field ecohealthalliance.org>; Charles H Calisher ; Brian R. Amman >; Wang Linfa >; Ralph S. Baric ; David S Blehert ; Cara Brook >; Kevin Castle ; Jeremy Coleman ; Peter Daszak ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Winifred F Frick, Ph.D. ; Gilbert, Amy T - APHIS >; David Hayman ; Hon S Ip >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson >; Kading,Rebekah ; Tigga Kingston ; Lorch, Jeffrey M Ian Mendenhall >; alisonpee ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; Jonathan D Reichard >; Jonathan M Sleeman ; Daniel Streicker ; Jonathan S. Towner
Cc: Paul Cryan
Subject: Re: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Hi Team,

Funny thing, bioRxiv actually rejected us! Apparently they don’t take “reviews”.

In any case we got **very positive reviews back from *PLoS Pathogens*** today, and the revised ms was just resubmitted (<24 hour turnaround). Woohooo! Finger’s crossed that the editors turn it around again quickly and we can see this published soon.

Attached is the cover letter, response to reviewers, and the resubmitted version of ms.

Cheers,
Kevin and Paul

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

On Jun 12, 2020, at 10:43 AM, Kevin Olival ecohealthalliance.org> wrote:

Dear all,

We successfully submitted to bioRxiv yesterday and it's currently in "review" with the editorial staff and should be posted within 48 hours. Big thanks to Paul for getting the final USGS approvals and ms formatting in place.

Hume and Charlie, I understand your very valid and "traditional" concerns here, there's a lot of riff-raff out there on pre-print servers and hence why we have the peer-review system. Nonetheless, given that there are other similar reviews being posted at the moment and the timeliness of this given the USGS/USFW Risk Assessment out last week, etc., would be best to get this out there while we're still in review at PLOS.

Best,
Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

On Jun 12, 2020, at 8:24 AM, DeeAnn Reeder > wrote:

Thanks all - I am in support of bioRxrv for this paper (although I don't systematically use it - in this fast moving CoV environment, for some papers I think it is a very good option).

Cheers - DeeAnn

On Thu, Jun 11, 2020 at 7:22 PM Hume Field ecohealthalliance.org> wrote:

> Thanks Kevin.. no prob, tho philosophically I'm with Charlie!
>
> Hume
>
> On Fri., 12 Jun. 2020, 1:23 am , > wrote:
>
> > No significant objections about the manuscript but I am not crazy about pre-print servers or their purpose. I am not only old, I am a traditionalist. Lots of crap being sent out as pre-print servers that wind up not being acceptable – or withdrawn.
> >
> > Charlie
> >
> > ---
> >
> > **From:** Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) <

Sent: Thursday, June 11, 2020 8:05 AM
To: Kevin Olival ecohealthalliance.org>; Wang Linfa ; Paul Cryan >; Ralph S. Baric ; David S Blehert Cara Brook >; Charles H Calisher ; Kevin Castle >; Jeremy Coleman ; Peter Daszak ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Hume Field ecohealthalliance.org>; Winifred F Frick, Ph.D. ; Gilbert, Amy T - APHIS >; David Hayman ; Hon S Ip < ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson Kading,Rebekah ; Tigga Kingston >; Lorch, Jeffrey M ; Ian MENDENHALL PhD alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina >; DeeAnn Reeder ; Jonathan D Reichard >; Jonathan M Sleeman ; Daniel Streicker ; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)

Subject: RE: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Thanks Kevin!

From: Kevin Olival ecohealthalliance.org>
Sent: Thursday, June 11, 2020 9:43 AM
To: Wang Linfa Paul Cryan < ; Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) >; Ralph S. Baric ; David S Blehert >; Cara Brook ; Charles H Calisher >; Kevin Castle ; Jeremy Coleman ; Peter Daszak ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Hume Field < ecohealthalliance.org>; Winifred F Frick, Ph.D. Gilbert, Amy T - APHIS >; David Hayman >; Hon S Ip >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah >; Tigga Kingston >; Lorch, Jeffrey M >; Ian MENDENHALL PhD ; alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; DeeAnn Reeder < ; Jonathan D Reichard < ; Jonathan M Sleeman >; Daniel Streicker ; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)

Subject: Re: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Dear all,

Update on our ms. It was submitted to PLOS Pathogens on June 2nd (you should have all received an email from the journal confirming this) and it is currently under review.

We are in the final stages of USGS approval to also submit to bioRxiv (pre-print server), and expect to finalize that and post it on bioRxiv in the next 24 hours. *Please let me know if there are any objections.*

Cheers,

Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eight Avenue, Suite 1201

New York, NY 10018

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

On May 28, 2020, at 4:38 PM, Kevin Olival > wrote:

Hi Folks,

Quick update on our paper — unfortunately got news yesterday that *PNAS* was not interested in this as a Perspectives piece, and rejected our proposal. We are currently pursuing options with editors at *PLOS Pathogens* to see if they want it as a review. Will keep you all posted.

Latest version attached that has cleared CDC and USGS review. We will still aim to get this on BioRxiv, but wanted to wait until we had it cleared first and ideally in review at a journal.

Cheers,

Kevin

<Olival et al. bat CoVs 20200520_v11.3.docx>

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eight Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

On 12 May 2020, at 10:13 PM, Kevin Olival ecohealthalliance.org> wrote:

Dear Co-authors,

Attached is the latest, submission ready version of our paper "**Possible risks of SARS-CoV-2 spillover to free-ranging wildlife: a case study of bats**". Thank you all for the last round of invaluable edits and comments. Paul and I have now gone through multiple revisions since you last saw the paper in an attempt to include everyone's feedback; so apologize for the delay in turning this around and moving towards submission.

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This has been a fantastic exercise in group writing! Big thank you to everyone.

Cheers,

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<Olival et al. bat CoVs 20200511_V9.1.docx>

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
460 West 34th Street, Suite 1701
New York, NY 10001

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics *and* promote conservation

--
DeeAnn M. Reeder, PhD
Professor
Department of Biology

From: DeeAnn Reeder
Sent: Friday, June 12, 2020 8:24 AM EDT
To: Hume Field ecohealthalliance.org>
CC: Charles H Calisher ; Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) >; Kevin Olival ecohealthalliance.org>; Wang Linfa ; Paul Cryan ; Ralph S. Baric ; David S Blehert ; Cara Brook ; Kevin Castle >; Jeremy Coleman ; Peter Daszak ecohealthalliance.org>; epstein ecohealthalliance.org>; Winifred F Frick, Ph.D. Gilbert, Amy T - APHIS >; David Hayman >; Hon S Ip >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah >; Tigga Kingston ; Lorch, Jeffrey M ; Ian MENDENHALL PhD >; alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina >; Jonathan D Reichard >; Jonathan M Sleeman ; Daniel Streicker Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) >
Subject: Re: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

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Kevin J. Olival, PhD

From: Hayman, David >
Sent: Friday, June 26, 2020 5:17 PM EDT
To: epstein ecohealthalliance.org>; Kevin Olival ecohealthalliance.org>
CC: DeeAnn Reeder >; Hume Field ecohealthalliance.org>; Charles H Calisher ; Brian R. Amman >; Wang Linfa >; Ralph S. Baric ; David S Blehert ; Cara Brook < >; Kevin Castle Jeremy Coleman ; Peter Daszak ecohealthalliance.org>; Winifred F Frick, Ph.D. ; Gilbert, Amy T - APHIS ; Hon S Ip >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson >; Kading,Rebekah >; Tigga Kingston ; Lorch, Jeffrey M Ian MENDENHALL PhD >; alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; Jonathan D Reichard Jonathan M Sleeman >; Daniel Streicker >; Jonathan S. Towner >; Paul Cryan >
Subject: Re: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Looks like it's accepted, so enjoy your weekends everyone and thanks for including me. Best wishes to you all.

Get Outlook for iOS

From: Jon Epstein ecohealthalliance.org>
Sent: Wednesday, June 17, 2020 8:35:07 AM
To: Kevin Olival < ecohealthalliance.org>
Cc: DeeAnn Reeder ; Hume Field ecohealthalliance.org>; Charles H Calisher >; Brian R. Amman >; Wang Linfa Ralph S. Baric David S Blehert >; Cara Brook >; Kevin Castle Jeremy Coleman ; Peter Daszak ecohealthalliance.org>; Winifred F Frick, Ph.D. >; Gilbert, Amy T - APHIS ; Hayman, David Hon S Ip >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah >; Tigga Kingston ; Lorch, Jeffrey M ; Ian MENDENHALL PhD ; alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina < >; Jonathan D Reichard Jonathan M Sleeman >; Daniel Streicker ; Jonathan S. Towner ; Paul Cryan

Subject: Re: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Well done Kevin and Paul. Thank you for all the hard work you put into this!
Cheers,
Jon

On Tue, Jun 16, 2020 at 1:19 AM Kevin Olival ecohealthalliance.org> wrote:

> Hi Team,
>
> Funny thing, bioRxiv actually rejected us! Apparently they don't take "reviews".
>
> In any case we got **very positive reviews back from *PLoS Pathogens*** today, and the revised ms was just resubmitted (<24 hour turnaround). Woohooo! Finger's crossed that the editors turn it around again quickly and we can see this published soon.
>
> Attached is the cover letter, response to reviewers, and the resubmitted version of ms.
>
> Cheers,
> Kevin and Paul
>
> **Kevin J. Olival, PhD**
> *Vice President for Research*
>
> EcoHealth Alliance
> 520 Eighth Avenue, Suite 1201
> New York, NY 10018
>
> www.ecohealthalliance.org
>
> *EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.*

On Jun 12, 2020, at 10:43 AM, Kevin Olival ecohealthalliance.org> wrote:

Dear all,

We successfully submitted to bioRxiv yesterday and it's currently in "review" with the editorial staff and should be posted within 48 hours. Big thanks to Paul for getting the final USGS approvals and ms formatting in place.

Hume and Charlie, I understand your very valid and "traditional" concerns here, there's a lot of riff-raff out there on pre-print servers and hence why we have the peer-review system. Nonetheless, given that there are other similar reviews being posted at the moment and the timeliness of this given the USGS/USFW Risk Assessment out last week, etc., would be best to get this out there while we're still in review at PLOS.

Best,
Kevin

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DeeAnn M. Reeder, PhD
Professor
Department of Biology

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

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New York, NY 10001

web: ecohealthalliance.org

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From: Kevin Olival ecohealthalliance.org>
Sent: Friday, May 29, 2020 2:02 PM EDT
To: Peter Daszak ecohealthalliance.org>
CC: David Hayman ; Wang Linfa ; Paul Cryan >; Brian R. Amman >; Ralph S. Baric ; David S Blehert >; Cara Brook Charles H Calisher Kevin Castle ; Jeremy Coleman epstein ecohealthalliance.org>; Hume Field ecohealthalliance.org>; Winifred F Frick, Ph.D. ; Gilbert, Amy T - APHIS >; Hon S Ip ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah >; Tigga Kingston ; Lorch, Jeffrey M < >; Ian MENDENHALL PhD >; alisonpeel ; Kendra Phelps ecohealthalliance.org.test-google-a.com>; Plowright, Raina >; DeeAnn Reeder >; Jonathan D Reichard ; Jonathan M Sleeman >; Daniel Streicker >; Jonathan S. Towner
Subject: Re: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Thanks Peter, *EcoHealth* is a great back up option. PLOS Pathogens review editor seemed quite receptive to it (we heard back today), so we're going to submit there first and see. I'll get it back in this weekend.

Cheers,
Kevin

On May 29, 2020, at 1:57 PM, Peter Daszak ecohealthalliance.org> wrote:

OK folks, you know this is coming, but if PLoS don't like it, EID don't like it, and 2 or three others,*EcoHealth* will be delighted if you submit it there. We will pledge to review it and get it back to you within 3 weeks, and if reviewer's comments are addressed, we will include a color image of your choosing. We'll push Springer to make it available online for free as well. All this assuming it gets through review process. Also, as Editor-in-Chief, I'll be recused automatically from the review process, which is also Double-Blind.

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
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USA

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From: Hayman, David >
Sent: Thursday, May 28, 2020 5:58 PM
To: Kevin Olival ecohealthalliance.org>; Wang Linfa >; Paul Cryan >; Brian R. Amman >; Ralph S. Baric ; David S Blehert ; Cara Brook >; Charles H Calisher < >; Kevin Castle >; Jeremy Coleman >; Peter Daszak < ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Hume Field ecohealthalliance.org>; Winifred F Frick, Ph.D. Gilbert, Amy T - APHIS v>; Hon S Ip William B. Karesh ecohealthalliance.org>; Christine Kreuder Johnson >; Kading,Rebekah >; Tigga.Kingston Lorch, Jeffrey M ; Ian MENDENHALL PhD >; alisonpeel Kendra Phelps ecohealthalliance.org.test-google-a.com>; Plowright, Raina ; DeeAnn Reeder

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Thanks Kevin.

If PLoS don't like it, it could interest Emerging Infectious Diseases as a Perspective.

Dave

From: Kevin Olival
Sent: Friday, May 29, 2020 08:38
To: Wang Linfa; Paul Cryan; Brian R. Amman; Ralph S. Baric; David S Blehert; Cara Brook; Charles H Calisher; Kevin Castle; Jeremy Coleman; Peter Daszak; Jon Epstein; Hume Field; Winifred F Frick, Ph.D.; Gilbert, Amy T - APHIS; Hayman, David; Hon S Ip; William Karesh; Christine Kreuder Johnson; Kading,Rebekah; Tigga Kingston; Lorch, Jeffrey M; Ian MENDENHALL PhD; alisonpeel Kendra Phelps; Plowright, Raina; DeeAnn Reeder; Jonathan D Reichard; Jonathan M Sleeman; Daniel Streicker; Jonathan S. Towner
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Professor
Department of Biology
Bucknell University

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Attachment(s): "smime.p7m"

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Thanks Kevin. Totally agree it's important to get it out as a pre-print in terms of timely accessibility. I was just taking the opportunity to reflect more broadly!

Look forward to promoting it on Twitter.

Hume

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Attachment(s): "Olival et al resubmission letter.docx","Olival et al response to reviewers.docx","Olival et al. bat CoVs_V11.8.docx"

Hi Team,

Funny thing, bioRxiv actually rejected us! Apparently they don't take "reviews".

In any case we got **very positive reviews back from *PLoS Pathogens*** today, and the revised ms was just resubmitted (<24 hour turnaround). Woohooo! Finger's crossed that the editors turn it around again quickly and we can see this published soon.

Attached is the cover letter, response to reviewers, and the resubmitted version of ms.

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Kevin and Paul

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Department of Biology

Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats

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Abstract

The COVID-19 pandemic highlights the substantial public health, economic, and societal consequences of virus spillover from a wildlife reservoir. Widespread human transmission of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) also presents a new set of challenges when considering viral spillover from people to naïve wildlife and other animal populations. The establishment of new wildlife reservoirs for SARS-CoV-2 would further complicate public health control measures and could lead to wildlife health and conservation impacts. Given the likely bat origin of SARS-CoV-2 and related beta-coronaviruses (β-CoVs), free-ranging bats are a key group of concern for spillover from humans back to wildlife. Here we review the diversity and natural host range of β-CoVs in bats and examine the risk of humans inadvertently infecting free-ranging bats with SARS-CoV-2. Our review of the global distribution and host range of β-CoV evolutionary lineages suggests that 40+ species of temperate-zone North American bats could be immunologically naïve and susceptible to infection by SARS-CoV-2. We highlight an urgent need to proactively connect the wellbeing of human and wildlife health during the current pandemic, and to implement new tools to continue wildlife research while avoiding potentially severe health and conservation impacts of SARS-CoV-2 "spilling back" into free-ranging bat populations.

Keywords: conservation, COVID-19; coronaviruses; spillover; spill-back; zoonoses

TEXT

Spillover of Pandemic Viruses.

The threat of emerging infectious diseases (EIDs) to wildlife health and biodiversity conservation is recognized [1], but cross-species transmission of novel pathogens, or spillover, is typically

viewed in the specific context of originating *in* a wildlife reservoir and transmitting *to* humans [2]. Research assessing EID risk has typically focused on identifying geographic regions [3, 4] and wildlife species [5-7] whereby spillover of zoonotic diseases into humans is most likely. Among recent pandemic zoonotic viruses, some have no evidence of transmission back to wildlife or domestic animal populations after establishment in people (e.g., human immunodeficiency virus, which causes acquired immunodeficiency syndrome), while others have repeatedly crossed species boundaries (e.g., pandemic H1N1 influenza A virus) [8, 9]. Evidence of 'reverse zoonotic' transmission, sometime referred to as "spillback", from people to wildlife and domestic animals is widespread [9]; however systematic surveys to determine the proportion of EIDs that spill back into novel wildlife hosts are lacking. Infection of bats by viruses of probable human origin has been recorded only twice [10, 11], and further transmission [12], or spread to a wider bat population, has not been recorded.

In December 2019, a novel coronavirus was detected from a cluster of 41 atypical pneumonia cases in Wuhan, China, and has since spread to cause a pandemic with significant global morbidity, mortality, and economic impact [13]. Phylogenetic evidence suggests that this virus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), and the clade of SARS-related coronaviruses (SARSr-CoVs) that it belongs in, evolved in Old-World bats of the family Rhinolophidae [14-16]. There is no epidemiological evidence of direct or indirect transmission of SARS-CoV-2 from bats to people, but a full genome of its closest known relative, with 96.2% sequence similarity, was reported from an Intermediate Horseshoe Bat (*Rhinolophus affinis*) sampled from Yunnan province, China, in 2013 [17]. The timing of SARS-CoV-2 spillover from bats, and any involvement of intermediate host species, remain undetermined [18, 19]. The United States (US) currently has the highest number of confirmed human cases of COVID-19, the disease caused by SARS-CoV-2. The consequences of this pandemic are many and include

the possibility of SARS-CoV-2 transmission from humans to free-ranging wildlife populations. Given the likely bat origin of SARS-CoV-2, free-ranging bats are a key group of concern for spillover from humans. Humans frequently handle and come into close contact with North American temperate-zone bats during the course of ecological research, wildlife rehabilitation, wildlife/pest control, and disease investigations. Anticipating the need for similar risk assessments across many potentially vulnerable species of wildlife and domesticated mammals globally, here we examine the possibility of humans inadvertently infecting free-ranging North American bats with SARS-CoV-2. We further discuss the possible public health and wildlife conservation consequences of SARS-CoV-2 becoming endemic in bats outside its natural host range.

Threats of SARS-CoV-2 to North American Bats.

The pandemic spread of SARS-CoV-2 may directly or indirectly threaten North American bat populations in at least three different ways. First, SARS-CoV-2 might infect any of the diverse and historically isolated 40+ endemic species of temperate-zone North American bats, with or without causing disease, morbidity, and mortality. Second, SARS-CoV-2 might infect and become established in one or more North American bat species, creating novel reservoirs capable of causing human infections (e.g., bat rabies lyssaviruses in the New World [20]). Third, if SARS-CoV-2 infection persists in North American bats of one or more species, it could potentially evolve, or recombine with endemic viruses [19, 21], to become more pathogenic or infectious to humans or other animals. In addition to new public health challenges, the latter outcomes could quickly shift public perception of bats from mostly beneficial wildlife with associated disease risks that are manageable, to bats posing unacceptable disease risks to human and animal health. Such a shift could increase the likelihood of negative human-bat interactions and conflicts, as well as undermine decades of concerted science, conservation,

and education efforts aimed at conserving these valuable animals [22-24]. The potential threat of SARS-CoV-2 transmission from humans to other animals applies to many species of wildlife and domesticated mammals, but the likely bat origin of SARS-CoV-2, and the current threats to bat populations due to another disease in North America, influenced us to focus this review on bats.

Lessons from an Epizootic -- Susceptibility of North American Bats to an Introduced Pathogen.

SARS-CoV-2 is not the first pathogen with the potential for inadvertent spread from people to North American bats. The COVID-19 pandemic follows the arrival of a fungal pathogen (*Pseudogymnoascus destructans*) that as early as 2006 began infecting hibernating bat populations in North America, spreading within and among species to alter the evolutionary trajectory of the continent's bats [25-28]. Genetic analyses indicate that *P. destructans* was introduced to North America [29], in our opinion likely by movement of humans or materials contaminated with fungal spores. White-nose syndrome (WNS), the disease caused by *P. destructans,* remains the only documented bat epizootic to cause multi-year, widespread mass mortality [30], although short-term bat die-offs have been also linked to Lloviu virus in Europe [31]. WNS has killed millions of North American bats, affected populations of at least 12 species of 3 genera, and has already spread across half of the US and Canada (whitenosesyndrome.org, accessed 11 May 2020). Effective methods to mitigate WNS spread and impacts remain elusive despite substantial research effort, and targeted mitigation actions have had limited success against its impacts [32]. It took years of concerted international scientific effort to identify the cold-growing fungus, determine that it likely originated somewhere in the temperate zones of Europe or Asia, understand its mechanisms of infection and

146 pathogenicity, develop strategies to limit accidental translocation, and track its rapid spread
147 through an immunologically naïve continental assemblage of hibernating bats [33-35].
148
149 The devastating impact of WNS on a diverse group of North American bats likely resulted from
150 evolutionary isolation of the continent's bat fauna from other parts of the world for millions of
151 years, despite other species of *Pseudogymnoascus* being present. Bats in both Europe and
152 Asia can become infected by *P. destructans*, but do not suffer mass mortality from WNS [36,
153 37]. The bat fauna spanning the higher latitudes of North America (in the US and Canada) is
154 composed almost entirely of endemic species belonging to the family Vespertilionidae.
155 Vespertilionid bats occur globally, but likely originated and diversified in North America tens of
156 millions of years ago before dispersing to other continents [38, 39]. No extant species of bat in
157 the Americas also occurs outside of the Americas [40, 41], and no bats migrate across the
158 Pacific or Atlantic oceans [42, 43]. The WNS epizootic demonstrates that a large proportion of
159 these historically isolated bats can be vulnerable to a pathogen introduced from another
160 continent during a single event. Additionally, bats already in a physiologically stressed condition
161 due to WNS or other pressures may be more susceptible to viral infection, experience
162 exacerbated disease outcomes, and/or increased viral shedding [44, 45]. The COVID-19
163 pandemic resembles WNS with respect to potential spread of a pathogen from another
164 continent through interconnected, multi-species assemblages of North American bats that might
165 be immunologically naïve, and highlights deficits in our understanding of temperate-zone bat
166 pathogens in North America.
167
168 **Gaps in Understanding Global Patterns of Bat-CoV Diversity, Evolution, and Host Range.**
169 Bats are among the world's most diverse mammals (approximately 1,400 species [46]), and the
170 global distribution and diversity of CoVs in bats proportionally reflects that of their hosts [47, 48].

Available evidence indicates that bats are natural reservoirs of CoVs, some of which have the potential to cause diseases in humans, domesticated animals, and wildlife [17, 47, 49-59]. Coronaviruses appear to have ancient and ancestral relationships with bats, diversifying globally through a process of within-host evolution and cross-taxonomic host-switching events [47, 59-61]. Bats are the likely mammalian progenitor hosts of all alpha (α-) and beta (β-) CoVs [58, 59, 62, 63] and potentially all coronaviruses [60]. Alpha-CoVs of likely bat origin include the causative agent of swine acute diarrhea syndrome (SADS), which caused mass mortality of over 25,000 piglets on farms in Guangdong province, China [57], and a variant strain of porcine epidemic diarrhea virus (PEDV) that spread rapidly from China in recent decades and caused mass piglet mortality in multiple US states [64]. Human CoVs NL63 and 229E also likely had their evolutionary origins in bats [59, 65]. Two recent human disease epidemics (severe acute respiratory syndrome [SARS], Middle East respiratory syndrome [MERS]) and now the current COVID-19 pandemic are caused by viruses that probably originated from β-CoVs circulating in bat populations in regions where outbreaks occurred [17, 19, 50-54, 58, 66-68].

The emergence of diseases like SADS, PEDV, SARS, MERS, and now COVID-19 strongly indicates a close association between CoVs that become pathogenic in humans and the wildlife reservoirs from which they originate [17, 50-54, 67]. The evolutionary relationships of CoVs within bats are consistent with geographically structured transmission cycles, with occasional transmission among related bat species [47, 58, 69]. These phylogeographic factors are also universal determinants of viral sharing among all mammals [70]. However, bat-virus association patterns can be particularly difficult to discern because bats often roost together in multi-species aggregations that can facilitate viral sharing, with each species capable of harboring multiple CoV lineages [47, 58, 68, 71]. Host shifts from bats to more divergent taxa are more difficult to predict -- firstly, because the potential host breadth for many CoVs is broad [55, 56, 60, 72],

196 and, secondly, because host susceptibility and onward transmission involve complex, multi-
197 stage processes [2, 12]. Bat-CoV associations likely remain substantially under-sampled and
198 understudied in temperate-zone North America [47, 71, 73, 74].
199
200 **Are Viruses like SARS-CoV-2 Already Present in North American Bats?**
201 Our examination of CoV evolutionary lineages and global distribution patterns of the diversity of
202 bat species they infect suggests that temperate-zone North American bats could be
203 immunologically naïve to infection by viruses like SARS-CoV-2. Alpha and β-CoVs have been
204 detected in bats on most continents, sometimes with both types occurring in bats of the same
205 species [58, 68]. However, an exception to this pattern is the lack of published evidence that β-
206 CoVs infect bats of temperate-zone North America, despite several search efforts which used
207 methods suitable to detect both α- and β-CoVs [59, 71, 74, 75]. Multiple novel α-CoVs have
208 been detected and described in vespertilionid bats of the US and Canada, infecting species
209 both living in close contact with humans and in remote wild areas [59, 71, 74-76]. However,
210 SARSr-CoVs and β-CoVs of the viral subgenus *Sarbecovirus* have thus far been detected
211 almost exclusively in species of the Old-World Chiropteran suborder Yinpterochiroptera (Fig.
212 1*A*, Table S1) [47, 58, 69]. The few exceptions to this pattern are the detection of novel Clade 3
213 and Clade 1 *Sarbecovirus* (*sensu* [53]) viruses in the Wrinkle-lipped Free-tailed Bat (*Mops*
214 *plicatus*, family Molossidae) in China [77] and the vespertilionid Leisler's Noctule (*Nyctalus*
215 *leisleri*) cohabiting a Bulgarian cave during autumn with several species of rhinolophids in which
216 other SARSr β-CoVs were concurrently detected, suggesting cross-species infections (Fig. 1 *A*)
217 [78]. Putative detections of a Clade 1 *Sarbecovirus* were also reported from guano samples of
218 the vespertilionid Brown Long-eared Bat (*Plecotus auritus*) and the molossid European Free-
219 tailed Bat (*Tadarida teniotis*) on Sardinia, where the same novel β-CoV was described in the
220 Greater Horseshoe Bat (*R. ferrumequinum*) [79].

Viruses in the β-CoV subgenera *Hibecovirus* and *Nobecovirus* also have been reported mostly from Old-World bat families Rhinolophidae, Hipposideridae, Rhinonycteridae, and Pteropodidae, except for novel viruses of the latter subgenus detected in four species of the vespertilionid genus *Scotophilus* in Asia and Africa (Fig. 1 *B* and *C*; Table S1) [47, 58, 69].

Bat β-CoVs of the subgenus *Merbecovirus* (MERS-related lineages) occur in a greater diversity of bat families and across more global regions than the other subgenera (Fig. 1 *D*) [47, 58, 69]. These widely distributed MERS-like viruses can cause disease in humans (e.g., MERS) and notably appear to be the only bat β-CoVs to diversify among several families of the globally distributed suborder Yangochiroptera (Fig. 1 *D*, Table S1) [47, 58, 69].

Lack of Evidence for β-CoVs in Temperate-zone North American Bats.

The several hundred species of extant bats spanning the Americas all belong to the suborder Yangochiroptera, which likely diverged from the Old-World suborder Yinpterochiroptera more than 50 million years ago (Fig. 2) [80]. The only β-CoVs detected in the Americas to date belong to the subgenus *Merbecovirus*, and appear restricted to two exclusively Neotropical bat families (Phyllostomidae and Mormoopidae) and one that is globally distributed (Molossidae). Distinct CoV lineages in the subgenus *Merbecovirus* were described from three species of *Pteronotus* (family Mormoopidae), four species of *Artibeus*, and Seba's Short-tailed Bat (*Carollia perspicillata*; family Phyllostomidae) from tropical regions of Mexico (Table S1) [47, 81]. Novel β-CoVs of the subgenus *Merbecovirus* were detected in two neotropical bat species of the family Molossidae: Wagner's Bonneted Bat (*Eumops glaucinus*) in southern Brazil and the Broad-eared Free-tailed Bat (*Nyctinomops laticaudatus*) in southern Mexico [81, 82]. *In vitro* infections have shown that primary kidney cells from the Jamaican Fruit-eating Bat *Artibeus*

246 *jamaicensis* can be infected with MERS-CoV, and virus replication and shedding was reported
247 in experimentally-infected bats of this species, but without obvious clinical signs of disease [83].
248 Similar to the evidence for natural invasion of bat rabies viruses among New World bats [84],
249 available evidence suggests β-CoVs may have arrived through South America and have long
250 been evolving in Neotropical bats. Although some bat hosts of *Merbecoviruses* overlap
251 geographically with species of temperate-zone North American bats, none occur outside of the
252 Neotropics. Sampling has been limited, but we are not aware of any published detections of
253 *Merbecoviruses* or any other β-CoVs in temperate-zone North American vespertilionid bats.
254
255 Our inference of true patterns of CoV occurrence and distribution in bat populations is limited by
256 uneven global sampling. Yet, SARSr-CoVs (*Sarbecovirus* spp), a focus of many surveillance
257 efforts, have been almost exclusively documented in Old-World Yinpterochiroptera. SARSr-
258 CoVs were only found in the ultra-diverse and globally distributed bat suborder Yangochiroptera
259 under conditions with plausible transmission from co-roosting *Rhinolophus* sp. bats [53, 85].
260 This absence of evidence for SARS-like β-CoVs in yangochiropteran bats in general, and in
261 temperate-zone vespertilionid bats of North America in particular, likely represents a unique
262 biogeographic pattern driven by underlying factors of host susceptibility or life history. These
263 observations also point to the susceptibility of vespertilionid bats under circumstances of
264 SARSr-CoV environmental exposure, and that they may not be naturally immune to these
265 viruses.
266
267 Bats rank among the most ecologically important mammals and play varied roles in most of
268 Earth's ecosystems; bats pollinate and disperse seeds of numerous plants in tropical regions,
269 and all over the world bats are primary nocturnal predators of flying insects [23, 24]. Across the
270 Holarctic, chiropteran species diversity is greatest among hibernating vespertilionid bats. At

least 25 of the ecologically diverse vespertilionid species of bats in the US and Canada hibernate [86], which might influence their susceptibility to or interactions with viruses, as has been postulated for common vespertilionids infected with α-CoVs and rabies virus [44, 87-89]. Hibernation strategies vary among species of bats (e.g., degree of sociality, thermoregulatory behaviors, habitat selection) [90], but bat body temperatures during hibernation generally remain consistently below 10ºC for periods lasting 7-9 months per year [91], providing a potential mechanism to limit viral replication and spread [92]. Experimental studies to assess the ability of SARS-CoV-2 or other β-CoVs to survive and replicate in bats (cell lines and individuals) at low temperatures [92, 93] would provide additional insight into risk of reverse zoonosis. However, appropriate tools for studying such possibilities are lacking, particularly immortalized cell lines from several hibernating, vespertilionid bats [59]. These tools would also enable interrogation of other physiological features of vespertilionids that may influence susceptibility, such as receptor-binding affinity and the expression of receptors across tissues. Scientists did not discover and isolate the obligately psychrophilic fungus that causes WNS until they collected samples in bat hibernation sites and moved culture dishes for incubation into laboratory refrigerators [25]. Similar innovative explorations outside the typical temperature conditions of laboratory experimentation could help assess risk of SARS-CoV-2 infecting the more than two dozen species of bats in the US and Canada that hibernate to survive harsh temperate-zone winters.

Proactively Connecting the Wellbeing of Human and Bat Populations.

Scientists have long recognized the risk of pathogen spillover from humans to bats [94-96], but bat researchers in North America have not systematically addressed this risk prior to WNS. Outside of reservoir host studies, few bat researchers studied infectious diseases in bats before WNS emerged in 2007 [73], nor studied bat viruses (other than rabies) before bats were

296 retrospectively connected to the SARS epidemic [15, 66, 97]. Fortunately, bat and wildlife
297 disease researchers recently began addressing these knowledge gaps in more detail [7, 97, 98].
298 Possible explanations for why bats might host particularly pathogenic viruses include
299 characteristics of their life history (e.g., long-lived, wide ranging, multi-species aggregations,
300 daily and seasonal heterothermy) [97], unique physiology for repairing their damaged DNA [99],
301 unique ability to suppress some of their innate immunity pathways [100-105], high species
302 diversity [48], and unmatched metabolic range and high body temperatures during flight [106].
303 Bats also cryptically come into close contact with humans, increasingly in urban and peri-urban
304 settings as a result of native habitat loss, often crossing human-wildlife interfaces [107-113].
305
306 Except for *Lyssavirus* infections, bats rarely show substantial signs of sickness from the same
307 pathogens that cause virulent disease in humans. Bats cope with viral infections in ways that we
308 do not yet fully comprehend but learning how they do so may reveal important insights to
309 develop therapeutics and ultimately to protect human health [103-105]. *In vitro* and laboratory
310 studies demonstrate that bats can specifically regulate naïve immunity pathways to effectively
311 cope with viral infection [114]. For example, dendritic cells generated from the bone marrow of
312 the Egyptian Rousette (*Rousettus aegyptiacus*) infected with Marburg virus downregulate
313 immune-stimulatory pathways and maturation of cells targeted by the virus, while upregulating
314 pathogen-sensing pathways [115]. Unique bat immune regulation may occur with MERS-CoV
315 infection, at least under experimental conditions [101]. Egyptian Rousette bats experimentally
316 challenged with SARS-CoV-2 by intranasal inoculation became transiently infected, shed virus,
317 and one co-housed bat became infected, but showed no clinical signs of disease other than
318 rhinitis [116]. Our potential lack of understanding of clinical signs of illness in bats and the
319 cryptic habits of many species also generally inhibit our ability to easily detect spillover of
320 pathogens from human to bat populations. This may add to uncertainty about cross-species

transmission and dispersal of CoVs among human and animal communities. Laboratory findings suggest human viruses that likely originated in bats, such as HCoV-NL63, are capable of infecting bat cells, at least *in vitro* [59]. SARS-CoV-2 and other CoVs have some of the longest genomes among all RNA viruses and despite having specialized RNA proofreading machinery [117, 118], they are still prone to recombination and copy errors in hosts, sometimes resulting in functional adaptations (e.g., altered receptor binding capacity or temperature adaptation of enzymes) [119]. CoVs can even recombine with functional fragments of other virus families, such as when a bat-derived CoV gained a functional gene from a reovirus [21]. Spillover of SARS-CoV-2 from infected humans to North American bats they handle or come in close contact with could lead to the virus becoming either less or more pathogenic to bats or other wildlife, domesticated animals, or humans through genetic mixing in one or more novel hosts. The public-health and conservation consequences of a more virulent virus could be severe, whereas genetic mixing in a bat host that resulted in a less-virulent virus might go unnoticed.

Need for an Interdisciplinary Response.

Effectively managing risks of human disease caused by emerging zoonotic pathogens *and* ensuring the health and conservation of wildlife species, that are potential reservoirs of those disease agents, can be synergistic goals under a One Health framework. Spillover risk (from or to wildlife) is often greatest in disturbed ecosystems where there is an elevated frequency of human-wildlife interactions or disruption of ecological patterns [3, 120-124]. Thus, effective bat conservation and management requires understanding both pathogens that cause disease in bats, as well as human activities and ecological contexts that increase direct and indirect interactions with bats that could present health risks [2]. Furthermore, fear-based reactions to disease risk from wildlife, such as culling infected bat populations or indiscriminate killing, often have negative unintended consequences for the interconnected health of both humans and bats

(e.g., culling of bats in a Uganda mine led to a more than doubling of Marburg virus prevalence in the bats living there) [30, 125-127]. Temperate-zone vespertilionid bats inhabiting human dwellings in the US and Canada represent a particularly relevant human-wildlife interface, where conservation and management actions to proactively address the potential consequences for pathogen spillover are worth careful consideration [73].

Conservation-compatible surveillance of bat viruses has demonstrated the potential for mutually beneficial collaboration between public health scientists and conservation stakeholders [94, 113, 125, 128, 129]. Disease-focused studies that integrate ecological principles into a rigorous study design provide the most informative context to interpret bat-virus associations and patterns of richness globally [130-132]. Assessing the risks of SARS-CoV-2 spillover into North American bats presents a timely opportunity to form multidisciplinary scientific teams that include experts on emerging infectious diseases and ecologists with expertise on North American bats [128]. Scientists researching emerging infectious diseases can benefit from sampling opportunities and methods that bat researchers have developed for observing, counting, and non-invasively sampling bats [73, 133]. Bat researchers can learn about human and animal health monitoring and supporting laboratory methods, including biosafety, secure handling/transport of CoV-positive samples, and training in the proper use of personal protective equipment (PPE) from professionals with expertise in veterinary and medical sciences [113, 131, 134, 135]. A shared goal of all stakeholders is to identify and implement simple, widely available diagnostic tests for detecting SARS-CoV-2 infection that are species-independent, practical for field and laboratory use, highly specific and sensitive, and that do not require strict biosafety containment [136]. All investigators can also work together to develop mutually beneficial goals, such as joint risk communications to the public with effective and balanced messaging about bat populations and higher risk activities for human-bat contact.

Adopting a precautionary approach in the face of global COVID-19 transmission among human populations, national and international wildlife organizations have advised limiting capturing and handling of bats in the field to minimize the risk of humans infecting wild bats with SARS-CoV-2 until further assessment can be made [137, 138]. The emergence of WNS in 2007 prompted a similar surge in interdisciplinary collaboration that enabled the rapid advances already mentioned and introduced changes to guidance for PPE use and disinfection practices for bat researchers and recreational cavers. Similarly, the emergence of SARS-CoV-2 and other viruses will likely alter the *status quo* of bat research, emphasizing the need to carefully weigh risks and benefits of wildlife research in the context of population-altering diseases. For example, PPE including respiratory protection is a standard practice adopted by many bat virus researchers, but by few others studying and regularly handling bats [134, 139]. The urgent research priority of a rapid, quantitative risk assessment and analysis of various mitigation options is currently underway [137, 140]. One key question is whether the proper use of optimal PPE, including bidirectional N95 or equivalent masks, along with effective risk communication and adherence to other basic biosafety practices [134, 141, 142] during field work, can significantly reduce the transmission risk of SARS-CoV-2 from humans to bats. In the interim, until new guidelines are established for handling and for close-proximity work with bats, we have outlined gaps in our understanding of SARS-CoV-2 spillover risks at the interface between humans, domesticated animals, and free-ranging wildlife. Temporarily shifting to 'hands-off' bat research methods also seems prudent, wherever possible, and could facilitate ongoing work with reduced risk.

Examples of 'Hands-off' Research Strategies.

Multiple research strategies that do not involve close contact with free-ranging bats already exist for addressing critical gaps in understanding CoV diversity, distribution, evolution, and potential health effects in temperate-zone bats. For example, a combination of host-cell receptor analyses and *in vitro* and *in vivo* experimental infections across a diversity of bat and other mammalian species have helped inform potential host range expansion for SARS-CoV-2. The receptors that many CoVs use to gain access to host cells, such as angiotensin-converting enzyme 2 (ACE2) and dipeptidyl peptidase-4 (DPP4/CD26), have undergone positive selection in bats, resulting in diverse and recombinant CoV strains [72, 143]. These strains can likely bind to numerous variants of a host receptor protein and facilitate spillover into other animal species [72, 144]. SARS-CoV-2 targets and strongly binds to mammalian ACE2 cell receptors [72, 145, 146]. Beta-CoVs of the subgenus *Merbecovirus* (like those known to occur in the Americas) are not known to target ACE2 cell receptors, instead using as a receptor DPP4/CD26 or possibly other receptors [53, 144]. Current *in silico* predictions that bats will likely have low susceptibility to SARS-CoV-2 based on ACE2 structural analyses conflict with *in vitro* evidence and do not comprehensively account for ACE2 amino acid sequence variation (including intraspecific variation) that occurs within bats [17, 72, 145]. Assessing SARS-CoV-2 host range will require additional virus-host receptor binding assays *in silico* and *in vitro* [17, 53, 72, 144, 145], together with future experimental infection studies for confirmation of Koch's postulates. In addition, *in vitro* studies could evaluate species variability in innate immune responses. These investigations will help quantify the potential for North American bat infection and transmission among free-ranging populations.

Examples of other 'hands-off' methods applicable to both bat disease and conservation research include: virus discovery and characterization focused on existing specimens archived in scientific museums or through partnerships and collaboration with established national bat

disease monitoring or surveillance programs [147, 148]; monitoring echolocation calls to determine the occurrence, distributions, and seasonal or nightly activity patterns of bats [133, 149]; digital imaging methods for counting bats and studying physiology and behaviors in the context of disease [90, 108]; sampling guano from below bat roosts to determine bat species and individual identity, population dynamics, and daily or seasonal patterns of bat occupancy and pathogen shedding [71, 150-152], and mathematical modeling to predict susceptible host species, virus sharing among hosts, spread patterns, or to estimate mortality in affected populations [5, 70, 122, 135]. Promising areas for innovation include making technologies for bat research more accessible to a broader global user base, less expensive, easier to use, and scientifically reproducible through open-source hardware, software, and laboratory methods [153, 154]. In addition to research, standardized field protocols and probabilistic sampling strategies are needed for monitoring bats and their viruses at continental scales (www.nabatmonitoring.org) [155, 156], as are longitudinal studies across multiple sites to better understand the ecological drivers of CoV dynamics and spillover [157]. Developing simple management tools and methods for rapidly assessing risks of virus spillover from humans to wildlife, while maintaining scientific rigor, could also help with future disease response. It might also be useful to prepare a suite of tools, protocols, and risk communication strategies for natural resource managers and public health officials to immediately deploy while risks are being assessed. Such prepared management resources could include public outreach material and guidelines for enhanced use of PPE for those in closest contact with potentially susceptible wildlife.

Conclusion.

Many questions remain about the risk of SARS-CoV-2 to naïve wildlife populations, the influences of human behavior on those risks, and the potential for establishment of new CoV

445 reservoirs. Cross-species virus transmission events are relatively rare, requiring an infectious
446 reservoir host to be in contact with a recipient host when conditions concurrently favor
447 susceptibility and onward transmission [12, 113, 114]. The currently unknown, but possible and
448 potentially high-consequence, risk of SARS-CoV-2 transmission and establishment in North
449 American bats (or other free-ranging mammals) warrants precaution [116, 140]. Strategically
450 managing interactions between people and potentially susceptible or at risk species can
451 decrease the probability of cross-species virus spillover [113]. Humans that frequently handle
452 and come into close contact with North American temperate-zone bats, such as bat
453 researchers, wildlife rehabilitators, wildlife/pest control workers, and disease investigators, can
454 help decrease any chances of spillover by adopting basic PPE and biosafety practices and
455 carefully evaluating how their actions might adversely affect bat populations. We are at a critical
456 nexus of biosecurity and natural resource conservation that will require ingenuity and diligence
457 to continue important research on bats whilst simultaneously evaluating the ecological future of
458 SARS-CoV-2. Our actions during this current pandemic could profoundly influence and protect
459 the health of both humans and wildlife in North America.
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Data Accessibility

Olival, K.J., P.M. Cryan, B.R. Amman, R.S. Baric, D.S. Blehert, C.E. Brook, C.H. Calisher, K.T. Castle, J.T.H. Coleman, P. Daszak, J.H. Epstein, H. Field, W.F. Frick, A.T. Gilbert, D.T.S. Hayman, H.S. Ip, W.B. Karesh, C. Kreuder Johnson, R.C. Kading, T. Kingston, J.M. Lorch, I.H. Mendenhall, A.J. Peel, K.L. Phelps, R.K. Plowright, D.M. Reeder, J.D. Reichard, J.M. Sleeman, D.G. Streicker, J.S. Towner, and L-F. Wang. 2020. Supporting Data Table 1 -- Possible risks of SARS-CoV-2 spillover from humans to free-ranging wildlife: a case study of bats: U.S. Geological Survey data release, https://doi.org/10.5066/P9U461PJ.

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959 **Figure Legends**

960

961 **Fig. 1.** Global patterns of bats and associated beta-coronaviruses (β-CoVs). (*A*) red-shaded
962 distributions of bat species in which SARS-related β-CoVs of the subgenus *Sarbecovirus* have
963 been detected; (*B*) pink-shaded distributions of bat species known to host β-CoVs of the
964 subgenus *Hibecovirus*; (*C*) brown-shaded distributions of bats in which β-CoVs of the
965 *Nobecovirus* lineage have been detected; and (*D*) green-shaded distributions of bats known to
966 host MERS-related β-CoVs of the subgenus *Merbecovirus*. Different colors and shade styles
967 within each panel represent different families of bats. See table S1 for species lists and data
968 sources and for the first identification of a β-CoVs in the subgenus *Embecovirus* in a bat. Maps
969 created using ArcMap (ESRI, Redlands, California, USA) and bat ranges derived from spatial
970 data on terrestrial mammals from the International Union for the Conservation of Nature (IUCN
971 2020. The IUCN Red List of Threatened Species. January 2019 [version 6.2].
972 https://www.iucnredlist.org; Downloaded on 11 April 2020).

973

974 **Figure 2. Old-World and New-World bats.** Overlapping species distribution outlines of bats in
975 the globally distributed suborder Yangochiroptera (blue) and Old-World Yinpterochiroptera
976 (yellow). Maps created using ArcMap (ESRI, Redlands, California, USA) and bat ranges derived
977 from spatial data on terrestrial mammals from the IUCN (International Union for the
978 Conservation of Nature (IUCN 2020. The IUCN Red List of Threatened Species. January 2019
979 [version 6.2]. https://www.iucnredlist.org; Downloaded on 11 April 2020).

Detailed Response to Reviewers -- COMMENTS FROM AUTHORS IN BLUE

Manuscript #PPATHOGENS-D-20-01177

Dear Dr. Olival,

Thank you very much for submitting your manuscript "Title - Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats

Short Title - Possibility for SARS-CoV-2 transmission from humans to free-ranging bats" for consideration at PLOS Pathogens. As with all papers reviewed by the journal, your manuscript was reviewed by members of the editorial board and by several independent reviewers. The reviewers appreciated the attention to an important topic. Based on the reviews, we are likely to accept this manuscript for publication, providing that you modify the manuscript according to the review recommendations.

Reviewer #1: This review discusses the possibility of SARS-CoV-2, now circulating worldwide, being introduced into naïve bat populations in North America. This is a prescient warning, as related beta-coronaviruses do not normally circulate in bats in this region of the world, therefore their accidental 'reverse zoonosis' into a new geographically-limited host population would have new implications for both disease in wildlife, and potentially the evolution of further SARS-CoV-2 variants with zoonotic potential. Both of these aspects are discussed thoroughly in the review, which covers strategies to mitigate the risk to bats of SARS-CoV-2 when doing field research on bats, as well as the necessary types of laboratory experiments and analyses required to understand the susceptibility of North American bats to SARS-CoV-2. The text is well written, and both authorative and informative. Furthermore, the figures are clear and visually appealing. The review will be of wide interest to those in the fields of zoonotic and pandemic infectious diseases, as well as bat researchers in general.

I have only one very minor point for the authors to check:

Lines 325-326: when referring to reference 101, is it fair to name SARS-CoV-2, as presumably the work in that manuscript did not include SARS-CoV-2?

Author Response: Thank you for catching this. We agree that SARS-CoV-2 should not be mentioned in this context and removed it from this sentence in the revision. An earlier version of the ms made general reference to lack of a strong immune response in bats during beta-coronavirus challenge experiments and cited the recent infection trial with the fruit bat *Rousettus aegyptiacus* and SARS-CoV-2:

> 116. Schlottau K, Rissmann M, Graaf A, Schön J, Sehl J, Wylezich C, et al. Experimental transmission studies of SARS-CoV-2 in fruit bats, ferrets, pigs and chickens. The Lancet. 2020. doi: https://dx.doi.org/10.2139/ssrn.3578792.

To recapture the prior point and update the revised manuscript with the latest published research, we also added the sentence:

> Unique bat immune regulation may occur with MERS-CoV infection, at least under experimental conditions [101]. **Egyptian Rousette bats experimentally challenged with SARS-CoV-2 by intranasal inoculation became transiently infected, shed virus, and one co-housed bat became infected, but showed no clinical signs of disease other than rhinitis [116]**.

Please note that we also added reference [116] to the Conclusion section and provided a new citation to a USGS risk assessment report now published as reference [140].

Reviewer #2: The review article addresses a relevant and timely topic that has not been reviewed before. It is well structured, well written and discusses available data and possible implications carefully. In only have a few minor points to address:

L.124: Please add a reference for the bat rabies lyssavirus distribution.

"Second, SARS-CoV-2 might infect and become established in one or more North American bat species, creating novel reservoirs capable of causing human infections (e.g., bat rabies lyssaviruses in the New World **[20]**)."

> 20. Banyard, A.C., A. Davis, A.T. Gilbert and W. Markotter. 2020. Bat Rabies. *In* Rabies: scientific basis of the disease and its management (Fooks, A.R. and Jackson, A.C. eds), Academic Press. Pp 231-276.

L.163-170: In my opinion, the text does not require so much detail on the Vespertilionidae family, e.g. the fact that they are "the only bat family to increase in diversity northward out of the tropics and consistently reach high latitudes" seems irrelevant to me regarding susceptibility of this family to a new pathogen. I suggest shortening of this paragraph.

We agree. The point of introducing the bat family Vespertilionidae here in such detail was to set up later findings and discussion about their historical isolation in North America. We hope the more concise revised version achieves this goal. The revision, shown here with text struck and additions in bold, now reads:

> The bat fauna spanning the higher latitudes of North America (in the US and Canada) is composed almost entirely of **endemic** species belonging to the ~~world's largest bat~~ family ~~–~~Vespertilionidae~~, with at least 500 described species [38]~~. Vespertilionid bats occur globally, but likely originated and diversified in North America tens of millions of years ago before dispersing to other continents~~ this second-largest family of mammals is the only bat family to increase in diversity northward out of the tropics and consistently reach high latitudes (50ºN)~~[39, 40]. No extant species of bat in the Americas also occurs outside of the Americas [41, 42], and no bats migrate across the Pacific or Atlantic

oceans [43, 44]. The WNS epizootic demonstrates that a large proportion of these historically isolated bats can be vulnerable to a pathogen introduced from another continent during a single event.

L.174-176: The sentence "The COVID-19 pandemic resembles WNS with respect to potential for pathogen spread through interconnected, multispecies populations" should be explained: Do the authors refer to WNS spread in bat populations or is there also evidence for spread in other animals? If it refers to bat populations is there evidence that SARS-CoV-2 has the potential to spread in multispecies bat populations? To me it was unclear what sort of populations the authors refer to.

We thank the reviewer for pointing out this ambiguity. Part of the problem was that we mistakenly referred to "…multi-species populations…" yet elsewhere always referred to populations in the single-species context. We also did not include any continent-specific wording to make our focus on potentially naïve bat populations of North America more apparent. Our intent was to raise the possibility that SARS-CoV-2 might have the potential to spread through multiple species (and genera) of co-occurring North American bats, as we have seen with the introduced pathogen that causes white-nose syndrome. Therefore, we revised the sentence to read:

> The COVID-19 pandemic resembles WNS with respect to potential ~~for~~ **spread of a** pathogen ~~spread~~ **from another continent** through interconnected, multi-species **assemblages of North American bats** that might be immunologically naïve, and highlights deficits in our understanding of temperate-zone bat pathogens in North America.

Board of Editors
PLoS Pathogens

15 June 2020

Dear Editors,

This letter accompanies our revised manuscript (#PPATHOGENS-D-20-01177) “Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: a case study of bats”.

We sincerely thank the editors and reviewers for their overall positive comments on our manuscript, and for considering it for publication in *PLoS Pathogens*. Guided by the very helpful, but relatively minor, reviewer comments we improved the article for this resubmission (**see attached response to reviewers for details**). A version of the manuscript showing all changes we made since submission, including improvements to the references cited section, is included with the revision package.

We hope that our revisions address the concerns raised and that our findings are now suitable for publication in *PLoS Pathogens*.

Thank you again for considering our manuscript.

Sincerely,

Kevin Olival and Paul Cryan

ecohealthalliance.org

cryanp

From: Peter Daszak ecohealthalliance.org>
Sent: Friday, May 29, 2020 1:57 PM EDT
To: Hayman, David ; Kevin Olival ecohealthalliance.org>; Wang Linfa < >; Paul Cryan ; Brian R. Amman ; Ralph S. Baric < ; David S Blehert Cara Brook >; Charles H Calisher ; Kevin Castle ; Jeremy Coleman >; epstein ecohealthalliance.org>; Hume Field ecohealthalliance.org>; Winifred F Frick, Ph.D. ; Gilbert, Amy T - APHIS >; Hon S Ip ; William B. Karesh ecohealthalliance.org>; Christine Kreuder Johnson >; Kading,Rebekah ; Tigga.Kingston Jeffrey M <jlorch >; Ian MENDENHALL PhD >; alisonpeel ; Kendra Phelps ecohealthalliance.org.test-google-a.com>; Plowright, Raina >; DeeAnn Reeder ; Jonathan D Reichard ; Jonathan M Sleeman ; Daniel Streicker ; Jonathan S. Towner
Subject: RE: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

OK folks, you know this is coming, but if PLoS don't like it, EID don't like it, and 2 or three others,*EcoHealth* will be delighted if you submit it there. We will pledge to review it and get it back to you within 3 weeks, and if reviewer's comments are addressed, we will include a color image of your choosing. We'll push Springer to make it available online for free as well. All this assuming it gets through review process. Also, as Editor-in-Chief, I'll be recused automatically from the review process, which is also Double-Blind.

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street
New York, NY 10001
USA

From: Hayman, David < >
Sent: Thursday, May 28, 2020 5:58 PM
To: Kevin Olival ecohealthalliance.org>; Wang Linfa Paul Cryan Brian R. Amman ; Ralph S. Baric >; David S Blehert >; Cara Brook ; Charles H Calisher ; Kevin Castle ; Jeremy Coleman >; Peter Daszak ecohealthalliance.org>; Jon Epstein < ecohealthalliance.org>; Hume Field ecohealthalliance.org>; Winifred F Frick, Ph.D. >; Gilbert, Amy T - APHIS ; Hon S Ip < ; William B. Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah >; Tigga.Kingston Lorch, Jeffrey M >; Ian MENDENHALL PhD >; alisonpeel Kendra Phelps ecohealthalliance.org.test-google-a.com>; Plowright, Raina >; DeeAnn Reeder ; Jonathan D Reichard ; Jonathan M Sleeman >; Daniel Streicker Jonathan S. Towner
Subject: Re: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Thanks Kevin.

If PLoS don't like it, it could interest Emerging Infectious Diseases as a Perspective.

Dave

From: Kevin Olival
Sent: Friday, May 29, 2020 08:38
To: Wang Linfa; Paul Cryan; Brian R. Amman; Ralph S. Baric; David S Blehert; Cara Brook; Charles H Calisher; Kevin Castle; Jeremy Coleman; Peter Daszak; Jon Epstein; Hume Field; Winifred F Frick, Ph.D.; Gilbert, Amy T - APHIS; Hayman, David; Hon S Ip; William Karesh; Christine Kreuder Johnson; Kading,Rebekah; Tigga Kingston; Lorch, Jeffrey M; Ian MENDENHALL PhD; alisonpeel ; Kendra Phelps; Plowright, Raina; DeeAnn Reeder; Jonathan D Reichard; Jonathan M Sleeman; Daniel Streicker; Jonathan S. Towner
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Latest version attached that has cleared CDC and USGS review. We will still aim to get this on BioRxiv, but wanted to wait until we had it cleared first and ideally in review at a journal.

Cheers,
Kevin

From: Hayman, David
Sent: Thursday, May 28, 2020 5:57 PM EDT
To: Kevin Olival < ecohealthalliance.org>; Wang Linfa ; Paul Cryan Brian R. Amman ; Ralph S. Baric ; David S Blehert ; Cara Brook ; Charles H Calisher ; Kevin Castle >; Jeremy Coleman >; Peter Daszak ecohealthalliance.org>; epstein ecohealthalliance.org>; Hume Field ecohealthalliance.org>; Winifred F Frick, Ph.D. >; Gilbert, Amy T - APHIS ; Hon S Ip ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson >; Kading,Rebekah >; Tigga Kingston ; Lorch, Jeffrey M >; Ian MENDENHALL PhD >; alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina >; DeeAnn Reeder ; Jonathan D Reichard Jonathan M Sleeman >; Daniel Streicker ; Jonathan S. Towner >
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From: Kevin Olival ecohealthalliance.org>
Sent: Friday, May 15, 2020 9:18 AM EDT
To: Paul Cryan >; Brian R. Amman >; Ralph S. Baric ; David S Blehert < Cara Brook >; Charles H Calisher ; Kevin Castle >; Jeremy Coleman >; Peter Daszak ecohealthalliance.org>; epstein ecohealthalliance.org>; Hume Field ecohealthalliance.org>; Winifred F Frick, Ph.D. ; Gilbert, Amy T - APHIS ; David Hayman >; Hon S Ip ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah ; Tigga Kingston ; Lorch, Jeffrey M ; Ian MENDENHALL PhD ; alisonpeel >; Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; DeeAnn Reeder ; Jonathan D Reichard >; Jonathan M Sleeman Daniel Streicker ; Jonathan S. Towner < ; Wang Linfa >
Subject: Re: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PNAS (new plan)
Attachment(s): "smime.p7m"

Dear all,

Quick update: We sent the paper in to*PNAS* as a potential Perspective piece yesterday, still waiting to hear back from editors. We'll keep everyone posted. Still waiting on some final clearance before we post to a pre-print server.

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
460 West 34th Street, Suite 1701
New York, NY 10001

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics *and* promote conservation

> On May 12, 2020, at 10:13 AM, Kevin Olival ecohealthalliance.org> wrote:
>
> Dear Co-authors,
>
> **Attached is the latest, submission ready version of our paper**"**Possible risks of SARS-CoV-2 spillover to free-ranging wildlife: a case study of bats**". Thank you all for the last round of invaluable edits and comments. Paul and I have now gone through multiple revisions since you last saw the paper in an attempt to include everyone's feedback; so apologize for the delay in turning this around and moving towards submission.
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> Also, for those that have secured USG approval already, please let me know if these needs to be updated or if you need any more information.
>
> This has been a fantastic exercise in group writing! Big thank you to everyone.
>
> Cheers,

Kevin

<Olival et al. bat CoVs 20200511_V9.1.docx>

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Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
460 West 34th Street, Suite 1701
New York, NY 10001

www.ecohealthalliance.org

From: Jon Epstein ecohealthalliance.org>
Sent: Tuesday, November 13, 2018 11:16 AM EST
To: Kading,Rebekah
CC: Stokes, Martha M. ; Katie Leahy ; Megan Hudson ; Kingston, Tigga
Subject: Re: thank you!

Thanks, Rebekah.
I'm glad you thought it was worthwhile. I thought it was really productive, too, and very glad to have you there.
I think Marty, Katie and Megan deserve most of the credit for how well the meeting worked out and the assembly of people, but I'm also giving special props to Tigga for her bat artistry skills (and scientific insight, of course... but mostly drawing :)).

Talk to you soon.

Cheers,
Jon

On Tue, Nov 13, 2018 at 10:35 AM Kading,Rebekah > wrote:

> Dear Marty, Katie, Megan, Jon, and Tigga -
>
> I just wanted to send a quick message to thank you for all your hard work on our BOHRN meeting last week! I know that took an amazing amount of coordination to get so many more people there, and I thought it was a very productive time! It was nice to have formal talks from some folks, and the white paper exercise was a great way to get people working together. I appreciate all the time and energy you each put into BOHRN -- it is a unique group with an important purpose and I am excited about the trajectory we are on so far! I'll look forward to touching base again soon about planning the Uganda meeting in the spring.
>
> Take care and have a great week -
>
> Best regards,
> Rebekah
>
> **Rebekah C. Kading, PhD**
>
> Assistant Professor
>
> Department of Microbiology Immunology and Pathology
>
> Colorado State University

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street, Ste. 1701

New York, NY 10001

web: ecohealthalliance.org

From: Kevin Olival, PhD ecohealthalliance.org>
Sent: Monday, May 15, 2017 8:57 AM EDT
To: Leahy, Catharine (US) < Mary J. Lancaster Ph.D. ; Martha M CIV Stokes ; Sander, William E CTR (US) Joram Buza ; Vivek Kapur Jon Epstein ecohealthalliance.org>; gavin.smith < ; Ian MENDENHALL PhD ; kityrob ; Devaney, Caitlin (US) ; Kading,Rebekah <
Subject: Re: UPDATE: Global Bat Alliance Network (convened on behalf of CBEP)

Dear all,

As mentioned, here is Tigga's book chapter on global bat conservation networks that I mentioned. The chapter is available for free download, as is the whole book!

http://link.springer.com/chapter/10.1007%2F978-3-319-25220-9_17

Cheers,
Kevin

Kevin J. Olival, PhD
Associate Vice President for Research

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

www.ecohealthalliance.org

> On May 15, 2017, at 7:00 AM, Leahy, Catharine (US) > wrote:
>
> <Bat meeting notes 9Feb2017.docx>

From: GSE Events >
Sent: Friday, May 22, 2020 12:51 PM EDT
To: kityrob ; abelwade >; epstein ecohealthalliance.org>; Tigga.Kingston ; Kading,Rebekah spwa >; ian.mendenhall

CC: Stokes, Martha M CIV (USA) >; Jamechia Hoyle >; Katie Leahy Aleman, Nicki D CTR DTRA COOP THRT REDUCT (USA)

Subject: Re: World One Health Congress and BTRP TRN Side Meeting - BOHRN

Dear BOHRN TRN Steering Committee Members,

We hope you have been able to remain safe during these times and that this email finds you well. As you may already know, the World One Health Congress has been rescheduled to take place on October 30 - November 3 in response to worldwide travel restrictions and to coincide with International One Health Day on November 3rd. We wanted to inform you that the BTRP TRN side meetings have been rescheduled in tandem with the Congress, now aiming to take place on November 3 - 4. This is a change we are trying to implement, however, we understand the current scope of world events and anticipate further changes as we go forward. Our utmost priority is everyone's safety and we will continue to monitor the situation to act accordingly. We will be sure to keep you informed of all updates.

Please let us know if you have any questions and stay safe.

Kind Regards,

GSE Logistics Team

Global Systems Engineering, LLC
A Certified HUBZone Company
www.globalsyseng.com

From: Caitlin Devaney
Date: Tuesday, March 10, 2020 at 2:30 PM
To: "kityrob " , "abelwade " < , "epstein " "Tigga.Kingston " >, "Rebekah.Kading " >, "spwa " >, "ian.mendenhall
Cc: "Stokes, Martha M CIV (USA)" , Jamechia Hoyle , Katie Leahy >, Megan Hudson "Aleman, Nicki D CTR DTRA COOP THRT REDUCT (USA)"
Subject: World One Health Congress and BTRP TRN Side Meeting - BOHRN

Dear BOHRN TRN Steering Committee Members,

On behalf of Dr. Martha Stokes, please accept this Save the Date to attend the World One Health Congress in Edinburgh, Scotland 15-17 June 2020 and participate in side meetings on BTRP's Threat Reduction Networks and planning for BOHRN.

Tentatively, we plan to hold two sessions at the end of the week: Thursday, 18 June - an afternoon TRN session that will include a wide group of BTRP-funded participants from its other research networks to discuss network metrics for sustainability; Friday, 19 June - a side meeting for BOHRN to map out its schedule and strategy, aligning with funding opportunities from BTRP and other entities. Attached is a tentative schedule for the week, for your reference. Due to travel and budgetary constraints we are unable to invite the entire steering committee, but intend to have productive discussions and meet objectives with the smaller group on this Save the Date email.

Please let us know if you will be able to attend the WOHC and side meetings on 18-19 June. Official invitation with travel instructions, details on arrangements, and more formal agenda will be forthcoming. Please note that there is a potential for the WOHC and BTRP side meetings to be postponed, given the current travel uncertainties related to COVID-19. We will be monitoring the status of the conference, and will keep you apprised of any cancellations should they occur. As always, let us know if you have any questions!

We hope to see you in Edinburgh!!

V/r,
Caitlin Devaney

CAITLIN DEVANEY | ***Program Manager***
Global Systems Engineering, LLC

From: Kingston, Tigga >
Sent: Friday, May 22, 2020 1:48 PM EDT
To: Kading,Rebekah >; GSE Events ; kityrob >; abelwade >; epstein ecohealthalliance.org>; hotmail.com ian.mendenhall
CC: Stokes, Martha M CIV (USA) ; Jamechia Hoyle Katie Leahy ; Aleman, Nicki D CTR DTRA COOP THRT REDUCT (USA)

Subject: RE: World One Health Congress and BTRP TRN Side Meeting - BOHRN

That's a great idea Rebekah!

From: Kading,Rebekah
Sent: Friday, May 22, 2020 12:32 PM
To: GSE Events >; kityrob ; abelwade epstein ecohealthalliance.org>; Kingston, Tigga >; spwa ; ian.mendenhall

Cc: Stokes, Martha M CIV (USA) ; Jamechia Hoyle >; Katie Leahy ; Aleman, Nicki D CTR DTRA COOP THRT REDUCT (USA) >
Subject: Re: World One Health Congress and BTRP TRN Side Meeting - BOHRN

Greetings everyone! Thank you for the update - I will stay tuned to see how the situation unfolds. I am available on those dates should that work out. We could try a Zoom meeting sometime in the interim, if that would be helpful to get everyone "together"? I know many BOHRN members have been collaborating and contributing to the pandemic response in a variety of ways, which I think represents some successful grassroots mobilization of the network. Might be encouraging to have something of a group call to hear about what folks have been up to and if there's anything we can band together more formally to accomplish despite being scattered. Just an idea to throw out there!
Kind regards,
Rebekah

Rebekah C. Kading, PhD

Assistant Professor

Department of Microbiology Immunology and Pathology

Colorado State University

From: GSE Events
Sent: Friday, May 22, 2020 10:51 AM
To: kityrob < ; abelwade ; epstein ecohealthalliance.org>; Tigga.Kingston >; Kading,Rebekah ; spwa ; ian.mendenhall

Cc: Stokes, Martha M CIV (USA) Jamechia Hoyle ; Katie Leahy ; Aleman, Nicki D CTR DTRA COOP THRT REDUCT (USA)
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Note: This email and any attachments may contain confidential or proprietary information.
If you are not the intended recipient, any use or distribution is prohibited; please notify the sender and delete from your system.

From: Prof. Joram Buza >
Sent: Monday, May 15, 2017 12:02 PM EDT
To: "Kevin Olival, PhD" ecohealthalliance.org>
CC: "Leahy, Catharine (US)" < ; Mary J. Lancaster Ph.D. <
Martha M CIV Stokes >; "Sander, William E CTR (US) ("
; Vivek Kapur ; Jon Epstein ecohealthalliance.org>;
gavin.smith ; Ian MENDENHALL PhD <
kityrob "Devaney, Caitlin (US)" <
Kading,Rebekah
Subject: Re[2]: UPDATE: Global Bat Alliance Network (convened on behalf of CBEP)

Dear Kevin
Thanks for sharing.

Buza

--
Sent from Gmail Email App for Android

Monday, 15 May 2017, 03:57PM +03:00 from Kevin Olival, PhD ecohealthalliance.org:

> Dear all,
>
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> Cheers,
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> **Kevin J. Olival, PhD**
> *Associate Vice President for Research*
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> EcoHealth Alliance
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> www.ecohealthalliance.org
>
> *EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.*
>
> On May 15, 2017, at 7:00 AM, Leahy, Catharine (US) wrote:
>
> <Bat meeting notes 9Feb2017.docx>

From: Aleksei Chmura ecohealthalliance.org>
Sent: Sunday, August 30, 2020 6:26 PM EDT
To: Kading,Rebekah
CC: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance
Attachment(s): "2020 Research Scientist and Project Manager Job Ad.pdf"

Dear Dr. Kading,

We just interviewed Anna Fagre for a position here at EcoHealth Alliance as a Research Scientist and Project Manager. Our hiring committee thought she was terrific with the right background and attitude for our team. Anna listed you as a reference. If you would be willing to send some comments about Anna, that would be terrific!

I have attached our position advertisement, so you may know more about the position - though based on her skillset, the specifics would evolve a bit. This position would focus primarily on our emerging infectious disease projects based in Southeast Asia including our recently awarded, NIAID funded EID-SEARCH program:

- https://www.ecohealthalliance.org/program/south-east-asia-research-collaboration-hub

I look forward to your reply and should a phone call be more convenient, we could do that as well.

On behalf of our whole committee, I sincerely appreciate your time.

-Aleksei

Aleksei Chmura, PhD
Chief of Staff

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-4182

)
www.ecohealthalliance.org

EcoHealth Alliance

JOB ADVERTISMENT

POSITION TITLE: Research Scientist and Project Manager

POSITION SUMMARY

Reporting directly to the President, the Research Scientist will assist senior research scientists on our NIH-funded and projects to examine the dynamics of pathogen transmission within and among wildlife populations, livestock, and humans; as well as the risk of spillover, patterns of infection, phylogenetic relationships of emerging zoonotic diseases. The candidate should be self-motivated and proactive. The Research scientist will need to have a collaborative approach to research, a positive attitude towards solving complex problems, and creativity. This position is a critical part of our science base and the will actively and collaboratively engage in expanding the boundaries of our research as well as help create our 'think-tank' on emerging infectious diseases. Above all, a passion for understanding the process of zoonotic disease emergence is key.

RESPONSIBILITIES

- Collaborate and/or lead in the design and implementation of a multi-country field study of zoonotic disease emergence from bats, rodents, and primates as well as the role of human behavior in disease emergence and analyze the resulting data. Extensive foreign travel, particularly in southeast Asia will be expected.
- Work on modeling and other projects that broadly integrate evolutionary, ecological, and biodiversity data into emerging disease and zoonotic disease models.
- Liaise with EcoHealth Alliance and other scientists to generate hypotheses and to assist with development of models and plan avenues of scientific investigation
- Engage with EcoHealth Alliance scientists and consortium partners on our other projects as well as on federally funded programs on AI, Ebola, Nipah, RVFV, and other emerging diseases.
- Work closely with the President, science staff, and collaborators to design and execute analytical projects to understand the process of zoonotic disease emergence including examination of the roles of host-specific and evolutionary drivers of disease emergence.
- Represent EcoHealth Alliance and work with stakeholders and collaborators at local, national, and international levels.
- Manage Staff, liaise with international partners, and report proactively to funders
- Assist with grant and manuscript writing
- Be responsible for grant management and program coordination
- Use a strong fact basis and collaborative approach to formulate alternative and creative solutions to problems and sensitive issues.

QUALIFICATIONS

- Minimum of Ph.D. in: Biology, Ecology, Evolutionary Biology, Public Health, or related field in the life sciences
- Strong quantitative analytical skills
- Experience with statistical analyses, particularly using R
- Experience with phylogenetic and evolutionary analyses a plus.
- Previous experience in public health or infectious diseases
- Previous experience writing grants and with international grants and program administration of large projects with key components including field and laboratory work and analyses
- 1-to-3 years' experience working on projects funded by US Federal agencies as well as prior non-profit, academic, or equivalent positions
- Demonstrated writing and research skills including Publications in peer-reviewed scientific journals
- Ability to conduct literature reviews, data collation and cleaning, and exploratory data analyses
- Strong writing and verbal communication skills with a keen eye for detail
- Proven ability to work independently
- Self-driven, highly motivated, organized, and willing to perform research and administrative duties
- Strong interpersonal skills; a willingness to place team before self and a strong sense of diplomacy
- Previous experience in Southeast Asia is a plus
- Cultural sensitivity
- Willingness to work some mornings, evenings, weekends as necessary
- Fluency in written and spoken English required

At EcoHealth Alliance, our vision is a workplace with a diverse and talented staff where people want to come, to stay, do their best work, and grow. We recruit, employ, train, compensate and promote our staff without regard to race, ethnicity, color, religion, gender, gender identity or expression, sexual orientation, national origin, disability, age, veteran status, or socioeconomic status. This position is based at EcoHealth Alliance in New York City and will entail extensive domestic and international travel. EcoHealth Alliance offers a competitive salary and a comprehensive benefit package including health, dental, and vision coverage, and a 403(b) pension plan. EcoHealth Alliance is proud and deeply committed to being an equal opportunity employer. For further information about EcoHealth Alliance, please visit our website: www.ecohealthalliance.org.

HOW TO APPLY

Send an email with a *single* attachment in PDF format containing (a) a cover letter, (b) CV, and (c) three references to jobs@ecohealthalliance.org with "**2020 RESEARCH SCIENTIST AND PROJECT MANAGER JOB APPLICATION**" in the subject line. If you would like to be considered for more than one job position, please indicate that in your cover letter and list your order of preference. Emails without the subject line or with multiple attachments will not be reviewed. No formal text is required within the body of your email, since emails will not be evaluated. All inquiries will receive an automatic response confirming receipt. *Only* appropriately qualified candidates will be contacted. Closing date for this position: 15th July 2020.

Thank you for your interest in EcoHealth Alliance!

From: Megan Hudson <
Sent: Tuesday, February 26, 2019 2:00 PM EST
To: nisreen.hmoud ; joram.buza
tigga.kingston ; kityrob >; spwa
; abelwade >; wanda.markotter
; pilotdovih ; abubasha
; meryem.lemrani >; wava
; c_demetria < ; paalviola
>; phelps ecohealthalliance.org>; epstein
; Kading,Rebekah >; sara.b
; sarabumrungsri ; julianas
; wiantoro >; benjamin_lee
>; lisamariep ; pipat
>; vudinhthong ; iroro.tanshi
>; benneth.obitte ; jjlutwama
; jit ; astghik.ghazaryan
ioseb.natradze >; ksidamonidze < ;
mariano.sanchez-lockhart.ctr >; farlowscience
; payscue >; bbrooks
; docshusmitadutta shahanajshano
>; aril ecohealthalliance.org>; eric.laing.
; stsang ; bhbird
ahandel ; tgoldstein <
CC: Stokes, Martha M CIV (USA) ; Becker, Stephen M CTR DTRA J3-7 (US)
; Katie Leahy >
Subject: Reminder: Bat One Health Research Network Survey

All,

As a reminder, please take a few moments to answer the following questionnaire. This survey will help us to identify BOHRN's efforts and progress towards its overarching goals and evaluate the networks threat reduction efforts. Please follow the link and complete the survey no later than 28 February: https://www.surveymonkey.com/r/6FQPQR3

Regards,

Megan

From: Megan Hudson >
Date: Wednesday, February 20, 2019 at 12:00
To: "nisreen.hmoud >, "joram.buza " < ,
"tigga.kingston " , "kityrob " , "spwa "
, "abelwade " , "wanda.markotter
, "pilotdovih " , "abubasha
, "meryem.lemrani " , "wava "
, "c_demetria " < , "paalviola
, "phelps ecohealthalliance.org>,
"epstein >, "rebekah.kading
>, "sara.b " < , "sarabumrungsri
, "julianas , "wiantoro "
, "benjamin_lee , "lisamariep "
, "pipat66 >, "vudinhthong "
, "iroro.tanshi , "benneth.obitte
, "jjlutwama , "jit8 "
"astghik.ghazaryan "ioseb.natradze "
, "ksidamonidze , "l.urushadze
>, Katie Leahy < >, Megan Hudson
>, Chris Russell , Jason Hudson
"mariano.sanchez-lockhart
"farlowscience " , "payscue "
"bbrooks " "docshusmitadutta " ,
"shahanajshano " >, "aril ecohealthalliance.org>,
"eric.laing.ctr , "stsang >, "bhbird
, "ahandel " "tgoldstein
Cc: "Stokes, Martha M CIV (USA)" , "Becker, Stephen M CTR DTRA J3-7 (US)"
Katie Leahy >
Subject: Bat One Health Research Network

Dear all,

On behalf of Dr. Marty Stokes, please find the final report for the BOHRN Workshop in Vienna.

As discussed in Vienna, there are several action items for the BOHRN network. In order to move forward on several of these items, we ask that you take a few moments to answer the following questionnaire. This survey will help us to identify BOHRN's efforts and progress towards its overarching goals and evaluate the networks threat reduction efforts. Please follow the link and complete the survey no later than 28 February: https://www.surveymonkey.com/r/6FQPQR3

Additionally, please use the following Drop Box link for access to the BOHRN Workshop participant list with pictures and the quad charts submitted by all participants. You may also access the video of the BOHRN Workshop here.

We had hoped to make a more formal announcement regarding solicitation for BOHRN special projects around this time; however, BTRP is internally still reviewing necessary criteria for award and will not be ready to make a more formal announcement until the April / May timeframe. The announcement will be released via the www.bohrn.net website.

Please let us know if you have any questions or concerns.

Kind Regards,

Megan

Megan Hudson
Project Lead | Global Systems Engineering

From: Megan Hudson
Sent: Monday, September 10, 2018 9:44 AM EDT
To: cryanp ; epstein ecohealthalliance.org>; Kading,Rebekah ; vkapur ; tigga.kingston ; olival ecohealthalliance.org>; raina.plowright >; c demetria
CC: Stokes, Martha M CIV (US) ; Katie Leahy < ; Aleman, Nicki D CTR DTRA PARTNERSHIP AND INSP (US) ; Becker, Stephen M CTR DTRA J3-7 (US)
Subject: Reminder: BOHRN November IMED Meeting Invitation

All,

As a reminder, please respond NLT **14 September** if you are able to attend the BOHRN/IMED Meeting in Vienna on 8-12 November 2018. The BOHRN meeting will be held 8-9 November.

We are looking for nominations to grow the BOHRN network, please send any nominations of subject matter experts or other participants who would be beneficial to this discussion **no later than Today, 10 September 2018**.

IMED will take place 9 – 12 November at the Hilton Vienna. The 2018 IMED will focus on innovation and changes in political and societal responses to outbreaks. The theme of IMED aligns with our overall BOHRN objectives and we encourage all BOHRN members to stay and participant in the conference.

We need you to confirm your attendance to BOHRN and IMED NLT 14 September.

v/r,

Megan

Megan Hudson
Task Lead | Global Systems Engineering
6303 Little River Turnpike #208
Alexandria, VA 22312

http://globalsyseng.com

Travel instructions:
Please contact Nicki Aleman **NLT 14 September 2018** if you intend to travel; you will likely need to provide her with your passport information, to and from destinations, and travel dates. CBEP's logistics support coordinators will work with you to secure plane reservations. Please note that they try to work with your preferences, but must remain within the boundaries of the Department of Defense regulations for travel.

From: Megan Hudson
Date: Thursday, September 6, 2018 at 10:54
To: "cryanp " , "epstein ecohealthalliance.org>, "rebekah.kading , "vkapur , "tigga.kingston olival ecohealthalliance.org>, "dreeder " , "raina.plowright " >, "ian.mendenhall , "c_demetria

Cc: "Stokes, Martha M CIV (US)" , Katie Leahy , "Aleman, Nicki D CTR DTRA PARTNERSHIP AND INSP (US)" "Becker, Stephen M CTR DTRA J3-7 (US)"
Subject: BOHRN November IMED Meeting Invitation

All,

On behalf of Dr. Marty Stokes you are receiving this email, as part of a save the date to attend our BOHRN Steering Committee meeting and International Meeting on Emerging Diseases and Surveillance (IMED) 8 – 12 November 2018 in Vienna, Austria.

Our meeting will take place on 8 – 9 November (hotel/meeting location TBD). The BOHRN steering committee meeting will aim to meet the objectives the group identified in Saskatoon. The following objectives were suggested based on your survey responses:

1. Prioritizes funding needs based on working groups' characterization of gaps and needs, to help organize and develop funding initiatives; and
2. Analyze progress of action plans and their yields establishing collaborate and sustainable projects

To facilitate these objectives, we will be asking each working group to present their progress. The progress updates for each working group are imperative to the outcomes for this meeting.

As discussed during the June BOHRN meeting, an objective of this meeting is to develop our outreach and populate working groups. Please send any nominations of subject matter experts or other participants who would be beneficial to this discussion **no later than 10 September 2018**.

IMED will take place 9 – 12 November at the Hilton Vienna. The 2018 IMED will focus on innovation and changes in political and societal responses to outbreaks. The theme of IMED aligns with our overall BOHRN objectives and we encourage all BOHRN members to stay and participant in the conference. **Therefore, we need you to confirm your attendance to BOHRN and IMED NLT 14 September.**

v/r,

Megan

Megan Hudson
Task Lead | Global Systems Engineering
6303 Little River Turnpike #208
Alexandria, VA 22312

http://globalsyseng.com

Travel instructions:
Please contact Nicki Aleman **NLT 14 September 2018** if you intend to travel; you will likely need to provide her with your passport information, to and from destinations, and travel dates. CBEP's logistics support coordinators will work with you to secure plane reservations. Please note that they try to work with your preferences, but must remain within the boundaries of the Department of Defense regulations for travel.

From: Grant, Evan H <
Sent: Wednesday, April 22, 2020 3:38 PM EDT
To: Gilbert, Amy T - APHIS ; Kevin Castle < ; Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) ; epstein ecohealthalliance.org>; dreeder ; Daniel Streicker >; Kading,Rebekah ; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) < ; Plowright, Raina >; wfrick ; a.peel >; Christine Kreuder Johnson
CC: Runge, Michael C >; Coleman, Jeremy T >; Sleeman, Jonathan M >
Subject: Results from Rd2 estimates and invitation to a Zoom presentation on the results of the analysis
Attachment(s): "SARSCoV2 Round2 Draft2.pdf"

Hi Expert team,
Thank you so very much for contributing to this assessment, on short notice, and using a process which may have been unfamiliar. Mike and I appreciate your contributions. We also learned a lot from the discussion that has helped us better understand the elements of transmission and infection that will drive the ultimate outcome.

Here I attach the revised distributions for each of the questions, following the discussions we had and your updated estimates. There was considerable revision in your estimates, which came in part from the median estimates but also a revision of the boundary limits and confidence. There remains significant uncertainty, which is expected given the emerging nature of this pathogen. These estimates were useful in estimating the risk of transmission to North American bat populations. We would have been unable to accomplish this without your expert judgement.

We are presenting these results this coming Friday, and cordially invite you to attend. Below please find the instructions to login to the presentation, hosted by Jonathan Mawdsley of the Association of Fish and Wildlife Agencies.

Kindest regards,
Evan and Mike

You are cordially invited to a Zoom presentation on the topic:

North American Bats and SARS-CoV-2: A Rapid Assessment of the Risk of Reverse Zoonotic Transmission

Authors:

Michael C. Runge, Evan H. Campbell Grant, U. S. Geological Survey Patuxent Wildlife Research Center

Jeremy T. H. Coleman, US Fish and Wildlife Service, National White-nose Syndrome Coordinator

Jonathan M. Sleeman, US Geological Survey, National Wildlife Health Center

FRIDAY, APRIL 24th, 2020, 1:00 PM – 2:30 PM Eastern

Jonathan Mawdsley is inviting you to a scheduled Zoom meeting.

Join Zoom Meeting
https://zoom.us/j/93063465687?pwd=dEV5ZGJ2WUttdjdBZmpzeWdsMnBVZz09

Meeting ID: 930 6346 5687
Password: 015861
One tap mobile
+16465588656,,93063465687#,,#,015861# US (New York)
+13126266799,,93063465687#,,#,015861# US (Chicago)

Dial by your location
+1 646 558 8656 US (New York)
+1 312 626 6799 US (Chicago)
+1 301 715 8592 US
+1 346 248 7799 US (Houston)
+1 669 900 9128 US (San Jose)
+1 253 215 8782 US

Meeting ID: 930 6346 5687
Password: 015861
Find your local number: https://zoom.us/u/acqLXCbB5b

Elicitation Results: Round 2

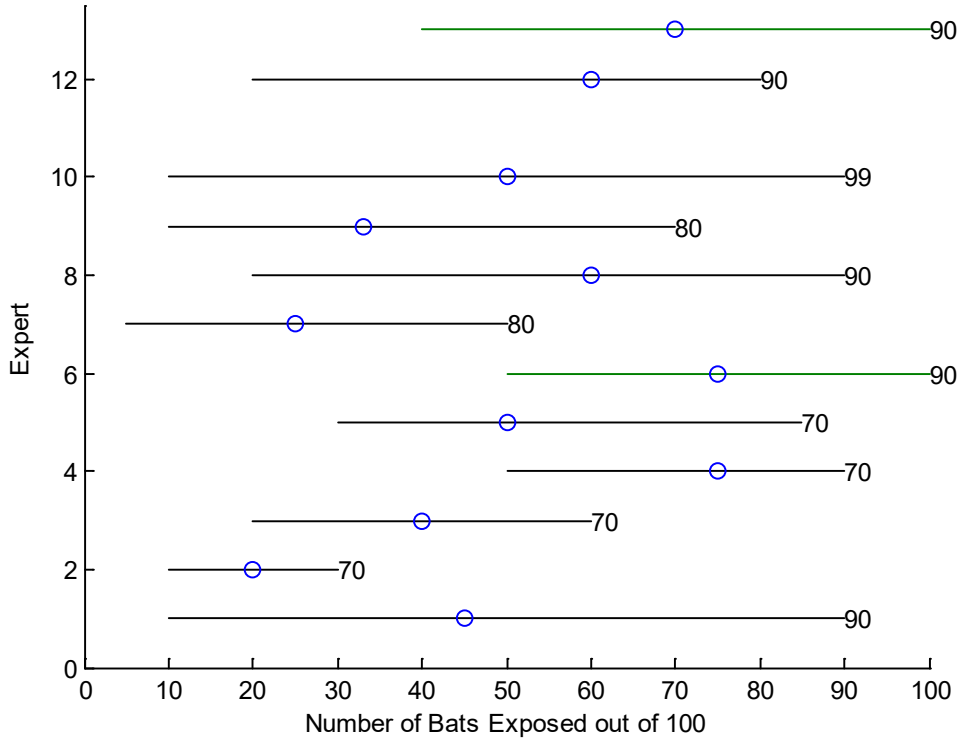
SARS-CoV-2 in North American Bats

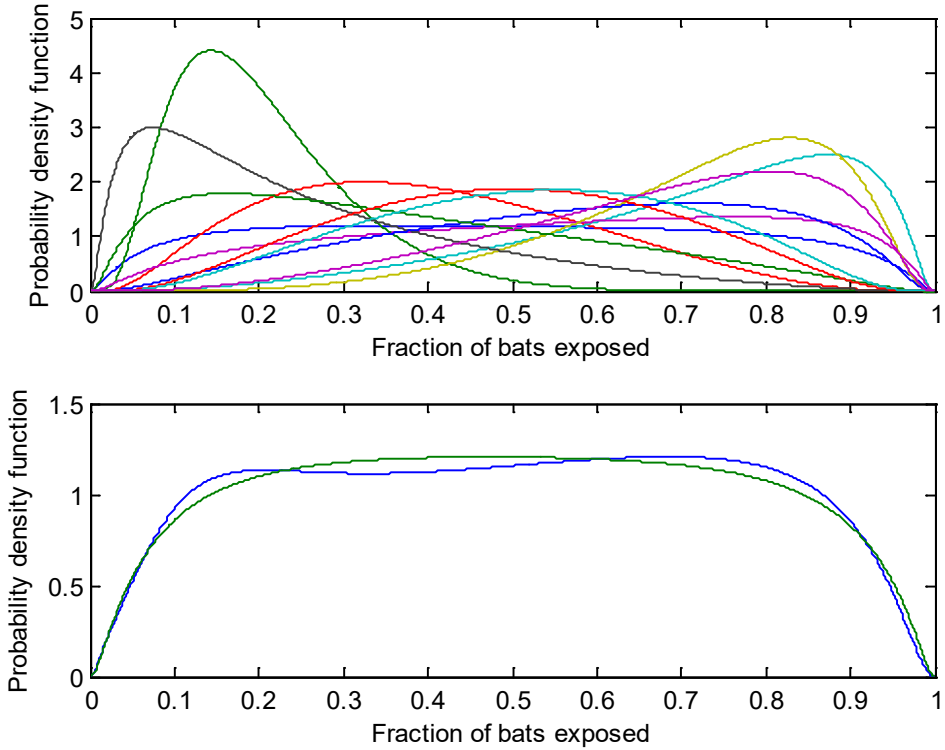
A Rapid Decision and Risk Assessment

April 22, 2020

PRELIMINARY RESULTS—NOT FOR DISTRIBUTION

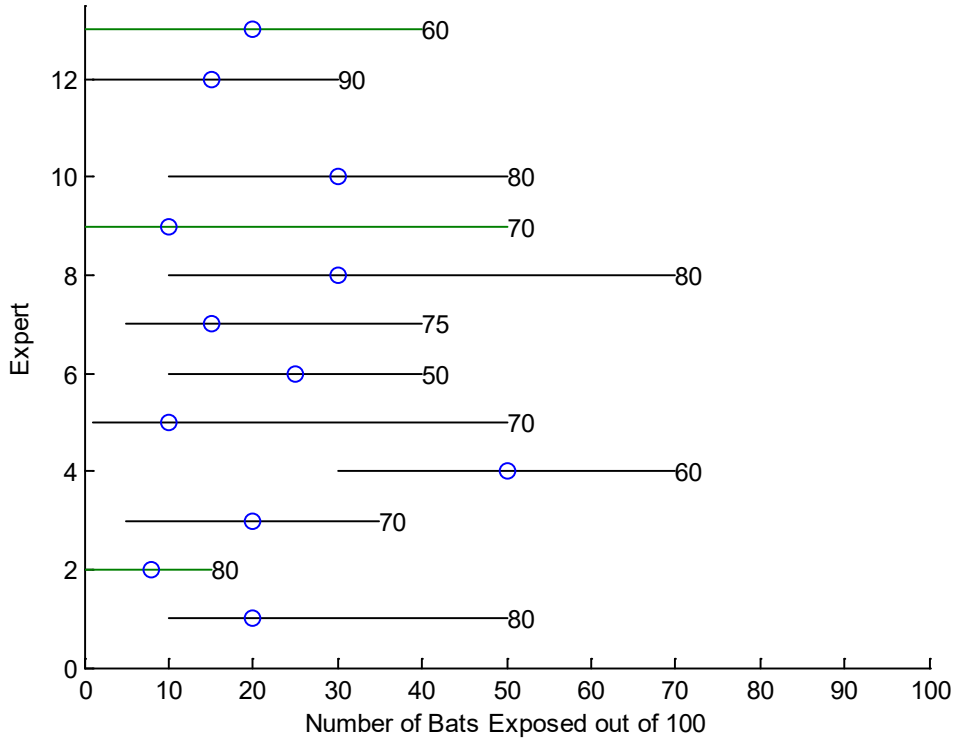
Q1 Exposure, RSM, handling

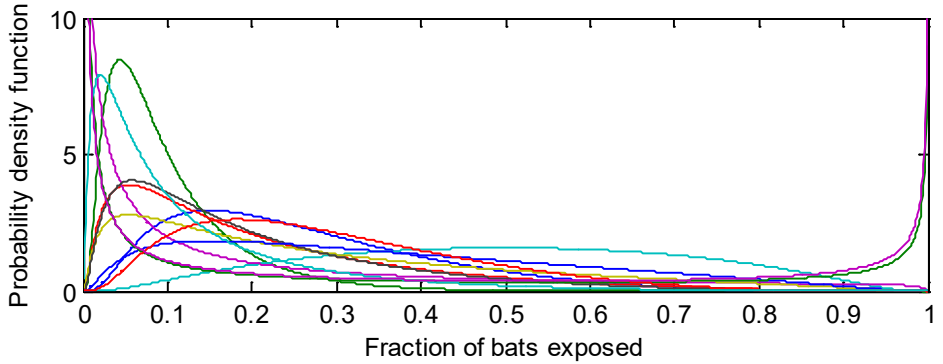


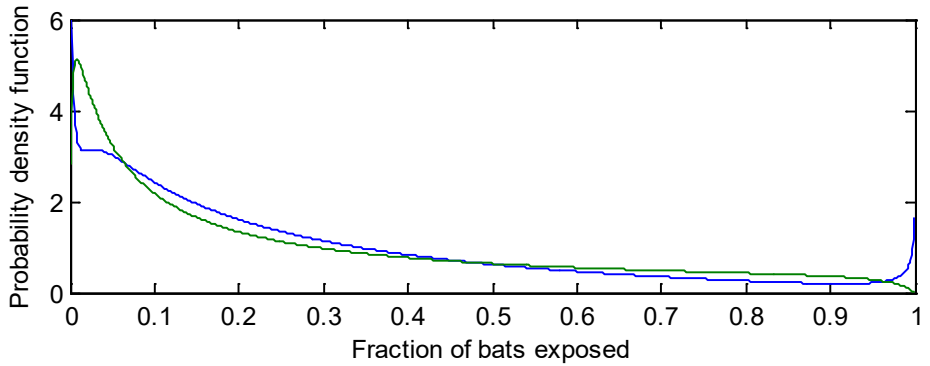


Aggregate estimate: 49.7 (15.3, 84.3)
(median, with 80% CI)

Q2 Exposure, RSM, enclosed

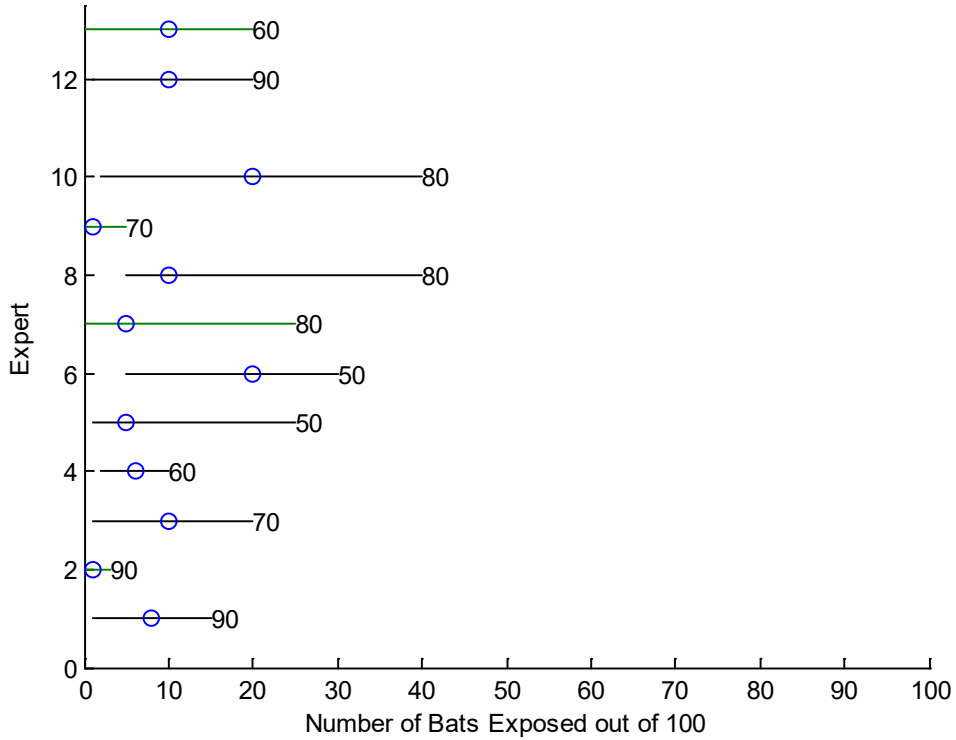


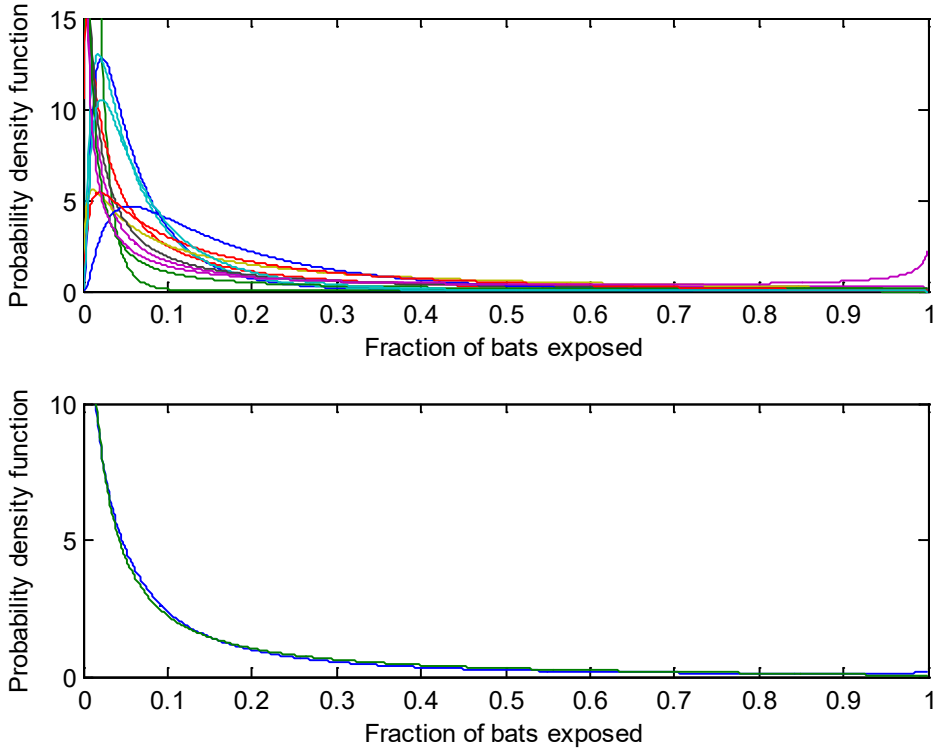




Aggregate estimate: 19.4 (2.2, 72.4)
(median, with 80% CI)

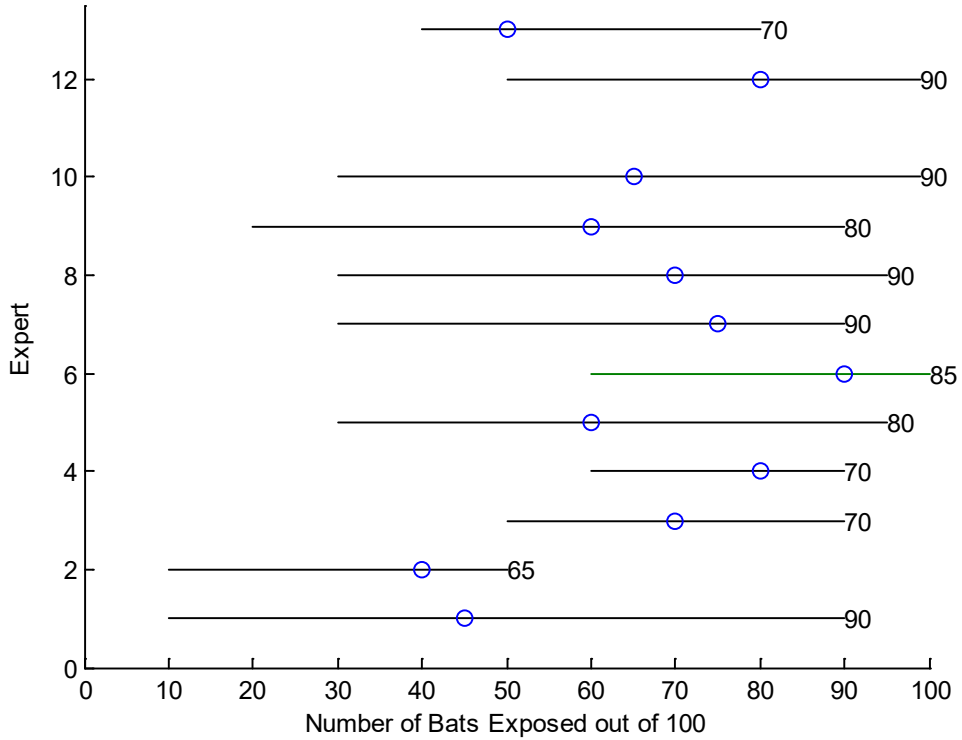
Q3 Exposure, RSM, proximity

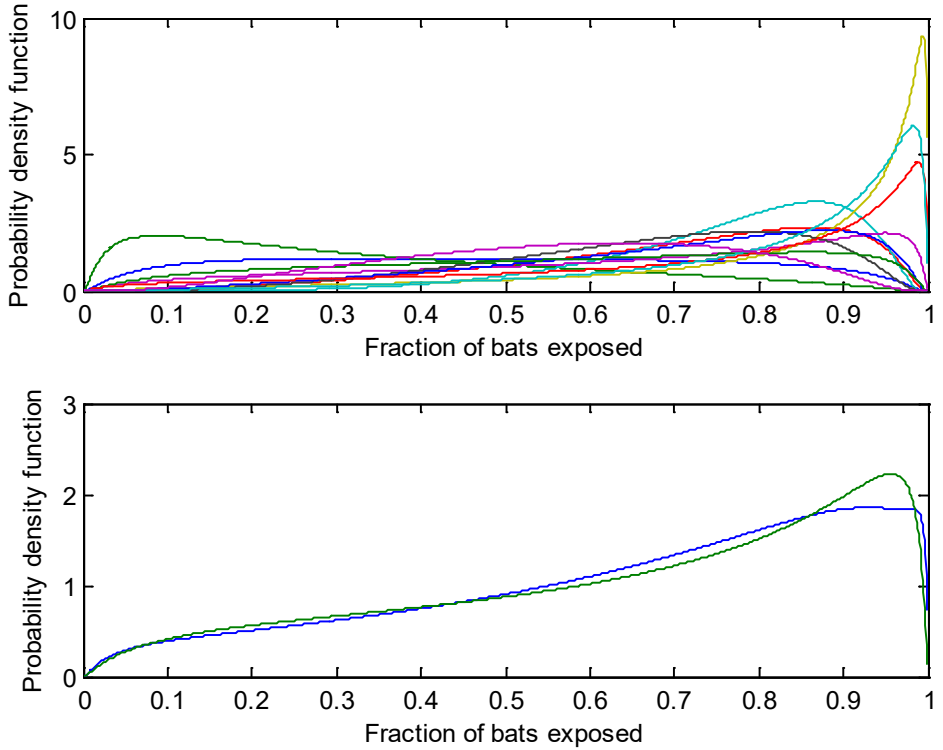




Aggregate estimate: 6.4 (0.6, 43.8)
(median, with 80% CI)

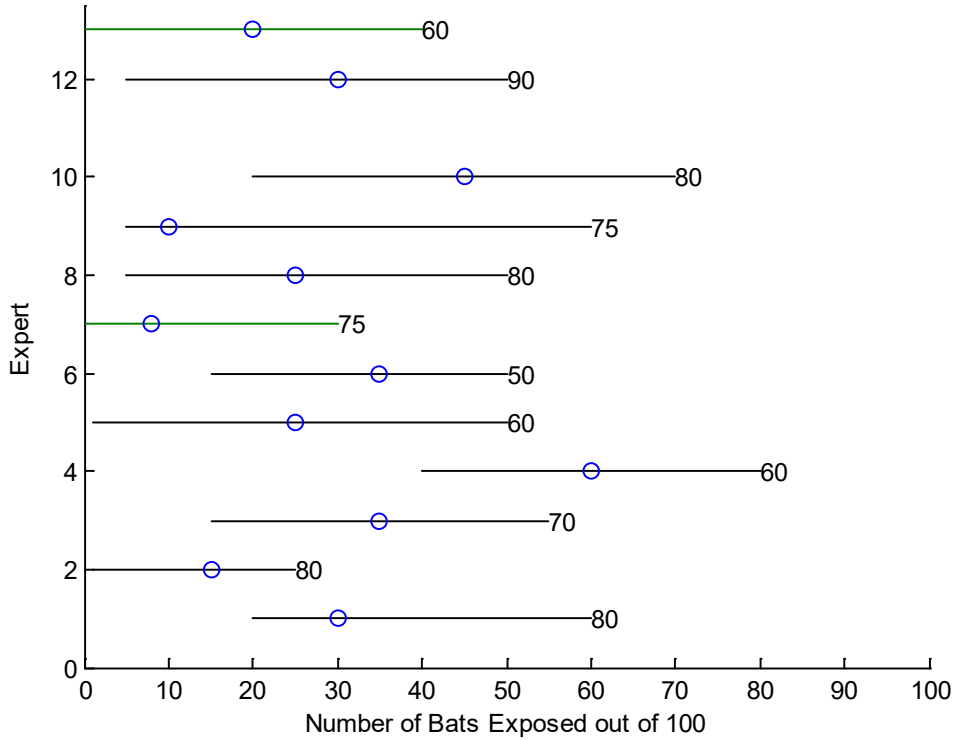
Q4 Exposure, WR, handling

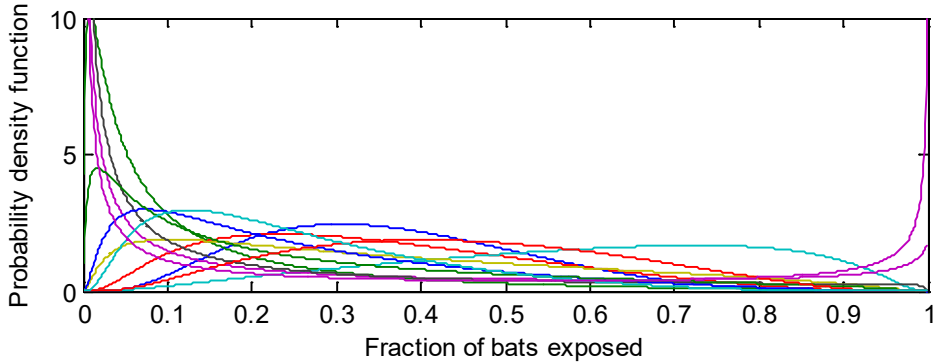


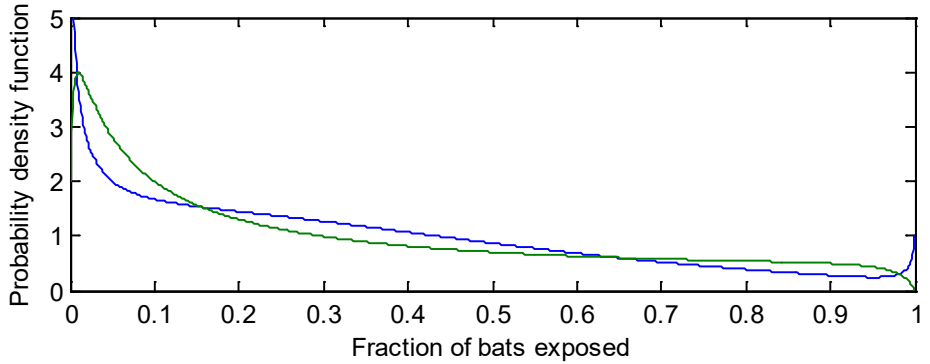


Aggregate estimate: 70.4 (24.4, 94.6)
(median, with 80% CI)

Q5 Exposure, WR, proximity

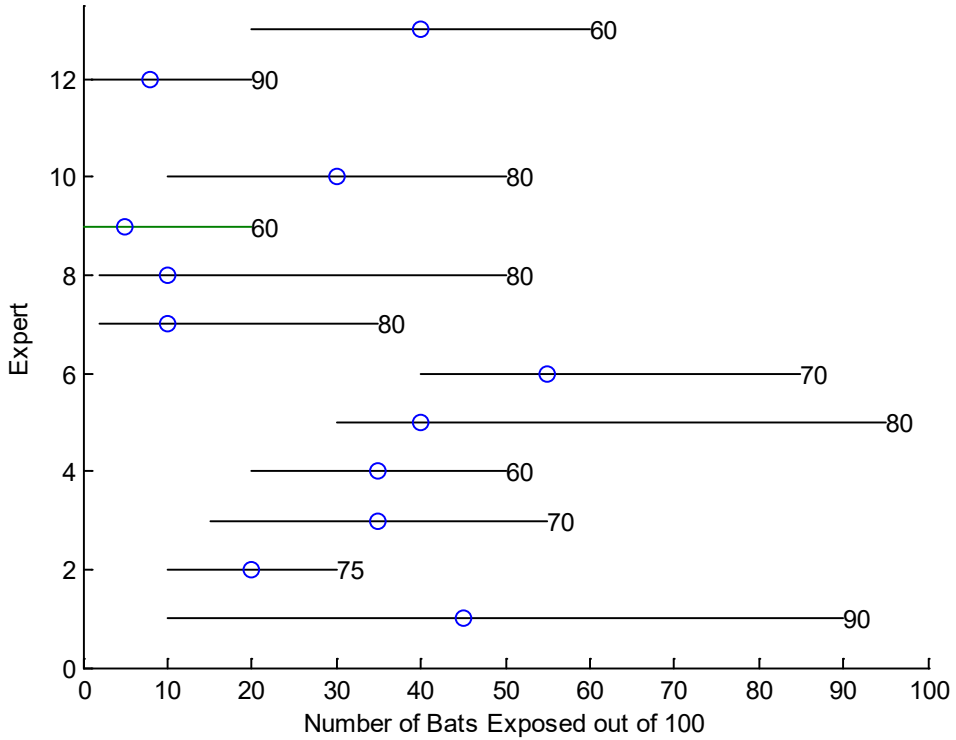


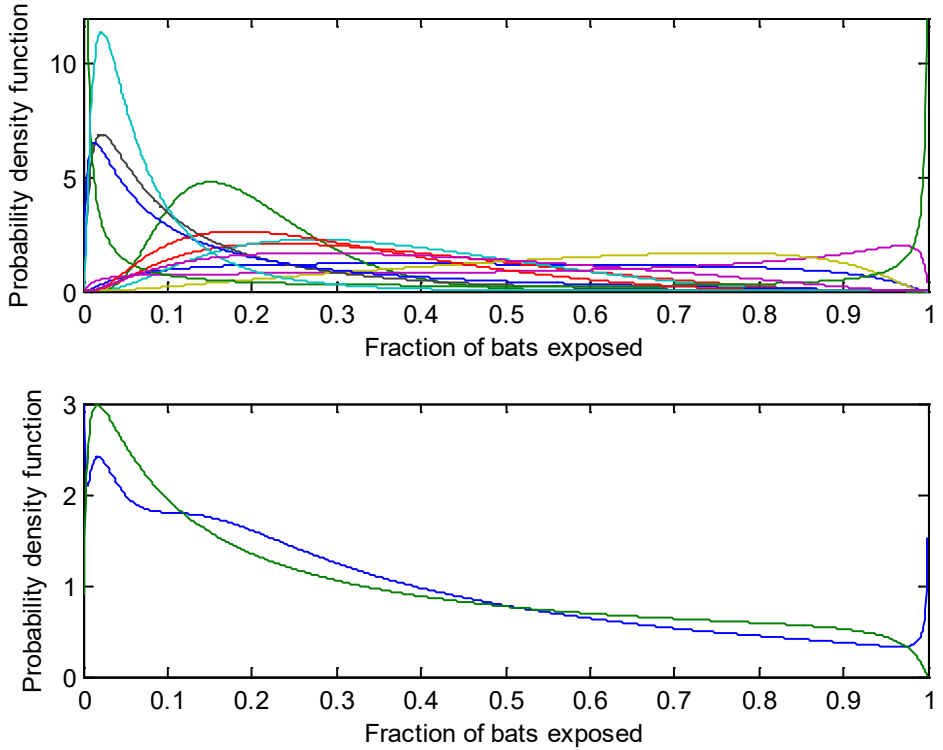




Aggregate estimate: 24.3 (2.8, 78.4)
(median, with 80% CI)

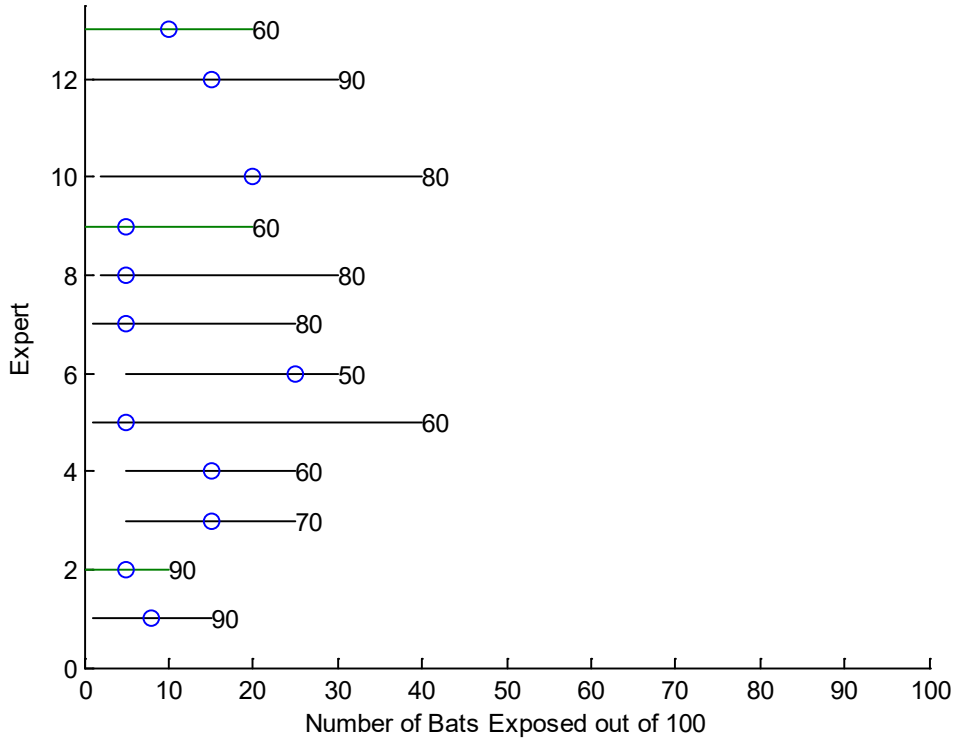
Q6 Exposure, WC, handling

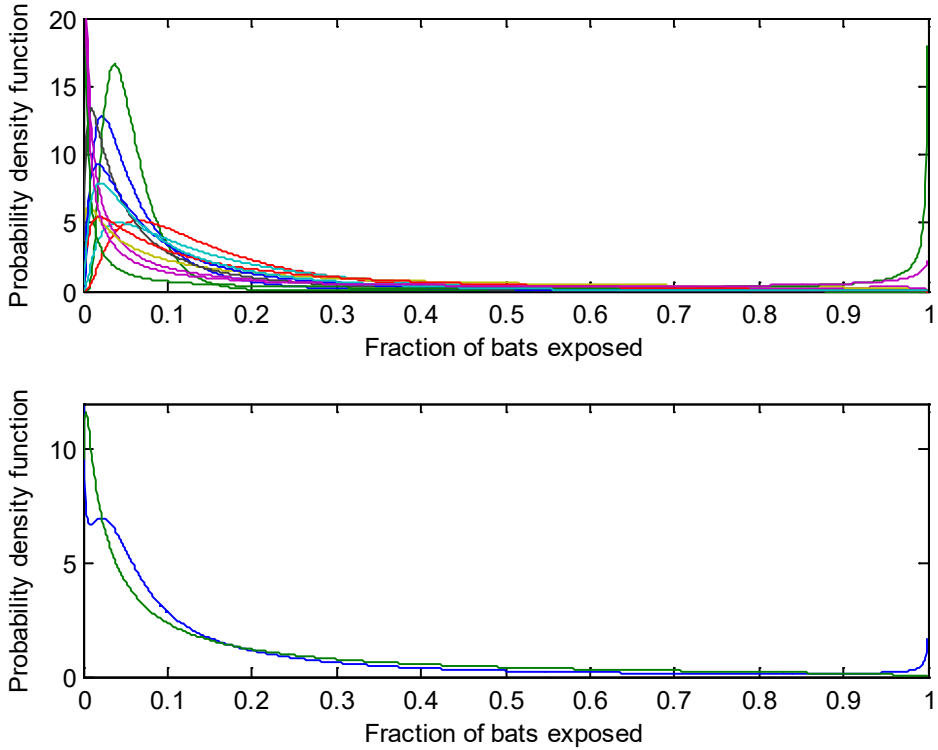




Aggregate estimate: 27.7 (3.7, 79.2)
(median, with 80% CI)

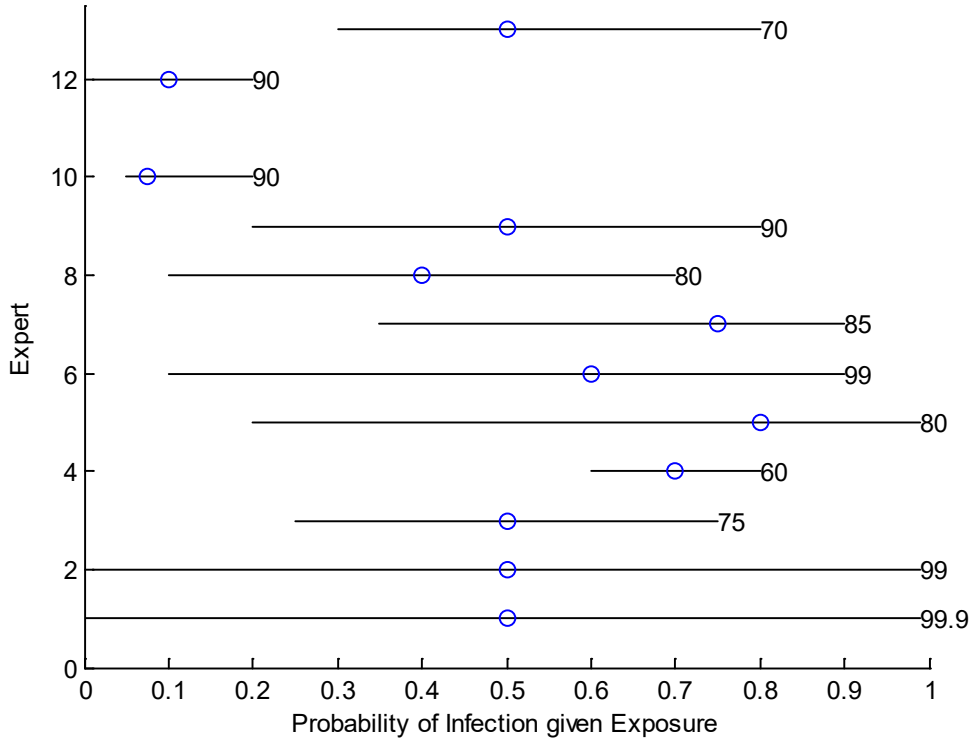
Q7 Exposure, WC, proximity

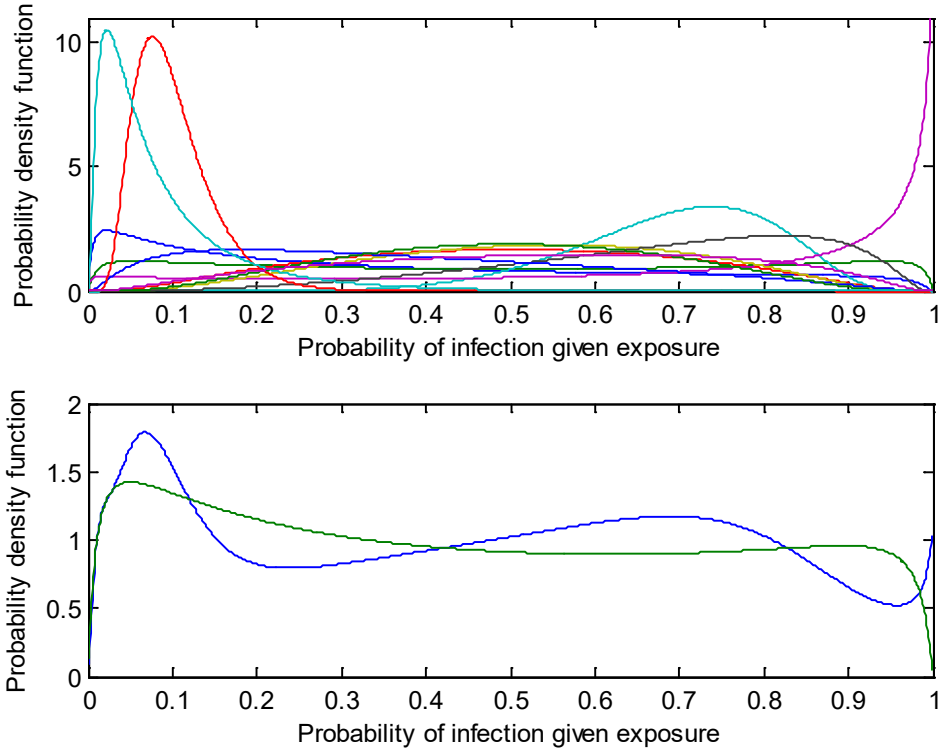




Aggregate estimate: 9.6 (1.0, 53.9)
(median, with 80% CI)

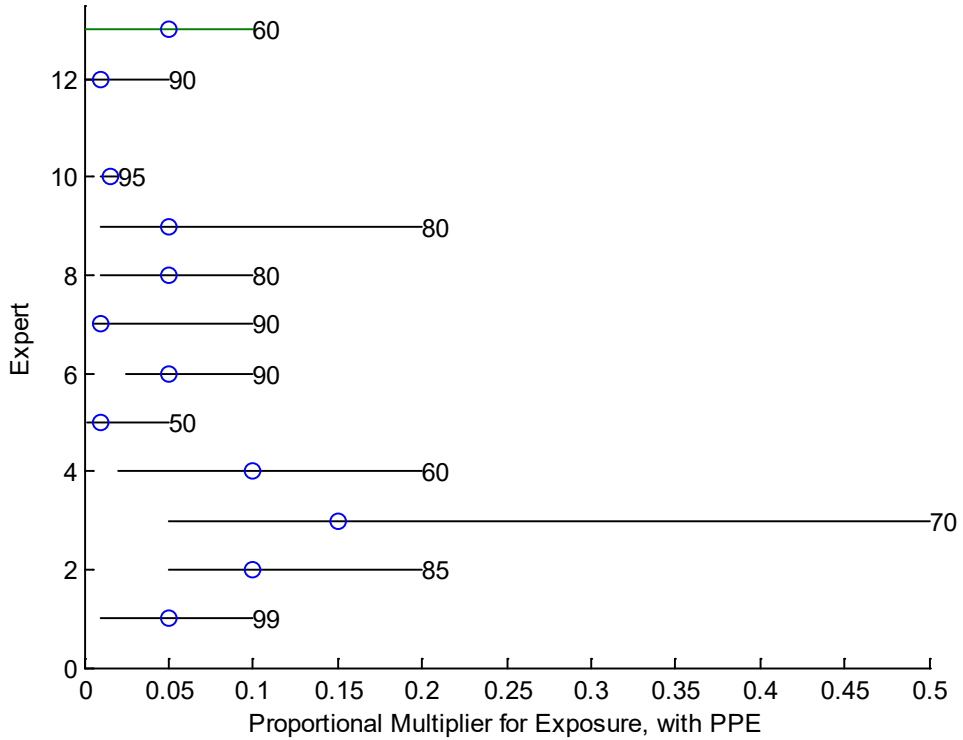
Q8 Infection, given exposure

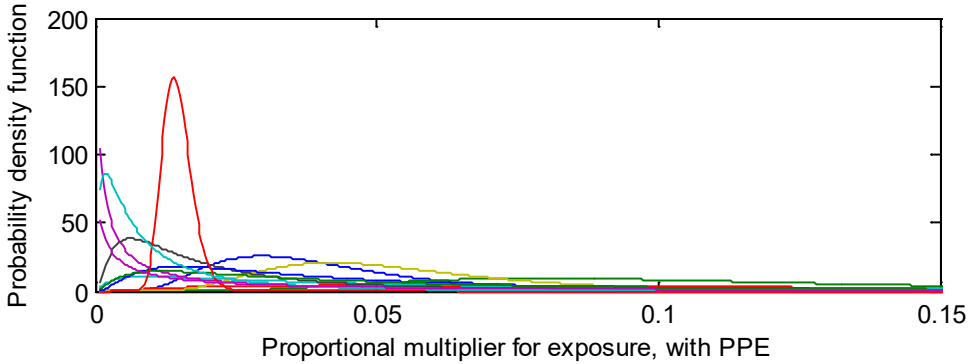


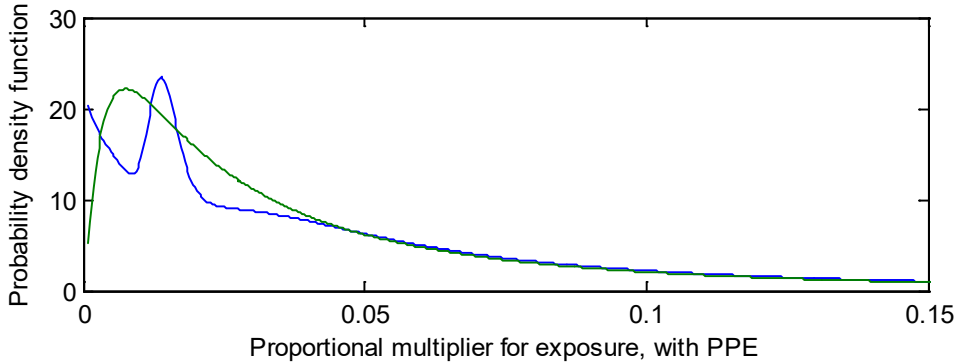


Aggregate estimate: 0.44 (0.08, 0.88)
(median, with 80% CI)

Q9 PPE effect, RSM, handling

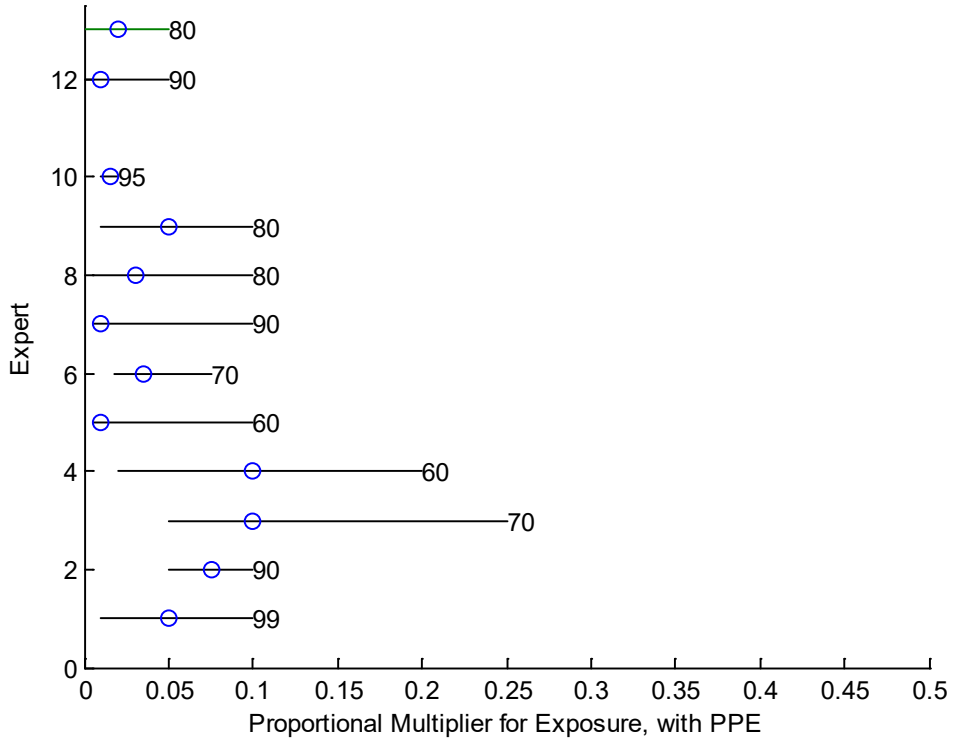


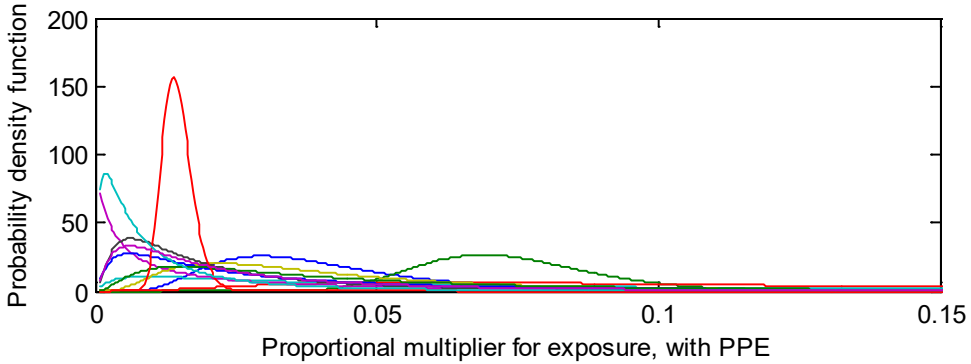


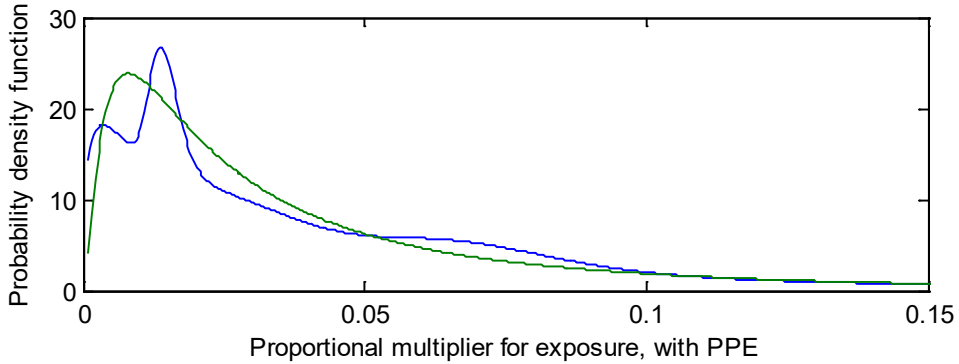


Aggregate estimate: 0.031 (0.007, 0.141)
(median, with 80% CI)

Q10 PPE effect, RSM, enclosed

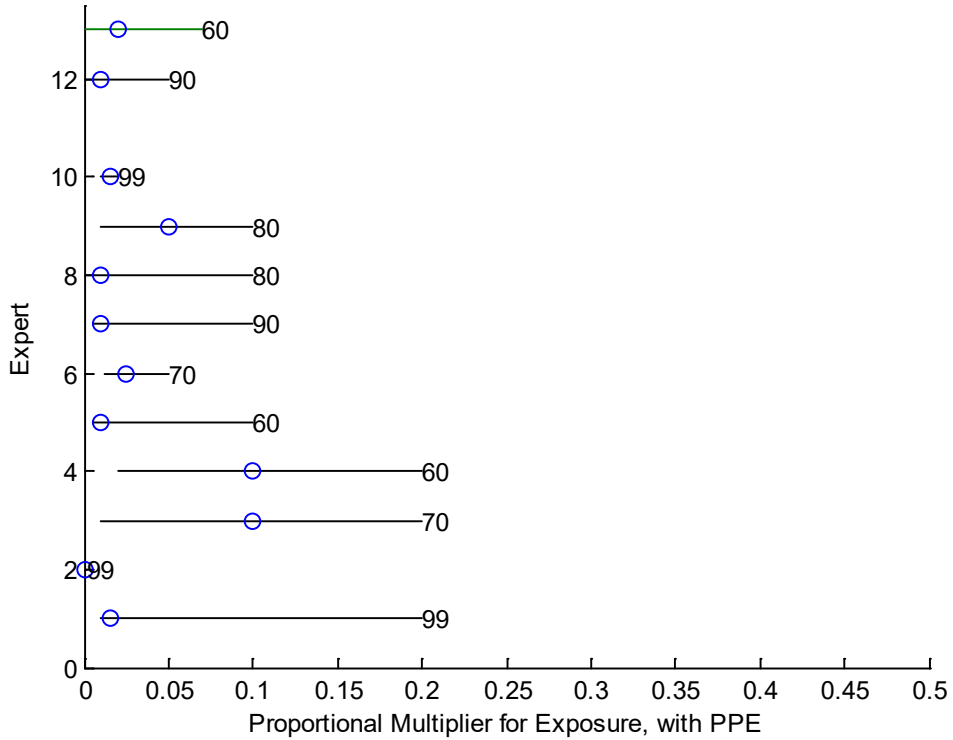


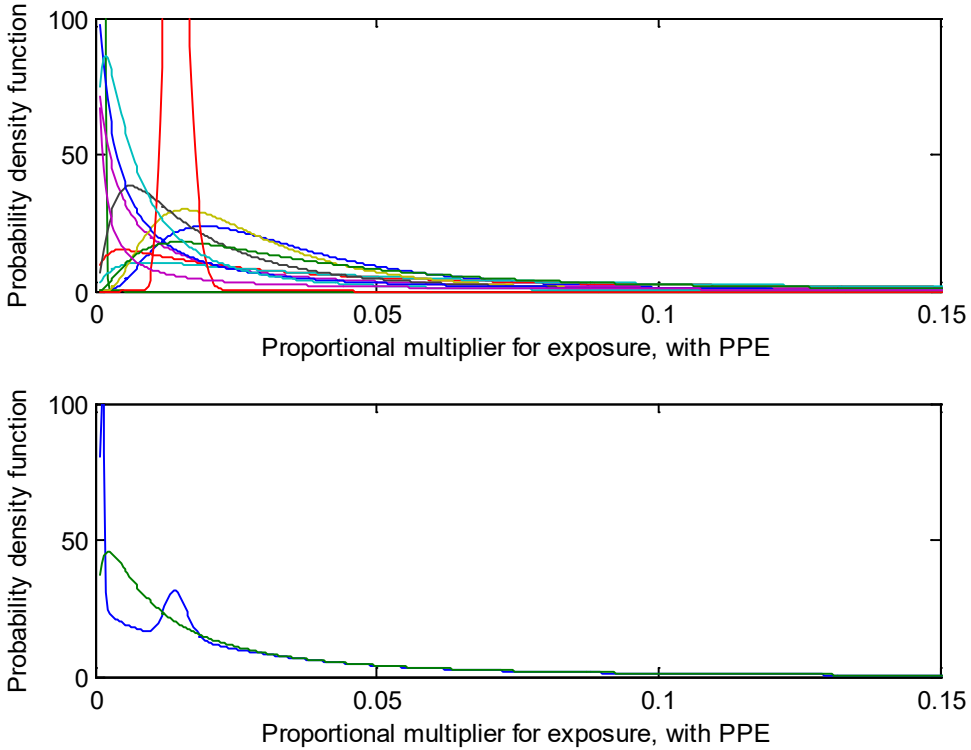




Aggregate estimate: 0.028 (0.007, 0.117)
(median, with 80% CI)

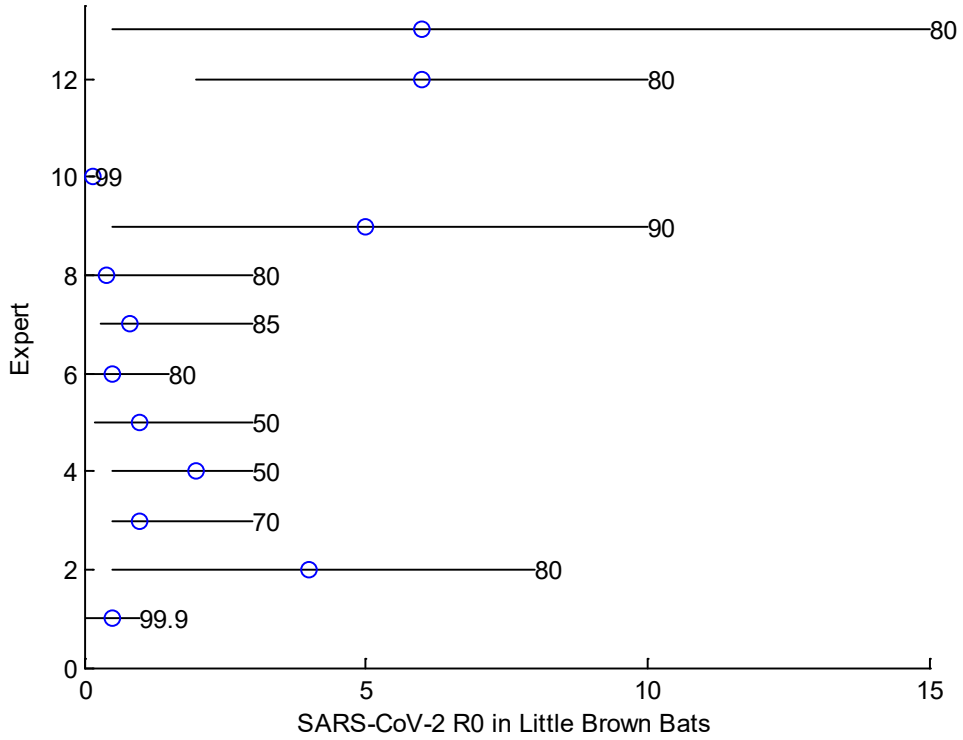
Q11 PPE effect, RSM, proximity

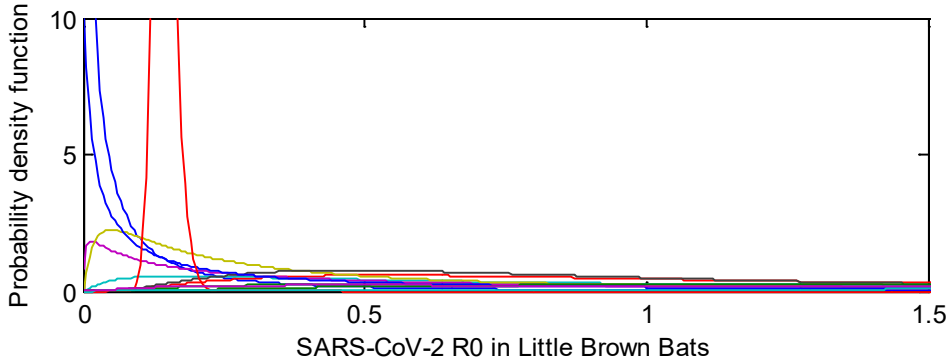


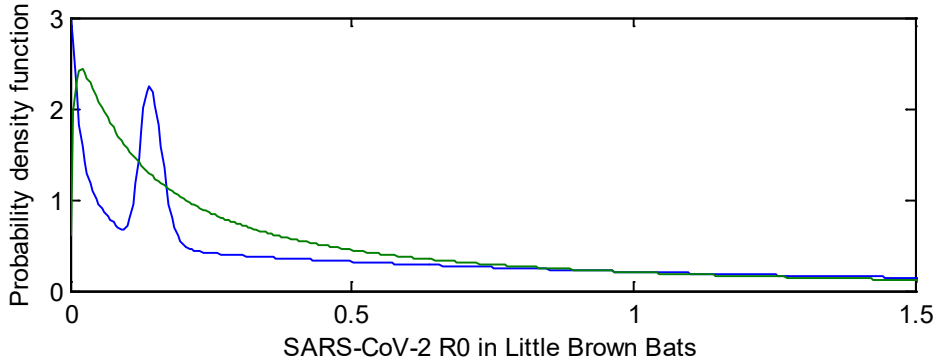


Aggregate estimate: 0.016 (0.003, 0.096)
(median, with 80% CI)

Q13 SARS-CoV-2 R_0 in little brown bats







Aggregate estimate: 0.45 (0.05, 4.38)
(median, with 80% CI)
prob(R_0 > 1) = 32.6%

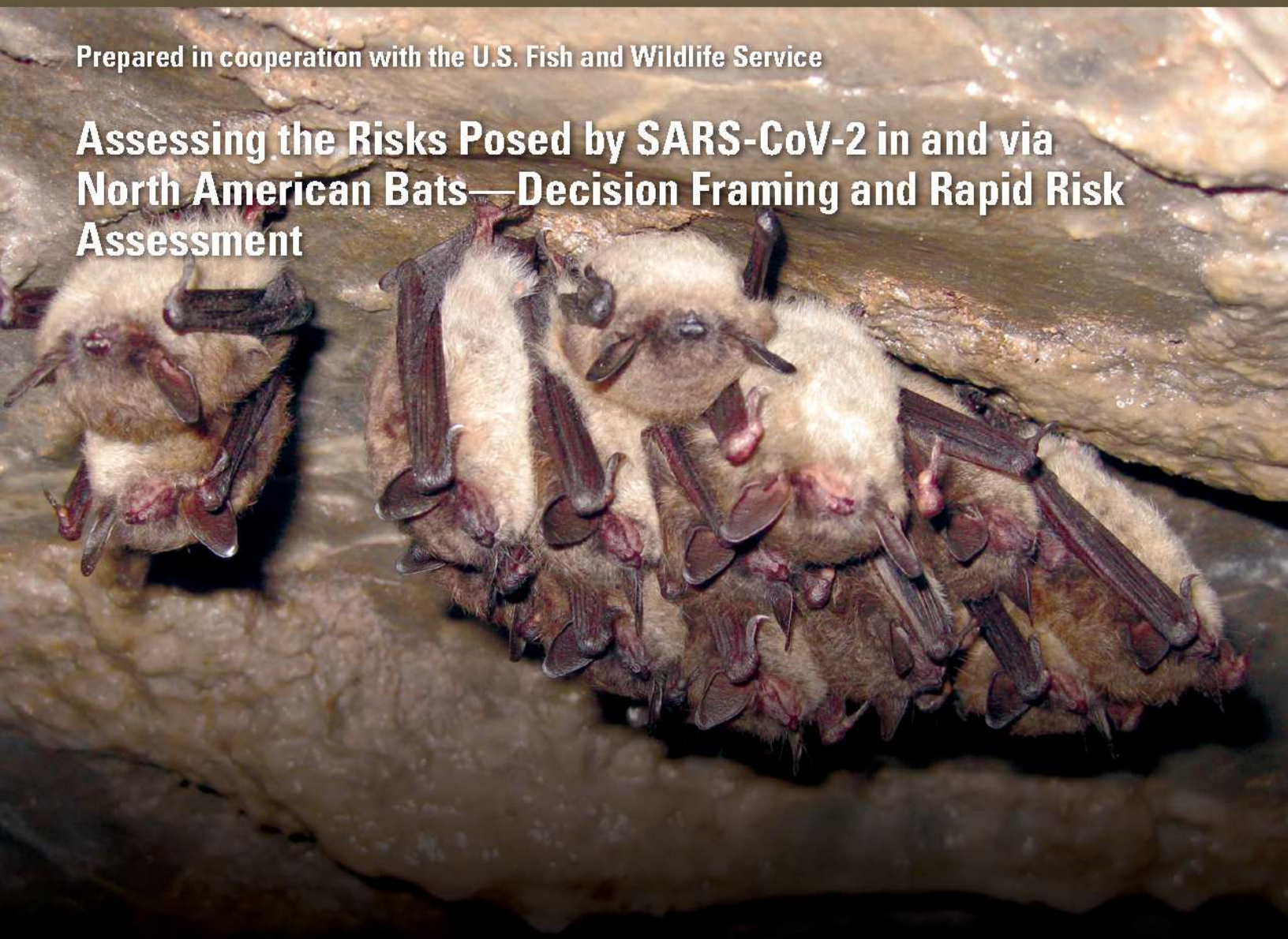
From: Grant, Evan H
Sent: Tuesday, June 02, 2020 1:39 PM EDT
To: Gilbert, Amy T - APHIS >; Kevin Castle ; Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) >; epstein ecohealthalliance.org>; dreeder ; Daniel Streicker >; kate.e.jones Kading,Rebekah >; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) ; Plowright, Raina >; wfrick >; a.peel >; Christine Kreuder Johnson >
Subject: SARS expert judgement - final report on the risk assessment
Attachment(s): "ofr20201060SARSCov2BatRiskAssessment.pdf"

SARS-bat Experts,
Thanks again for lending your expertise to this risk assessment. I attach here the report from this work.
Kindest regards,
Evan and Mike

USGS
science for a changing world

Prepared in cooperation with the U.S. Fish and Wildlife Service

Assessing the Risks Posed by SARS-CoV-2 in and via North American Bats—Decision Framing and Rapid Risk Assessment



Open-File Report 2020–1060

U.S. Department of the Interior
U.S. Geological Survey

Cover. A single *Myotis lucifugus* (little brown bat; black nose) in a cluster of *M. sodalis* (Indiana bats; pink noses). Photo by Riley Bernard, University of Tennessee.

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DAVID BERNHARDT, Secretary

U.S. Geological Survey
James F. Reilly II, Director

U.S. Geological Survey, Reston, Virginia: 2020

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The findings and conclusions in this article are those of the authors and do not necessarily represent the views of the U.S. Fish and Wildlife Service.

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Conversion Factors

U.S. customary units to International System of Units

Multiply	By	To obtain
	Length	
inch (in.)	2.54	centimeter (cm)
inch (in.)	25.4	millimeter (mm)
foot (ft)	0.3048	meter (m)
mile (mi)	1.609	kilometer (km)
mile, nautical (nmi)	1.852	kilometer (km)
yard (yd)	0.9144	meter (m)

Abbreviations

AFWA	Association of Fish and Wildlife Agencies
CDC	Centers for Disease Control and Prevention
CoV+	Actively shedding SARS-CoV-2 virus
DOI	U.S. Department of the Interior
ESA	U.S. Endangered Species Act, 16 U.S.C. §1531 et seq.
FWS	U.S. Fish and Wildlife Service
IACUC	Institutional Animal Care and Use Committee
IDEA	The Investigate-Discuss-Estimate-Aggregate Protocol
IQR	Interquartile range
NGO	Non-governmental organization
NPS	National Park Service
OIE	World Organisation for Animal Health (*Office International des Epizooties*)
PDF	Probability density function
PPE	Personal protective equipment
RSM	Research, Survey, Monitoring, and Management
USFS	U.S. Department of Agriculture, Forest Service
USGS	U.S. Geological Survey
WC	Wildlife Control
WCO	Wildlife Control Officer
WR	Wildlife Rehabilitation
WNS	White-nose syndrome

Assessing the Risks Posed by SARS-CoV-2 in and via North American Bats—Decision Framing and Rapid Risk Assessment

By Michael C. Runge[1], Evan H. Campbell Grant[1], Jeremy T. H. Coleman[2], Jonathan D. Reichard[2], Samantha E. J. Gibbs[2], Paul M. Cryan[1], Kevin J. Olival[3], Daniel P. Walsh[1], David S. Blehert[1], M. Camille Hopkins[1], and Jonathan M. Sleeman[1]

Abstract

The novel β-coronavirus, SARS-CoV-2, may pose a threat to North American bat populations if bats are exposed to the virus through interaction with humans, if the virus can subsequently infect bats and be transmitted among them, and if the virus causes morbidity or mortality in bats. Further, if SARS-CoV-2 became established in bat populations, it could possibly serve as a source for new infection in humans, domesticated animals, or other wild animals. Wildlife management agencies in the United States are concerned about these potential risks and have begun to issue guidance regarding work that brings humans into contact with bats, but decision making is difficult because of the high degree of uncertainty about many of the relevant processes that could lead to virus transmission and establishment. The risk assessment described in this report was undertaken to provide management agencies with an understanding of the likelihood that the various steps in the causal pathways would lead to SARS-CoV-2 infection of North American bats from people. This assessment focused on the active season for bats in the temperate zone of North America (April 15 through November 15), and used *Myotis lucifugus* (little brown bats) as a surrogate species. At the time of this work (April 2020), no empirical data about the effects of SARS-CoV-2 on North American bats were available, so a formal process of expert judgment was used to elicit estimates of the underlying parameters. Twelve experts in bat ecology, epidemiology, virology, and wildlife disease from the United States, United Kingdom, and Australia participated in the elicitation. A Monte Carlo simulation model was used to integrate the parameter estimates elicited from the experts and to predict the likelihood of exposure and infection in bats through a series of transmission pathways, with particular attention to capturing uncertainty in the predictions.

Given the current state of knowledge as expressed by the expert panel, the results of this assessment indicate that there is a non-negligible risk of transmission of SARS-CoV-2 from humans to bats. For example, if a research scientist were shedding SARS-CoV-2 virus while handling bats under the field protocols used in North America prior to the COVID-19 pandemic, the risk model indicates that 50 percent (uncertainty, 15–84 percent) of those bats could be exposed to virus, and 17 percent (uncertainty, 3–51 percent) could become infected. Use of personal protective equipment, especially a respirator, is expected to reduce the exposure risk. The expert panel estimated that exposure risk from research scientists could be reduced 94–96 percent (uncertainty, 86–99 percent) through proper use of appropriate N95 respirators (a type of mechanical filter worn over the nose and mouth), dedicated clothing (such as Tyvek coveralls), and gloves. Should any North American bats become infected with SARS-CoV-2, the expert panel estimated that there is an approximately 33-percent chance the virus could spread within a bat population.

This study, conducted by the U.S. Geological Survey in cooperation with the U.S. Fish and Wildlife Service, identified several critical uncertainties that could affect the estimate of risks associated with SARS-CoV-2 entering bat populations—notably, the underlying probability that a human would be shedding virus while working with bats, the likelihood of the virus replicating in bat tissue, and the likelihood of transmission of the virus within bat populations. Ongoing empirical work during May–October 2020 may shed light on these issues. Follow-up work is needed to better understand the probability of transmission of SARS-CoV-2 to bats from the general public; the manner in which the probabilities of exposure, infection, and transmission would differ during hibernation compared to the breeding season; and the likelihood of important effects, like morbidity and mortality in bats, the possibility of zoonosis from a North American bat reservoir, and effects of and on other wildlife.

[1]U.S. Geological Survey.

[2]U.S. Fish and Wildlife Service.

[3]EcoHealth Alliance.

Introduction

The novel β-coronavirus, SARS-CoV-2, that has caused a pandemic disease (COVID-19) in humans arose from a mammalian host, possibly an Old World bat in the family Rhinolophidae. The closest known virus discovered in wildlife was found in a *Rhinolophus affinis* (horseshoe bat) from Yunnan province in China (Zhou and others, 2020b), although the similarity is not an exact match. No SARS-related β-coronaviruses have yet been identified in New World bats, but a different type of β-coronavirus has been identified in New World species of bats from Mexico (Anthony and others, 2013; Anthony and others, 2017; Góes and others, 2016). This raises an important question about whether North and South American bats could be vulnerable to infection with SARS-CoV-2 via contact with humans, which in turn raises questions about whether there could be reciprocal spread to humans via a bat reservoir. This inquiry was designed to be a rapid assessment of the risk of transmission of SARS-CoV-2 from humans to North American bats, the management contexts in which this risk might be relevant, and possible mitigation actions that may be implemented by those who come into contact with bats or their habitats. The structure of this study could also serve as a model to rapidly assess the risk to bats in other geographic regions (for example, Europe or Latin America) or the risk to other wildlife taxa of concern (for example, felids and mustelids which may be susceptible to SARS-CoV-2; Shi and others, 2020).

The purpose of this report is to describe the risk assessment conducted by the U.S. Geological Survey, in cooperation with the U.S. Fish and Wildlife Service, to evaluate the potential for transmission of SARS-CoV-2 from humans to bats. This assessment focuses on potential activities undertaken by research scientists, wildlife rehabilitators, and wildlife control operators in North America during the summer field season (April 15 to November 15, 2020), with and without new protocols for such work.

Decision Framework

In late March 2020, State, Federal, and tribal wildlife management agencies in the United States began expressing concern about the possible transmission of SARS-CoV-2 from humans to bats and requested that the U.S. Geological Survey (USGS) lead a risk assessment that could inform their decision making. Prior to designing the risk assessment, the authors worked with a guidance committee composed of representatives from State and Federal wildlife management agencies (see Acknowledgments) to frame the decision context in which risk assessment would be used. We recognized that the motivation, statutory requirements, and authority to address the problem may stem from human health and wildlife conservation interests and needs, and that decisions involve a mixture of conservation and human health objectives, where tradeoffs are likely to occur. The construction of the decision framework was instrumental in informing the focus and structure of the risk assessment. The decision framework constructed in consultation with the representatives from decision-making agencies is described below.

Relevant Decision Makers and their Authorities

In the United States, there are many decision makers with authority to make decisions that affect bats and the interactions of bats and people. For most terrestrial mammal species that are not listed under the U.S. Endangered Species Act (ESA; 16 U.S.C. §1531 et seq.) and are not on Federal land, the State wildlife agencies have management jurisdiction. The status of bats under current State laws and regulations differs from State to State (O'Shea and others, 2018), but existing statutory and regulatory authorities generally involve several types of activity. First, States have authority to direct the activities of their own staff, such as conducting bat surveys or habitat and population management. Second, States permit the work of wildlife rehabilitators and can prescribe conditions of that work. Third, States permit nuisance wildlife control operators who perform such activities as removing bats from human dwellings. Fourth, States provide permits for a variety of research activities by scientists and environmental consultants. Fifth, States sometimes collaborate with educational institutions that may keep captive bats for purposes of exhibition. Sixth, States often require permits or registration for private citizens or groups who wish to hold bats. Seventh, State wildlife agencies, in conjunction with many partner agencies, often undertake public communication about the benefits of wildlife and healthy ways for humans to interact with wildlife.

Several U.S. Department of the Interior (DOI) agencies have management responsibilities for bats. The U.S. Fish and Wildlife Service (FWS) has authority under the ESA for any listed bat species; this authority includes permitting the activities of other Federal agencies that may affect listed species. The FWS Office of Law Enforcement is responsible for managing the importation of wildlife into the country. (The Centers for Disease Control and Prevention (CDC) also require permits for importation of bats). The FWS Wildlife and Sport Fish Restoration Program is a major funding source for State agencies' bat management efforts. The FWS supports the National White-Nose Syndrome Program, which provides funding for research, conservation, and monitoring of bats, and issues guidance to partners on matters related to white-nose syndrome (WNS). The FWS, through the National Wildlife Refuge System, manages land, wildlife, staff, and public access at Refuges, some of which provide habitat for bats. Refuge staff conduct research and monitoring activities. Refuges also issue special use permits for outside scientists to conduct research. Similarly, the National Park Service (NPS) has authority over the activities that occur within NPS

units. These activities include research and management, which involve contact with bats by park staff or cooperators; cave tours and bat viewing opportunities for the public; and permits for recreational caving by individuals or groups. The FWS Refuge System and NPS have extensive communication efforts aimed at educating the public about wildlife, including bats.

Within the U.S. Department of Agriculture, the U.S. Forest Service (USFS) has research and management responsibilities for bats on its Federal lands, often in coordination with other Federal and State partners. Similar to DOI agencies, the USFS manages land, sustains habitat for native fish and wildlife, and provides public access for recreational activities, including use of caves and mines. USFS scientists conduct research and monitoring activities. The USFS issues permits for outside scientists to conduct research on its lands. The National Forest System engages in public outreach and education about wildlife, especially bats.

Many agencies and institutions, including the USGS, FWS, NPS, USFS, universities, and non-governmental organizations, conduct scientific studies on bats. Under the Animal Welfare Act (7 U.S.C. §2131 et seq.) and other Federal and State laws and policies, researchers and agencies are required to consider the welfare of the animals being studied or used for educational or teaching purposes in captivity or the wild. Institutional Animal Care and Use Committees (IACUC) are responsible for review and approval of protocols involving animals used in research or teaching. IACUC review ensures that the welfare of animals is taken into consideration and that all approved activities include appropriate use of animals. Additionally, these entities often conduct internal reviews of scientific research study plans. IACUC and other research plan review mechanisms represent an additional tool with which agencies can manage the activities of their staff that involve interactions with animals.

Public health agencies at Federal, State, and county levels take action to benefit human health, and while they do not directly manage bats, they do play a role in the interactions humans have with bats. Because of the risk of rabies virus transmission, many interactions that members of the general public have with bats are reported to county health agencies, which help to manage the health risk of such exposure. In turn, county health agencies often report rabies statistics to State and Federal public health agencies (for example, CDC), enabling broader understanding of seasonal and geographic patterns and trends in the types of bats and other wildlife coming into contact with the public at a national scale (Pieracci and others, 2020).

Finally, zoos and wildlife parks frequently have captive populations of bats, including species native to North America as well as species from other parts of the world, with which North American bats may not naturally come into contact. Zoos and wildlife parks can control the proximity of humans to captive bats and the way the bats are handled by staff.

Management Objectives

Each agency with jurisdiction that affects the interactions of bats and humans has its own purposes, as derived from its enabling legislation, mission, or stakeholder input. We worked with representatives from State and Federal wildlife management agencies (see Acknowledgments) to develop a set of long-term outcomes (“fundamental objectives”) sought by these agencies through decisions related to bats and SARS-CoV-2. We recognize that some of these objectives may conflict with each other; indeed, that is what makes decisions difficult. By clearly articulating the set of objectives that are important to decision makers, the scientific assessments that are needed to inform difficult deliberations about appropriate and necessary mitigation actions can be better identified. Through discussions with these representatives, 10 objectives were identified. (The order of presentation of these objectives is not meant to imply anything about their relative importance.)

1. Minimize the morbidity and mortality of wild North American bats resulting from infection with SARS-CoV-2 or from management actions meant to mitigate transmission. If SARS-CoV-2 is introduced and transmitted to a naïve population of bats, it is possible the novel infection could lead to disease or death. In addition, some management actions meant to reduce disease transmission to bats could directly or indirectly cause mortality. Because many of these bat populations are already threatened by WNS and other stressors, any additional sources of mortality could affect long-term conservation.

2. Minimize the risk of SARS-CoV-2 becoming endemic in any North American bat population through sustained bat-to-bat transmission. We want to avoid anthropogenic establishment of a new endemic disease in bat populations for several reasons. Fundamentally, any anthropogenic change to the ecosystem outside the course of natural events is to be avoided. We are also concerned about this objective as a means to other objectives because a reservoir of SARS-CoV-2 in bats could lead to a reduction in the long-term conservation of bats (Objective 1), a risk to public health (Objective 3), or a risk to the health of other wildlife taxa or domesticated animals (Objective 5).

3. Minimize the risk of new SARS-CoV-2 cases in humans via transmission from North American bats. The long-term aim of public health agencies and other organizations will be to minimize the incidence and transmission of SARS-CoV-2 in humans. However, if a reservoir of SARS-CoV-2 becomes established in North American bats, it could represent a source for new exposure and infection; worse, if such a reservoir provides an opportu-

nity for evolution or recombination of the virus, the new viral strains could evade existing immune responses or reduce the efficacy of vaccines under development.

4. Minimize the indirect effect on human health from actions designed to mitigate SARS-CoV-2 transmission to bat populations. Particularly at this moment, when the equipment needed to manage the COVID-19 pandemic is in short supply, any use of such equipment (such as personal protective equipment; PPE) for bat-related activities may undermine public health efforts. The supply of PPE for human needs is expected to increase in the near future as manufacturing ramps up, decreasing the gap between demand and supply. Therefore, this may not be a limitation once the human health demand is satisfied.

5. Minimize the risk of SARS-CoV-2 infection in other North American wildlife or domesticated animal populations through a reservoir in North American bats. Other species of mammals and other taxa are known to be susceptible to β-coronaviruses, specifically SARS-related viruses. If SARS-CoV-2 becomes established in bat populations, it could possibly spill over into other susceptible wild and domesticated animals.

6. Maintain or maximize the ability of wildlife control operators and wildlife rehabilitators to carry out their functions for the benefit of humans and wildlife. The activities undertaken by wildlife control operators are necessary tools for managing conflict between humans and wildlife; these activities (like humane removal of bats from human dwellings and prevention of ingress) are important for human health (for example, minimizing rabies exposure) as well as for bat conservation. Likewise, the activities undertaken by wildlife rehabilitators may have a positive effect on wildlife, as well as a positive effect on public attitudes toward wildlife.

7. Maintain or maximize recreational activities, such as cave tours, recreational caving, and other activities that occur in bat habitat. Humans derive benefit from outdoor recreational activities; indeed, refuges, parks, and national forests have an important purpose in providing such opportunities.

8. Maximize the opportunities for scientific research on bats and within bat habitat. Research on bats and their habitats contributes to many facets of primary knowledge about the natural world. Conservation measures for other threats to bats, including WNS, benefit from on-going research. Additionally, the status of listed and candidate bat species requires a periodic assessment of population sizes. The fields of geology, hydrology, entomology, and numerous others benefit from on-going research that may overlap with bats and their habitats.

9. Maximize public appreciation for bats and their conservation. Past zoonotic diseases (such as the 2003–10 highly pathogenic avian influenza outbreak and the 2003 SARS outbreak) have created negative public responses to wildlife (wild birds and wild bats, respectively). The risk of SARS-CoV-2 in bats and the response to it could undermine recent gains in public appreciation for bats and bat conservation.

10. Maximize the ability to manage and conserve bat populations. Many of the agencies mentioned above have active programs to conserve bat populations. These programs sometimes require staff to handle or be in proximity to bats. Objectives 6 and 8 also contribute to the long-term conservation of North American bats.

Potential Mitigation Measures

The central causal chain that was motivating concern from State, Federal, and tribal wildlife agencies has three steps: the possible transmission of SARS-CoV-2 from humans to bats; sustained bat-to-bat transmission of SARS-CoV-2; and subsequent effects, for instance, of transmission from bats back to humans or to other wildlife. The representatives from State and Federal wildlife agencies that guided this work expressed an urgent need to identify actions they could take to interrupt this potential chain of events. We worked with the representatives to identify the types of actions within their jurisdiction that could be employed to minimize the risks associated with SARS-CoV-2 and achieve the objectives described above. Each of the decision-making bodies has a different set of management actions under its jurisdiction, and we did not try to match particular actions with specific agencies. Instead, we worked with them to describe the types of actions that could be taken in an attempt to achieve the objectives described earlier. It is worth noting that these actions are not mutually exclusive; indeed, a full strategy may involve deploying these actions in combination.

Federal and State agencies have a variety of mechanisms by which they may implement mitigation strategies. These mechanisms may come in the form of regulations, guidance, directives, conditions of funding, or permission.

- Various agencies have authority to issue permits (for example, for the take or harassment of Federally Threatened or Endangered bat species, to conduct research on bats, for research activities on National Wildlife Refuges and National Forests, for wildlife holding, for scientific take, for school programs and citizen scientists, for wildlife control operators, and to operate wildlife rehabilitation centers). Agencies may reject or rescind permission for activities that involve handling or proximity to bats or bat habitats. Additionally, permission may be granted so long as a permittee takes a set of risk-mitigation actions (for example,

from the list below). Permittees include university, tribal, Federal, and State agency researchers; environmental consultants; wildlife rehabilitators; and wildlife control operators.

- Multiple agencies (USGS, FWS, NPS, USFS) have Institutional Animal Care and Use Committees, institutional biosafety committees, and other research approval processes (for example, study plan review and approval) or benefit from these committees housed with non-governmental institutions (universities, professional societies, non-governmental organizations); the committees may compel researchers to comply with risk-mitigation measures as they apply to animal welfare concerns. These committees may suspend animal research that has received prior approval until risk mitigation measures germane to animal welfare are adopted.

- Agencies (for example, USGS science centers and Cooperative Research Units, FWS-WNS National Program, NPS visitor contact, and USFS) may issue guidance outlining voluntary measures, which differs from a permit in that the guidance is not compulsory. Agencies may issue guidance and provide training of wildlife rehabilitation and nuisance animal control entities to promote the adherence to best practices.

Potential mitigation actions may reduce the frequency of contact or the probability of transmission of SARS-CoV-2 from infected humans to susceptible bats or change the behavior of individuals interacting with bat populations.

1. The use of PPE, including appropriate N95 respirators or other face masks or shields, eye protection, latex or nitrile gloves, or dedicated clothing (for example, coveralls, Tyvek) to minimize exposure of bats from COVID-19-infected individuals may be required (for example, via agency permit, occupational safety and health programs, or IACUC).

2. Decontamination protocols, such as those provided by the National WNS Response Team to reduce the threat posed by the fungal pathogen *Pseudogymnoascus destructans*, may include best-practice protocols for disinfection of persons and equipment prior to and after handling bats or interacting with bat habitats.

3. Various agencies (for example, States, NPS, Association of Fish and Wildlife Agencies [AFWA], FWS-WNS National program, USFS) have avenues for public outreach, which are already in use to improve public understanding and tolerance of bats, and can be used to encourage the public to engage in behavior and adopt protective measures (including the use of PPE and distancing between humans and bats) to reduce the risk of transmission of SARS-CoV-2 to bats. In some circumstances, this public outreach is coordinated with State and local public health agencies or the CDC.

4. Land managers, including NPS, FWS, USFS, States, and tribes may suspend or limit access to bat populations or habitats. This may involve suspending group tours to caves and access to National Wildlife Refuges or requiring or encouraging distancing from bats. This may also involve directing permittees and agency personnel to delay or suspend some kinds of (non-essential) research.

5. Nuisance animal control activities (undertaken by wildlife control operators [WCO], which may include such activities as capturing individual bats in a home, trapping and transporting bats in an attic, and installing an exclusion device to restrict bat access to human dwellings) could be legally limited to currently established best management practices, which prevent the unnecessary human-bat interactions that are characteristic of less effective approaches. WCOs could be advised or required to not release hand-captured bats.

6. Wildlife rehabilitators may be instructed to avoid accepting bats for rehabilitation.

7. Wildlife rehabilitators may be instructed to not release captive bats or to suspend wildlife rehabilitation of bats. As appropriate testing becomes available, bats might only be released after testing negative for coronavirus.

8. Agencies may issue guidance or directives governing conditions for workers coming into contact with bats, such as a minimum amount of time (for example, 2 weeks) after any potential exposure to SARS-CoV-2, a negative test for active coronavirus infection, a positive serological test, or vaccination to SARS-CoV-2 (when it is available).

9. Agencies, universities, and non-governmental organizations (NGOs) may begin research projects on the risks of SARS-CoV-2 transmission between humans and bats and the effectiveness of potential mitigation options.

10. In the long term, if SARS-CoV-2 does become established in North American bat populations, there might be mitigation measures designed to prevent the virus from moving back to humans, wildlife, or domesticated animals. These may differ from actions identified above.

Causal Linkages between Actions and Objectives

An influence diagram is a graphical representation of a system. The influence diagram in figure 1 describes the causal chains—pathways within the human-bat system—that link the mitigation actions with the desired outcomes. Each arrow represents a process, which is governed by a parameter that describes the effect of an action on an outcome. Figure 1 shows the proposed causal linkages between the potential mitigation actions (orange rectangles) and the long-term objectives

(blue hexagons) described above. Key system states are represented as nodes in the diagram (green ovals).

The central causal logic that is motivating discussions about SARS-CoV-2 in North American bats can be described with three phases: (1) direct or indirect transmission of SARS-CoV-2 from a human to individual wild bats (dashed portion of fig. 1); (2) following this initial transmission, sustained bat-to-bat transmission of SARS-CoV-2, resulting in endemic disease within one or more bat populations (arrow labelled "Sustained bat-to-bat transmission" in fig. 1); and (3) ensuing consequences of endemic SARS-CoV-2 in bats, such as transmission to humans, other wildlife, or domesticated animals (arrows to hexagons in fig. 1). The influence diagram captures the expectation that many of the actions designed to mitigate the risks posed by SARS-CoV-2 have consequences to other important outcomes. The choice of mitigation measures may require decision makers to balance trade-offs among multiple objectives.

Some of the parameters underlying the central steps in figure 1 are transmission parameters (between humans and bats, among bats, between bats and other species, among locations, and between bats and humans) and bat mortality parameters. Mitigation actions are expected to affect the transmission rates, which may subsequently affect the bat mortality rates; we did not consider any actions that address bat mortality rates directly. We recognize that there is likely some background level of transmission (through the general public node, and possibly through a feral/domestic cat node) that may not be affected by any of the mitigation actions considered.

To estimate the consequences of a set of potential mitigation strategies (combinations of the 10 actions described above), we need estimates of parameter values for many of the arrows in the influence diagram (fig. 1). Given the novelty of SARS-CoV-2, there is a lack of robust scientific information for many of these parameters at this time. Values for the parameters may be borrowed from similar systems reported in the scientific literature, but the manner in which these are applied to North American bat populations requires expert judgment.

This influence diagram helps to identify the key parameters for which we require quantitative estimates to calculate the resulting risk, given the selection of a mitigation strategy (that is, one or more actions). In this first phase, we primarily focus on estimating the risk of transmission to bat populations via direct contact with humans (fig. 2), particularly during the time of year when bats are most active and may be in contact with the most humans, which are in the midst of the COVID-19 pandemic (2020). If it is possible to prevent the initial transmission, then all the later steps in the causal pathway are blocked. Further, even if transmission cannot be entirely prevented (for example, because of other pathways of transmission), the reduction in the magnitude of transmission may decrease the risks associated with later steps. We recognized the need to estimate the probability of sustained bat-to-bat transmission. This step is critical to many of the later consequences, so if that risk is very low, the need for mitigation might be less urgent.

The dynamics of initial transmission, although a portion of the larger picture, are nevertheless sufficiently complicated for the first step of our risk analysis. Key factors to consider include potential differences among bat species, regions, and initial population status (including population size and the occurrence of *Pseudogymnoascus destructans* and WNS); differences among the routes of transmission; and differences among the mitigation actions (for example, using PPE in research settings may include appropriate N95 respirators or less protective masks).

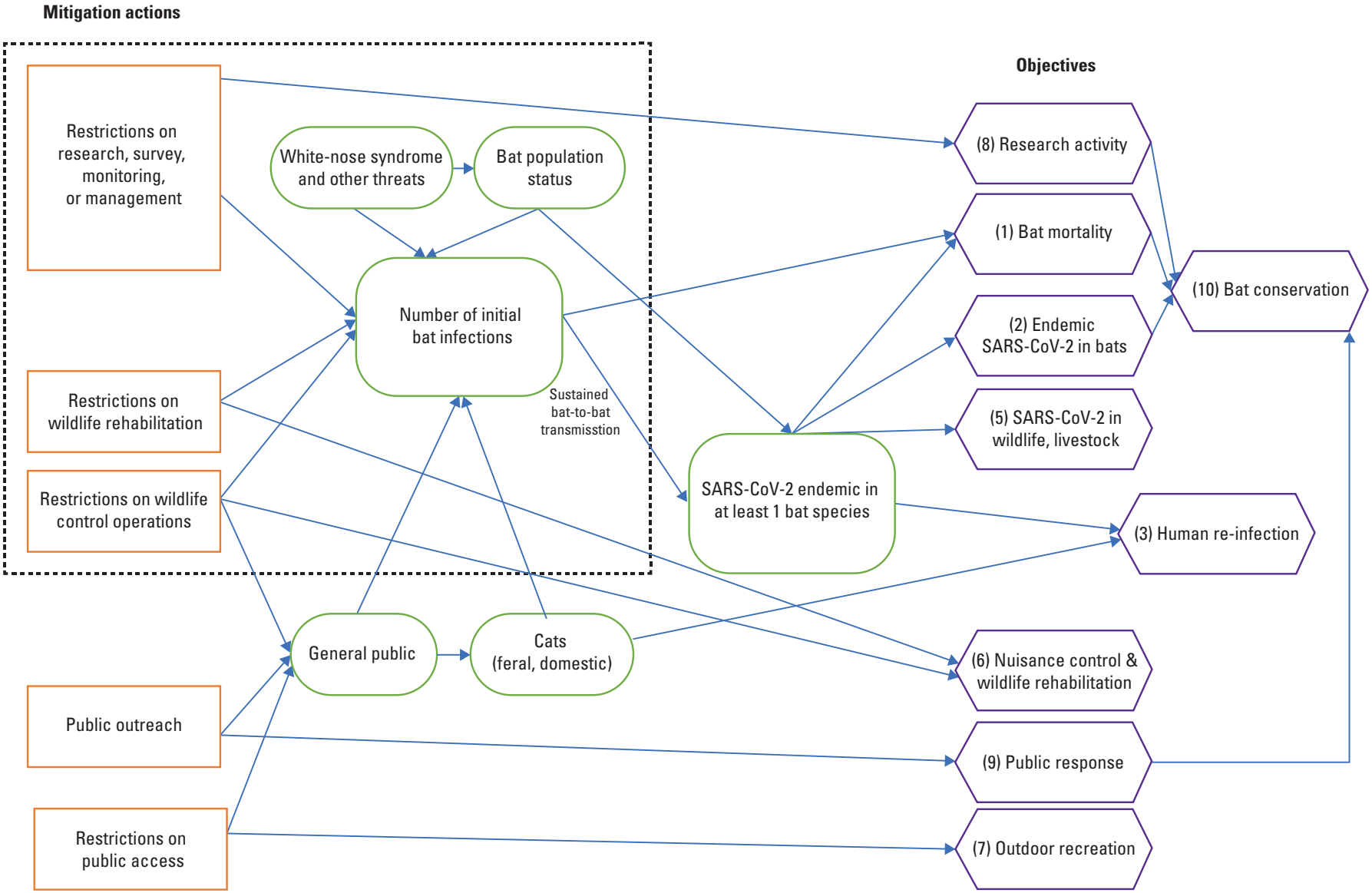

Figure 1. The causal linkages between actions and outcomes motivated by the risk of SARS-CoV-2 entering North American bat populations. The diagram includes potential mitigation actions (orange rectangles), key system states (green ovals), and long-term objectives (blue hexagons). The numbering of the objectives corresponds to the numbering in the "Management Objectives" section of this report. The portion of the diagram within the dashed line emphasizes the initial transmission dynamics analyzed in this assessment.

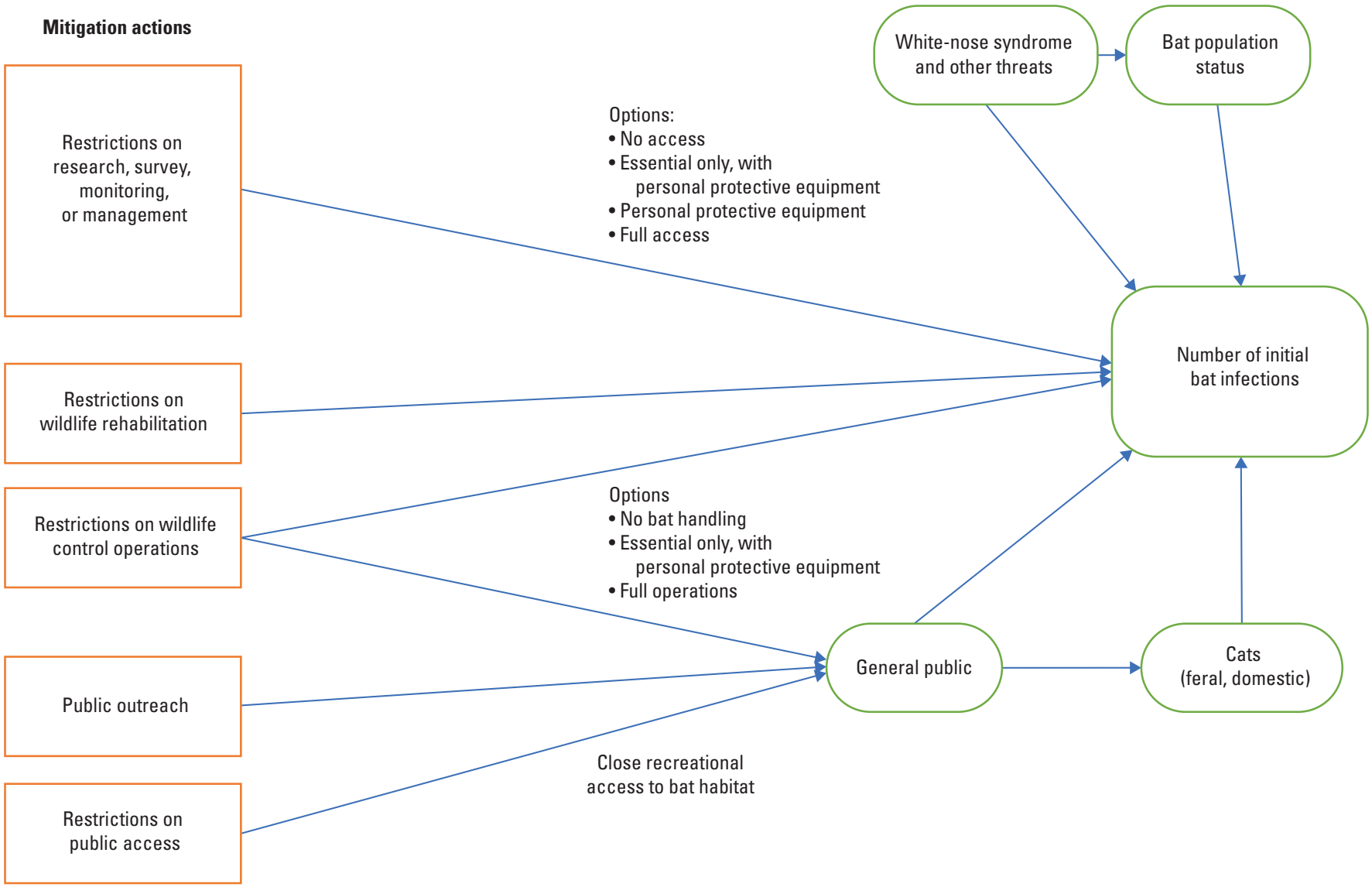

Figure 2. The part of the influence diagram that focuses on the routes of initial transmission of SARS-CoV-2 from humans to bats, with different levels of potential mitigation strategies.

Focal Questions

For this initial risk assessment, we wanted to answer the following five questions, recognizing that they are only a small subset of all the questions embedded in figure 1. These initial questions focus on the transmission risk from humans to bats and begin to address the likelihood of sustained transmission in bats. As a starting point, we chose the little brown bat as a surrogate for North American bats because of their widespread distribution (most of the United States north of Arizona, New Mexico, Texas, and Louisiana, and most of Canada south of the Northwest Territories and Nunavut) and frequent contact with humans (Fenton and Barclay, 1980). We chose to focus on the transmission pathways that may be directly affected by guidance from wildlife and research agencies. Finally, we chose to focus our assessment of risk over the near term (that is, the next 6 months), between April and the end of the 2020 bat active season (November, the beginning of hibernation). The five questions below focus on the baseline probability of transmission and the potential effect of mitigation strategies on the transmission probability. In later sections, we use these questions to motivate a mathematical model, then to develop methods, including expert elicitation, to estimate the relevant parameters.

1. Thinking specifically about little brown bats throughout their range in North America, how many individual wild bats would be infected by SARS-CoV-2 directly from humans undertaking research, survey, monitoring, or management (RSM) activities between now (April 2020) and the initiation of hibernation in autumn 2020, in the absence of any new restrictions, regulations, or protocols?

2. Thinking specifically about little brown bats throughout their range in North America, how many individual bats would be infected by SARS-CoV-2 and released into the wild by humans engaged in wildlife rehabilitation (WR) between now (April 2020) and the initiation of hibernation in autumn 2020, in the absence of any new restrictions, regulations, or protocols?

3. Thinking specifically about little brown bats throughout their range in North America, how many individual wild bats would be infected by SARS-CoV-2 directly by humans engaged in wildlife control (WC) between now (April 2020) and the initiation of hibernation in autumn 2020, in the absence of any new restrictions, regulations, or protocols?

4. (a) How much might the transmission risk owing to research, survey, monitoring, and management (Question 1) be reduced if the fieldwork protocols and guidance included all the following:

   - restriction of fieldwork to people without symptoms or contact with someone who had symptoms of COVID-19 in the last 14 days,
   - training and oversight in the proper use of PPE,
   - proper use of Tyvek or other dedicated clothing,
   - proper use of an appropriate N95 respirator, and
   - proper use of gloves when handling bats.

   (b) Is there any reason to believe this reduction in transmission risk owing to proper use of PPE would be different for wildlife rehabilitators or wildlife control operators compared to scientists or biologists engaged in research, survey, monitoring, and management?

5. What is the basic reproduction number, R_0, for SARS-CoV-2 in little brown bats during the active season? That is, for each infected little brown bat within a naïve population, how many other little brown bats would become infected with the virus?

Questions 1–3 are designed to estimate the probability of infection of bats with SARS-CoV-2 via three pathways of exposure (research and management, wildlife rehabilitation, and wildlife control operations), in the absence of any new guidance (status quo). Question 4 addresses the efficacy of PPE to reduce exposure and subsequent infection. Question 5 provides a rough estimate of the likelihood of sustained bat-to-bat transmission.

This initial focus leaves out many questions of interest. It does not address indirect pathways of transmission (for example, via the general public's contact with bats in their homes or during recreation, or via domestic and feral cats). The initial focus here is on pathways that State and Federal wildlife agencies may be able to directly interrupt. Likewise, this initial focus does not address the effects on the other fundamental outcomes of interest (including mortality of bats, transfer back to humans; fig. 1), but it does address the primary node through which the risk flows (exposure and infection of bats from humans). Because of the urgency to consider interventions available to management agencies in preventing transmission of SARS-CoV-2 from humans to bats, the focus of this assessment is on the pathways that can be affected in the near term.

Model for the Direct Transmission Pathways

The first three questions listed above address three transmission pathways. Because the pathways are fairly complex, we believed that it would be difficult for experts to directly answer Questions 1–3. Instead, for these questions, we have developed a mathematical model for the component elements of the pathways, and we focused elicitation on those elements.

For the first pathway, we consider the following model, which describes individual components of the transmission process from humans engaged in research, survey, monitoring, or management of bat populations. The model combines the average infection status of humans working with bats, the number of bats encountered (directly through handling and

indirectly by proximity), the probability of exposing the bats to the virus, and the probability a bat can be infected once it is exposed:

$$I_{ML}^{RSM} = p_{RSM}^{+}(H_{ML}^{RSM}\beta_{H}^{RSM} + E_{ML}^{RSM}\beta_{E}^{RSM} + P_{ML}^{RSM}\beta_{P}^{RSM})\sigma_{ML} \quad (1)$$

where

I_{ML}^{RSM} is the number of little brown bats (ML) directly infected over the course of the 2020 active season by people engaged in research, survey, monitoring, or management (RSM);

p_{RSM}^{+} is the probability that someone conducting such work is actively shedding SARS-CoV-2 virus on any given day of the 2020 active season;

H_{ML}^{RSM} is the total number of little brown bats physically handled by any RSM scientist over the course of the 2020 active season;

β_{H}^{RSM} is the probability that a bat handled by an RSM scientist who was actively shedding virus would be exposed to the virus (an "exposure probability"), in the absence of any new restrictions, regulations, or protocols, taking into account the handling time typical of RSM activities;

E_{ML}^{RSM} is the total number of little brown bats encountered by any RSM scientist within a 6-foot proximity in an enclosed space (such as a cave or attic), without handling, over the course of the 2020 active season;

β_{E}^{RSM} is the probability that a bat in an enclosed space within a 6-foot proximity of (but not handled by) a RSM scientist who was actively shedding virus would be exposed to the virus (an "exposure probability"), in the absence of any new restrictions, regulations, or protocols;

P_{ML}^{RSM} is the total number of little brown bats encountered by any RSM scientist within a 6-foot proximity but **not** in an enclosed space, without handling, over the course of the 2020 active season;

β_{P}^{RSM} is the probability that a bat **not** in an enclosed space but within a 6-foot proximity of (and not handled by) an RSM scientist who was actively shedding virus would be exposed to the virus (an "exposure probability"), in the absence of new restrictions, regulations, or protocols; and

σ_{ML} is the probability that a little brown bat exposed to a sufficient viral dose of SARS-CoV-2 would actually become infected by the virus (the "infection probability").

Note that we are separating the processes of exposure and infection. By exposure probability, we mean the likelihood that a particular interaction between an average bat and a person who is actively shedding SARS-CoV-2 virus will result in exposure of the bat to a sufficient viral dose to cause infection. By infection probability, we mean the probability that the virus replicates in the host (bat) tissue, conditional on that bat having been exposed to a sufficient viral dose. That is, the exposure process is about whether enough virus was transferred to make an infection possible; it is a property of the interaction between the biologist and that bat. The infection process is about the molecular, cellular, immunological, and physiological conditions that allow viral replication in the bat; it is a property of the interaction of the bat and the pathogen.

The parameters H_{ML}^{RSM}, E_{ML}^{RSM}, and P_{ML}^{RSM} were estimated by surveying State, Federal, and research agencies engaged in bat research (see "Methods" section). The parameter p_{RSM}^{+} was estimated from human epidemiological models of COVID-19, accounting for the expected cumulative incidence over the 2020 active season and the average length of time that an infected person is shedding virus (see "Methods" section). At this time, in the absence of empirical data, the three exposure probabilities, β_{H}^{RSM}, β_{E}^{RSM}, and β_{P}^{RSM}, and the infection probability, σ_{ML}, had to be estimated through expert elicitation.

We describe the second pathway of transmission, through the activities of wildlife rehabilitators, in a similar manner:

$$I_{ML}^{WR} = p_{WR}^{+}(H_{ML}^{WR}\beta_{H}^{WR} + P_{ML}^{WR}\beta_{P}^{WR})\sigma_{ML} \quad (2)$$

where the subscripts and superscripts now refer to people engaged in wildlife rehabilitation (WR), but the parameters are analogous to equation 1. Note that in this equation, there are only two "distances" of interaction: handling (*H*) and proximity (*P*, here meaning within a 6-foot proximity, whether enclosed or not); we expect that, in most cases, the interactions that wildlife rehabilitators have with bats involve handling, typically for more extensive periods of time than in other pathways.

The parameters H_{ML}^{WR} and P_{ML}^{WR} were estimated by surveying State agencies that permit or otherwise authorize wildlife rehabilitation organizations (see "Methods" section). At this time, the two exposure rates, β_{H}^{WR} and β_{P}^{WR}, were estimated through expert elicitation because we lack empirical estimates.

We assumed that the parameter p_{WR}^{+} did not differ from p_{RSM}^{+}. Likewise, we assumed the infection rate conditional on exposure, σ_{ML}, is the same in equations 1 and 2, as well as equation 3 below. That is, we assumed the infection rate is a function of the bat species but does not differ on the basis of the route of transmission because the effects of the route of transmission are captured in the exposure rates.

We describe the third pathway of transmission, through the activities of wildlife control operators, in a similar manner:

$$I_{ML}^{WC} = p_{WC}^{+}(H_{ML}^{WC}\beta_{H}^{WC} + P_{ML}^{WC}\beta_{P}^{WC})\sigma_{ML} \quad (3)$$

where the subscripts and superscripts now refer to people engaged in wildlife control operations (WC), but the parameters are analogous to those in equation 2.

The parameters H_{ML}^{WC} and P_{ML}^{WC} were estimated by surveying State agencies that permit or otherwise authorize wildlife rehabilitation organizations (see "Methods" section). The two exposure rates, β_H^{WC} and β_P^{WC}, were estimated through expert elicitation. As in equation 2, we assume that p_{WC}^{+} is identical to p_{RSM}^{+} and that σ_{ML} is the same across transmission pathways.

Equations 1, 2, and 3 specifically focus on the transmission rates under status quo conditions, by which we mean the ways wildlife biologists and other professionals in the United States most likely would have interacted with bats prior to the arrival of SARS-CoV-2 in North America. In particular, past concern about transfer of biological agents was primarily focused on rabies virus, histoplasmosis, and the fungus *P. destructans*. Typical protocols for *P. destructans* involve decontamination of clothing and footwear between sites and wearing nitrile gloves (with disposal or decontamination between bats), but use of face masks or respirators was not implemented or continued once it was determined humans were unlikely to be harmed by the fungus. Face masks are employed only in specific situations, primarily when working amidst large amounts of bat guano. We were also interested in assessing whether updating guidance and protocols for work with bats (including use of PPE) can reduce the transmission rates. To do this, we assume that the effect of such guidance is on the exposure parameters (the β parameters). For this initial risk assessment, we focus on guidance that allows all work with bats to continue but includes all of the mitigations described in Focal Question 4. We estimated the change in the β parameters as a result of use of enhanced PPE through expert elicitation.

Methods

Expert Elicitation

We used expert elicitation methods to estimate 12 parameters for which data are not yet available (the seven exposure rates in equations 1, 2, and 3; the infection rate in equations 1, 2, and 3; three multipliers of exposure rate that reflect the effect of enhanced PPE; and the basic reproduction number, R_0, for SARS-CoV-2 in little brown bats; see appendix 1). To reduce the effects of expert bias and overconfidence on the results, we conducted an elicitation using a modified Delphi process that includes two rounds of elicitation with feedback and discussion in between. Six steps were followed: (1) choosing experts, (2) training experts, (3) conducting a first round of elicitation, (4) reviewing and discussing the first round with the experts, (5) allowing experts to adjust their assessments in a second round of elicitation, and (6) aggregating the estimates across experts (Hanea and others, 2017). The modified Delphi approach requires experts to share and discuss the logic behind their opinions. In addition, to capture within-expert uncertainty, the four-point elicitation procedure was used (Speirs-Bridge and others, 2010), which consists of asking experts for their lowest, highest, and best estimates, and their confidence the true value lies within the reported interval. By using the scientific judgments from multiple experts, we included uncertainty in scientific understanding in the predictions of the effect of mitigation actions on the desired outcomes.

Through literature review and the professional contacts of two of the authors of this report (P.M. Cryan and K.J. Olival), a list was compiled of 43 experts whose expertise spans bat ecology, virology (especially of coronaviruses), epidemiology, and wildlife disease, with an emphasis on experts who had a demonstrated background in one or more of those fields. Seventeen experts from this list were invited to participate in the elicitation. The invited participants were selected to produce a group with diverse and complementary scientific backgrounds, from several countries, with a balanced gender representation. The invited participants included scientists from academic institutions, government agencies, and non-governmental organizations (see Acknowledgments).

Training

Formal expert elicitation is a new process for many, so the first step was to familiarize experts with the approach. This training step increases the quality of expert judgment for unknown qualities (Cooke, 1991). Before starting the elicitation concerning the questions of interest, we provided the expert panel a chance to practice the elicitation methods. Questions were provided for which the answers were known (that is, answers were identified values from the literature, but they were unlikely to be known precisely by experts). The questions were used to ensure that the instructions were understood by the experts and to allow the experts a chance to self-calibrate their estimates of uncertainty. We asked three questions (Appendix 1)—one for which we assumed the uncertainty had a normal distribution (forearm length of a little brown bat), one for which we assumed a log-normal distribution of uncertainty (R_0 of WNS), and one for which we assumed a logit-normal distribution (breeding probability)—which represented the kinds of parameters we would ask in the real elicitation. Experts were provided with a custom spreadsheet to record their answers, which plotted the probability distribution resulting from their responses. We did not use responses to the training questions to rank expert quality or weight experts when summarizing responses for the model.

The results of the training questions were summarized and sent to the experts prior to the first elicitation round. The exercise revealed some potential for linguistic uncertainty in two of the questions (R_0 and breeding probability), which we discussed in feedback to the experts prior to the first elicitation round.

Round 1

The experts were provided with a document that described the background of the study, a summary (a draft synthesis manuscript, including literature references) of the current state of knowledge on SARS-CoV-2 and bats, a detailed description of the quantities that were being elicited (see Appendix 1), instructions for completing the elicitation, and a spreadsheet that plotted the distribution that represented their uncertainty from their responses to the four-point elicitation. The experts were asked to work independently and return their responses within about 72 hours.

Group Discussion

The results from the first round of elicitation were compiled; for each question, the anonymous responses for each of the experts were shown graphically (for example, appendix fig. 2.1*A*), the fitted distribution for each expert was plotted (for example, fig. 2.1*B*), and the average distribution across experts was plotted (for example, fig. 2.1*C*). Two 2-hour video conference calls were held with the experts to discuss the first round of results, focusing on several topics: clarifying the interpretation of the questions, sharing insights of individual experts, discussing notable differences in how the experts answered the questions, and reinforcing the instructions for the four-point elicitation method. After the calls, the results of the first round and a brief written summary of the discussion (especially, to clarify the questions) were provided to the experts.

Round 2

The experts were asked to reconsider their responses to the questions, taking into account the group discussion, and independently provide a revised set of answers within 24 hours.

Aggregation of Experts

Separately for each parameter and expert, we fitted a probability distribution to the responses to the four-point elicitation, assuming the best estimate corresponded to the median and the confidence limits represented symmetric quantiles. We assumed that questions 1–8 were best represented with logit-normal distributions because the quantities elicited were proportions bounded by 0 and 1, which is the support for the logit-normal distribution. We assumed that questions 9–11 and 13 were best represented with lognormal distributions because the quantities elicited were bounded by 0 on the lower end and unbounded on the upper end, like the lognormal distribution. We fitted the distributions by regressing the inverse cumulative distribution function of the quantiles against the corresponding values.

The individual probability density functions (PDF) were aggregated, with equal weight, across experts. We then found the parameters of a logit-normal or lognormal distribution that best fit the average PDF, as measured by the Kullback-Leibler distance (Kullback and Leibler, 1951). The fitted, aggregated distribution provided an estimate, with uncertainty, for each parameter.

Other Parameters

Bat Handling Data

Seven State and four Federal wildlife agencies were queried for bat research or permit records to estimate the number of bats handled over the course of a field season for the three transmission pathways. The State and Federal agencies queried were a non-random sample, composed primarily of agencies that were on the guidance committee (see Acknowledgments).

Probability an Individual Human is Shedding SARS-CoV-2

To estimate the probability that a bat worker would be shedding SARS-CoV-2 at the time of an encounter with a bat (p^{+}_{RSM} in equation 1), three components were considered: cumulative incidence, which is the probability of the worker becoming infected with SARS-CoV-2 in the United States from April 15 through November 15, 2020 (C^{+}); the length of time an individual with COVID-19 is shedding virus (s); and the length of the period of time in question (t, 214 days, April 15–November 15, 2020). Then, the desired probability is given by

$$p^{+}_{RSM} = C^{+} * \frac{s}{t}. \quad (4)$$

Regarding the cumulative incidence (C^{+}), although a number of models can forecast SARS-CoV-2 infection in humans, most report only the peak number of hospital admissions and intensive care unit beds or provide forecasts for only the next approximately 4 months. We could not find any models that specifically forecast the cumulative incidence between April 15 and November 15, 2020, but there are a few models that forecast the incidence through the course of the epidemic. If we assume that the bulk of the epidemic in the United States will occur by November 15, those forecasts are helpful benchmarks. The forecast of Moghadas and others (2020) was used, which estimates the cumulative incidence for the COVID-19 epidemic in the United States under two values of R_0 for SARS-CoV-2 in humans (2.0, 2.5), resulting in 177 million and 233 million people infected through the end of the epidemic (representing 53.8 and 70.5 percent, respectively, of the total U.S. population infected, assuming a U.S. population

size of 329.1 million, https://www.census.gov/popclock/; accessed April 20, 2020). These estimates are similar to the forecast of Ferguson and others (2020) for 81 percent of the U.S. population to be infected, if R_0 is 2.4. We treated the two estimates from Moghades and others (2020) as the median and 90th quantile of a logit-normal distribution. For the 10th quantile for the cumulative incidence of COVID-19 disease in the United States by November 15, 2020, we divided the number of reported cases on April 20 (788,172; https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/cases-in-us.html) by a reporting rate of 0.066 for the United States (Bommer and Vollmer, 2020) and multiplied by 3 (assuming mid-April was roughly the peak infection rate in the United States, and the decline will involve three times as many cases as the increase); the result is a 10.9-percent cumulative infection rate through November 15. We fitted these three quantiles (10th, 50th, and 90th) to a logit-normal distribution.

We estimated shedding duration (s) using results from Zhou and others (2020a) who found a median duration of SARS-CoV-2 shedding for hospitalized patients to be 31.0 days from illness onset (interquartile range [IQR]: 24.0–40.0, minimum: 18, maximum: 48). Other studies (Wölfel and others, 2020; Zou and others, 2020) report shorter maximum durations, but that may be related to the lengths of observation studies. A linear model fitted to figure 1b of Wölfel and others (2020) estimates a maximum of 25 days of shedding. Zou and others (2020) report detection of viral DNA up to the end of the study period (21 days). To capture uncertainty in the duration of viral shedding, we fitted a normal distribution to the values (18, 31, 48), associating those values with three quantiles (0.025, 0.50, 0.975).

Simulation Model

To integrate the estimates of the parameters in equations 1, 2, and 3, and to propagate the uncertainty in those estimates through to the results, we built a Monte Carlo simulation model for those equations. We sampled each parameter from the probability distribution that represented its estimate. In most cases, the parameters were sampled independently, but for the 3 RSM exposure probabilities (the β parameters in equation 1), the 2 WR exposure probabilities (the β parameters in equation 2), the 2 WC exposure probabilities (the β parameters in equation 3), and the three PPE multipliers, we assumed that the parameters in those sets had a correlation of 0.50 to reflect the assumption that, for example, if the true exposure probability for RSM handling was on the high end of its uncertainty distribution, the true exposure probability for RSM proximity is likely to be at the high end of its uncertainty distribution. For each of 1,000 replicates in the simulation, equations 1 through 3 were used to calculate the number of infected bats from the sampled parameter values.

Results

Encounters with Bats

Federal and State wildlife agencies do not have a common system for documenting and recording encounters with bats by scientists, rehabilitators, and wildlife control operators, so the data on encounters were difficult to compare across agencies (table 1). Bat research, survey, monitoring, and management activities span all three types of encounter, with a mixture that depends on how the agency in question permits such activities, as well as the needs of the specific setting. Across agencies that were able to report encounters for all three modes, 45.8 percent involved handling, 11.5 percent involved proximity in an enclosed space, and 42.7 percent involved proximity in an unenclosed space. Wildlife rehabilitation invariably involves handling, not simply proximity to bats. Wildlife control operations have a mixture of activities that involve handling or proximity. Across the States that reported totals for two modes of encounter, 22.9 percent of the encounters by wildlife control operators involved handling, and 77.1 percent involved proximity without handling.

After the data in table 1 were collected from the wildlife agencies, we realized several unanticipated challenges: (1) the data are not collected in a common way across agencies, making comparisons difficult; (2) there may be duplicate counts because the same activity may be recorded by multiple agencies (for example, a research project conducted on USFS land in Virginia may be recorded both by USFS and by the Virginia Department of Game and Inland Fisheries); (3) it was not possible, in the available time frame, to gather comprehensive data across the United States; and (4) in many cases, the data on encounters are recorded for all bats, not by species. In light of these challenges, we were not able to estimate the H, E, and P parameters in equations 1, 2, and 3. Instead, we used the data in table 1 to estimate relative values for H, E, and P. Thus, in the results that follow, the number of potential infections is not expressed on an absolute scale, but on a relative scale, reflecting the probability of infection.

Expert Judgment

Of the 17 experts invited to participate in the elicitation process, 13 participated in either Round 1 or Round 2; in the final analysis, we included only the 12 experts who had participated in the group discussions and who submitted Round 2 estimates afterwards. The four-point responses, the individual fitted distributions, the mean aggregate distribution, and the fitted aggregate distribution are shown for each question in Appendix 2.

Table 1. Number of bats encountered during the 2019 active bat season.

[The entries show the number of bats of any species encountered during the 2019 active bat season, April 15–November 15, 2019, as reported through direct requests to the agencies listed in the table. Blank entries indicate only that the quantity was not recorded or estimated by the agency, whereas an entry of 0 indicates that the agency recorded no encounters in that category. Gray cells indicate no encounters were expected because the agencies in question do not oversee rehabilitation or wildlife control operations. CO CPW, Colorado Parks and Wildlife; CT DEEP, Connecticut Department of Energy and Environmental Protection; KY DFWR, Kentucky Department of Fish and Wildlife Resources; NYSDEC, New York State Department of Environmental Conservation; OR DFW, Oregon Department of Fish and Wildlife; VA DGIF, Virginia Department of Game and Inland Fisheries; WI DNR, Wisconsin Department of Natural Resources; FS, Forest Service; NPS, National Park Service; USGS, U.S. Geological Survey; WNS, white-nose syndrome surveillance program; k, thousand]

Agency	Research, survey, monitoring, and management			Wildlife rehabilitation		Wildlife control operations	
	Handling	Enclosed	Proximity	Handling	Proximity	Handling	Proximity
CO CPW	456	521		93		50	
CT DEEP	10	400	250	101		250	300
KY DFWR	6,750	675	[1]202,500	20	0	15	785
NYSDEC	625	0	0	335	0	[2]16k–63k	0
OR DFW	1,038	750	150	177		91	
VA DGIF	907	0	0	528	0	79	412
WI DNR	1,053	250	600	576	0	[3]103	[3]5
FS, CO	30	0	200				
FS, KY	130	11	153				
FS, OR	22	13	170				
FS, WI	90	26	101				
NPS, CO	410	0	0				
NPS, CT	0	0	0				
NPS, KY	299	[4]12,000	30				
NPS, VA and NY	200	0	0				
NPS, OR	75	0	0				
NPS, WI	0	0	0				
WNS Surveillance	2,192	147	732				
USGS[5]	1,860	575	5,700				
Total[6]	8,642	2,172	8,056	1,459	0	447	1,502

[1]The large number of bats in the proximity of scientists arises primarily from emergence counts from roost sites.

[2]This estimate includes bats handled by homeowners as well as wildlife control operators.

[3]Includes only wildlife control operators with permits to handle State threatened and endangered species (possibly only 25–30 percent of operators).

[4]This includes bats within 6 feet of tour guides at Mammoth Cave National Park over the duration of the summer.

[5]This includes all USGS scientists within the Ecosystems Mission Area who work on bats.

[6]For all columns within each category (Research, survey, monitoring, and management; Wildlife rehabilitation; Wildlife control), the total includes those agencies that reported entries for each mode of handling in the category, without a noted exception as to how the encounters were interpreted. That is, to be included in the totals for a category, an agency needed to report entries for each of the handling modes, and there needed to be no exceptions noted on any of the entries. If these conditions were not met, then none of the entries for that agency were included in the totals for that category.

For RSM workers, the detailed responses for the three exposure probabilities (Q1, Q2, and Q3) are shown in Appendix figures 2.1, 2.2, and 2.3, and the fitted aggregate distributions are summarized in figure 3. Using the fitted aggregate distribution, we estimated that a median 49.7 bats per 100 handled by actively shedding SARS-Co-V-2 virus (CoV+) RSM workers would be exposed to a sufficient dose of virus for infection (80-percent interval, 15.3–84.3); this is close to a uniform distribution between 0 and 100, indicating the experts had considerable uncertainty about the degree of this exposure. For Q2, the aggregated expert judgment is that a median 19.4 bats per 100 encountered within an enclosed space by CoV+ RSM workers would be exposed to a sufficient dose of virus to possibly lead to infection (80-percent interval, 2.2–72.4). For Q3, the aggregated expert judgment is that a median 6.4 bats per 100 encountered within 6 feet in an unenclosed space by CoV+ RSM workers would be exposed to a sufficient infectious dose of virus (80-percent interval, 0.6–43.8). Thus, although the experts expressed considerable uncertainty in the range of these exposure probabilities, the pattern showed a consistent decrease as the nature of the encounter became less proximal (fig. 3). Similar types of results were estimated for the exposure rates through the wildlife rehabilitation (figs. 2.4 and 2.5) and wildlife control (figs. 2.6 and 2.7) transmission pathways.

Conditional on exposure to a sufficient dose of SARS-CoV-2, the experts estimated that the median probability a little brown bat would develop an infection was 0.44 (80-percent interval, 0.08–0.88; fig. 2.8). During discussion, the experts noted their particular uncertainty about this parameter (represented by the nearly uniform aggregate distribution) and noted that this parameter is a critically important nexus in the causal diagram (fig. 1).

The experts expected that proper use of PPE (that is, an appropriate N95 respirator and other protective gear) would be effective at substantially reducing the exposure probability. The detailed responses of the experts are shown in figures 2.9, 2.10, and 2.11 (Appendix 2) as proportional multipliers on exposure probability. The fitted aggregate distribution, expressed as the percent reduction in exposure (1 minus the quantity elicited), did not differ substantially among the three modes of handling (fig. 4), ranging from a mean of 94 to 96 percent effective. When asked an open-ended question about whether the effectiveness of PPE would differ among scientists (RSM), rehabilitators (WR), and wildlife control operators (WC), the experts were inconclusive; about half thought there would not be tangible differences in the effectiveness of PPE, and the other half thought that differences in compliance among the three groups could possibly affect the amount by which exposure was reduced.

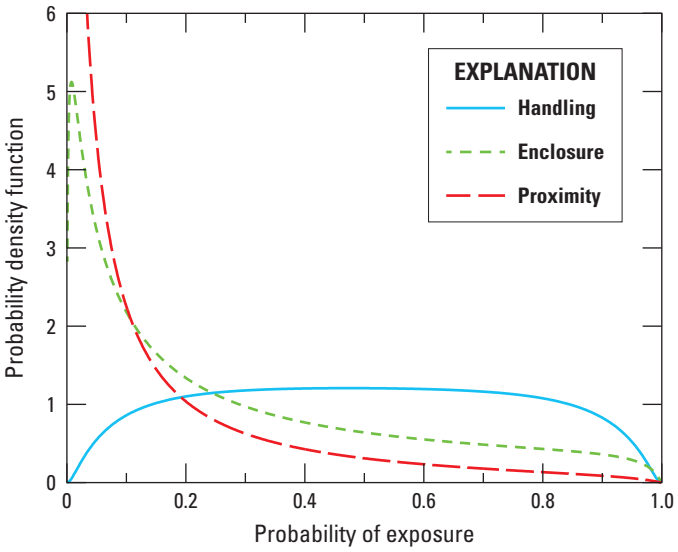

Figure 3. Aggregate probability distributions for the probability of exposure of bats from a SARS-CoV-2-positive research, survey, monitoring, and management worker, referenced in expert judgment questions Q1, Q2, and Q3.

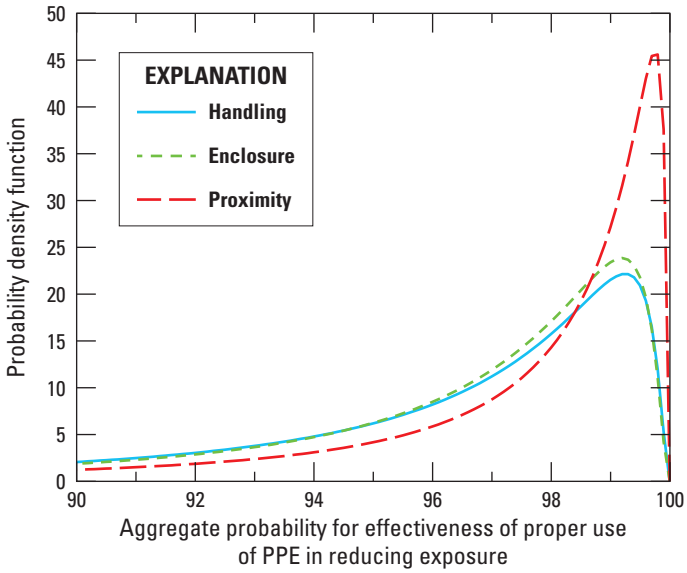

Figure 4. Aggregate probability distributions for the effectiveness of proper use of personal protective equipment in reducing exposure of bats to SARS-CoV-2 by a research, survey, monitoring, and management worker, referenced in expert judgment questions Q9, Q10, and Q11, expressed as the percent reduction in exposure.

Probability a Worker is Shedding Virus

The probability of a worker shedding SARS-CoV-2 virus during an encounter with bats over the course of summer 2020 (April 15–November 15), absent a change in field work practices, was estimated to be 0.057 (that is, 5.7 percent, median; 80-percent interval, 0.022–0.112; fig. 5). This is based on a cumulative incidence of 0.39 (median; 80-percent interval, 0.17–0.71) and a shedding duration of 33 days (median; 80-percent interval, 23–42) within a 214-day field season.

Probability of Bats Being Infected

Combining the probabilities of exposure and infection, for multiple modes of encounter under status quo conditions, we estimate that a CoV+ RSM scientist would infect 107 (median) per 1,000 bats (80-percent interval, 16–348); a CoV+ WR worker would infect 252 (median; 80-percent interval, 41–654) per 1,000; and a CoV+ WC worker would infect 50 (median; 80-percent interval, 5–268) per 1,000 (fig. 6).

Combining the probabilities of exposure and infection (fig. 6) with the probability that a worker is CoV+ (fig. 5),

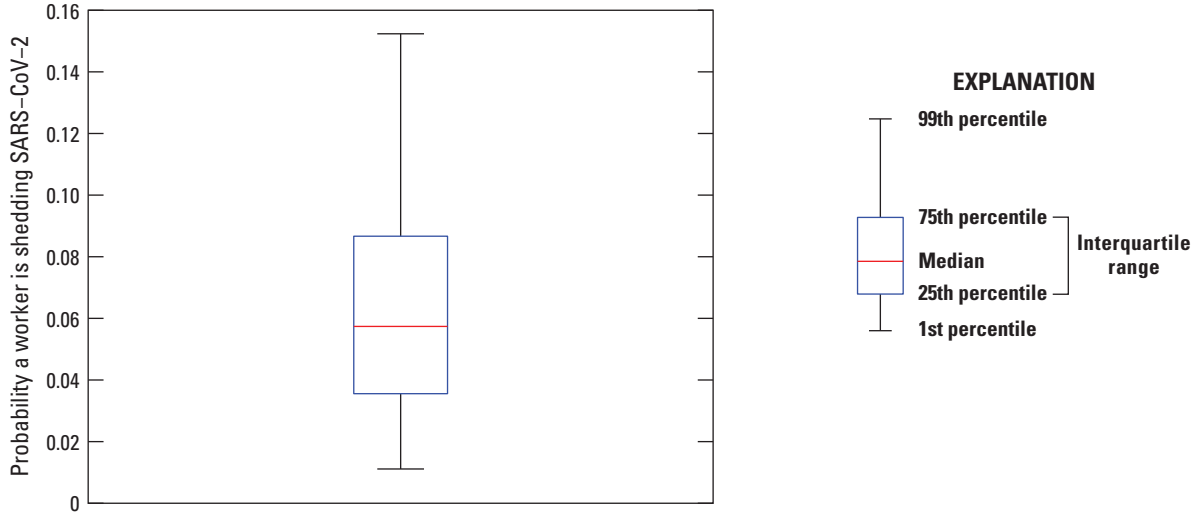

Figure 5. Probability that a worker is shedding SARS-CoV-2 during an encounter with a bat.

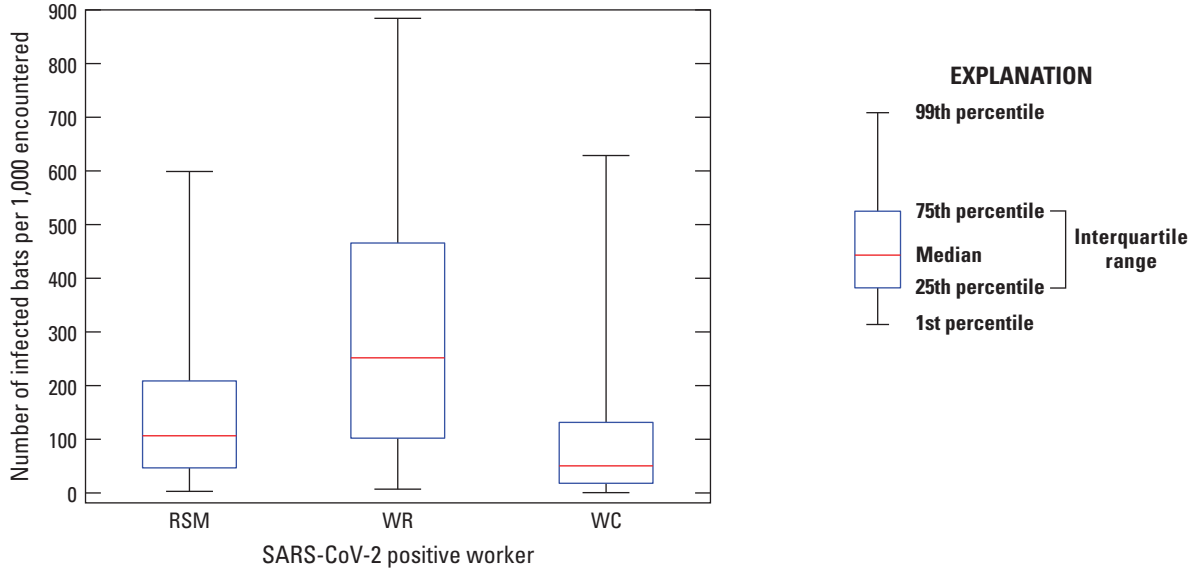

Figure 6. Number of bats per 1,000 exposed to and infected by virus from a SARS-CoV-2-positive worker, by transmission pathway, under status quo working conditions. (RSM, research, survey, monitoring, and management activities; WR, wildlife rehabilitation; WC, wildlife control operations.) These results were obtained with the assumed ratio of encounter modes (handling, enclosure, and proximity) estimated from the totals in table 1.

we estimate that an average RSM worker would infect 6.0 (median) per 1,000 bats (80-percent interval, 0.8–22.2); an average WR worker would infect 12.7 (median; 80-percent interval, 1.8–42.8) per 1,000; and an average WC worker would infect 2.7 (median; 80-percent interval, 0.3–16.6) per 1,000 (fig. 7), under status quo conditions. But if PPE protocols and training are implemented, the respective probabilities of infection drop to 0.2, 0.4, and 0.1 bats per 1,000, respectively (median values, with narrow uncertainty ranges; fig. 7).

Another way to understand the results in figure 7 is to consider the probability that the number of infections exceeds some threshold value. For example, the probabilities that at least 5 per 1,000 bats are infected is 55 percent for RSM (1.3 percent with PPE), 75 percent for WR (4.6 percent with PPE), and 35 percent for WR (0.6 percent with PPE). We use the exceedance threshold 5 per 1,000 to demonstrate this approach; the relevant threshold value reflects the decision maker's risk tolerance for introduction of infected bats to the wild population.

The effect of the mode of encounter on the infection rate in the RSM transmission pathway is notable (fig. 8). The combined probability that at least 5 bats per 1,000 are exposed to and infected by SARS-CoV-2 from an average RSM worker is 66 percent if handling is involved (3.1 percent with PPE), 40 percent if the bats are encountered in an enclosed space without handling (1.3 percent with PPE), and 24 percent if the bats are encountered in an unenclosed space (0.4 percent with PPE).

Probability of Transmission in Bat Populations

The experts expressed considerable uncertainty about the basic reproduction number (R_0) for SARS-CoV-2 in little brown bats (fig. 9; expert panel responses in fig. 2.12). The bulk of the fitted aggregate distribution was less than 1.0, with a median of 0.45 and an 80-percent interval of (0.05, 4.38), but the experts could not rule out the possibility that SARS-CoV-2 could be effectively transmitted in a little brown bat population. For the fitted aggregate distribution, the probability that the basic reproduction number (R_0) is greater than 1 is 32.6 percent.

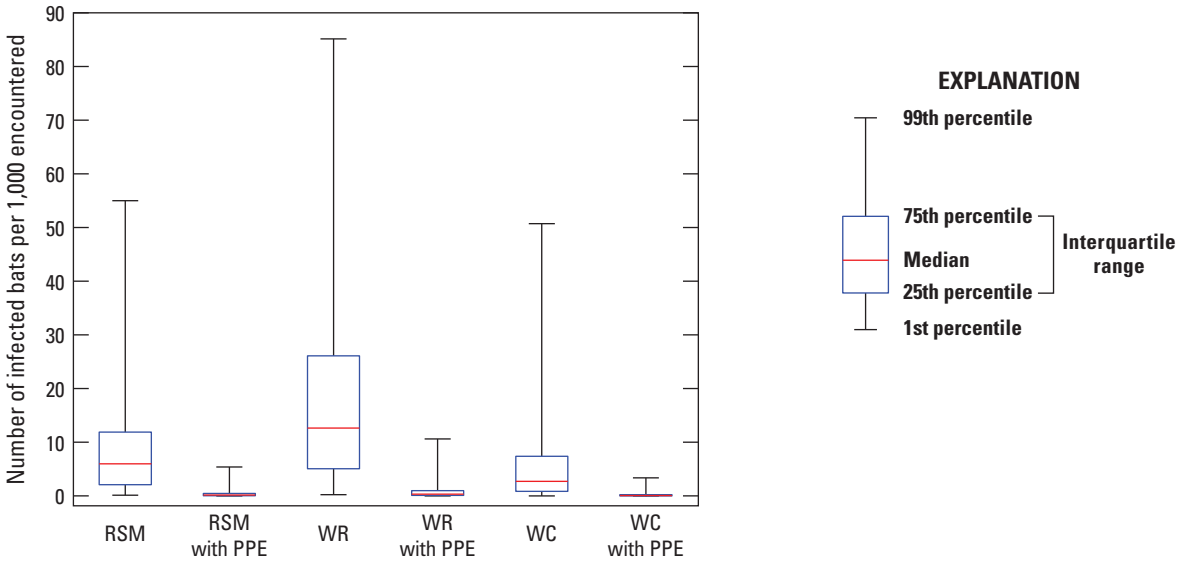

Figure 7. Number of bats per 1,000 exposed to and infected by SARS-CoV-2 from an average worker, by transmission pathway, without and with the proper use of personal protective equipment. (RSM, research, survey, monitoring, and management activities; WR, wildlife rehabilitation; WC, wildlife control operations; PPE, personal protective equipment)

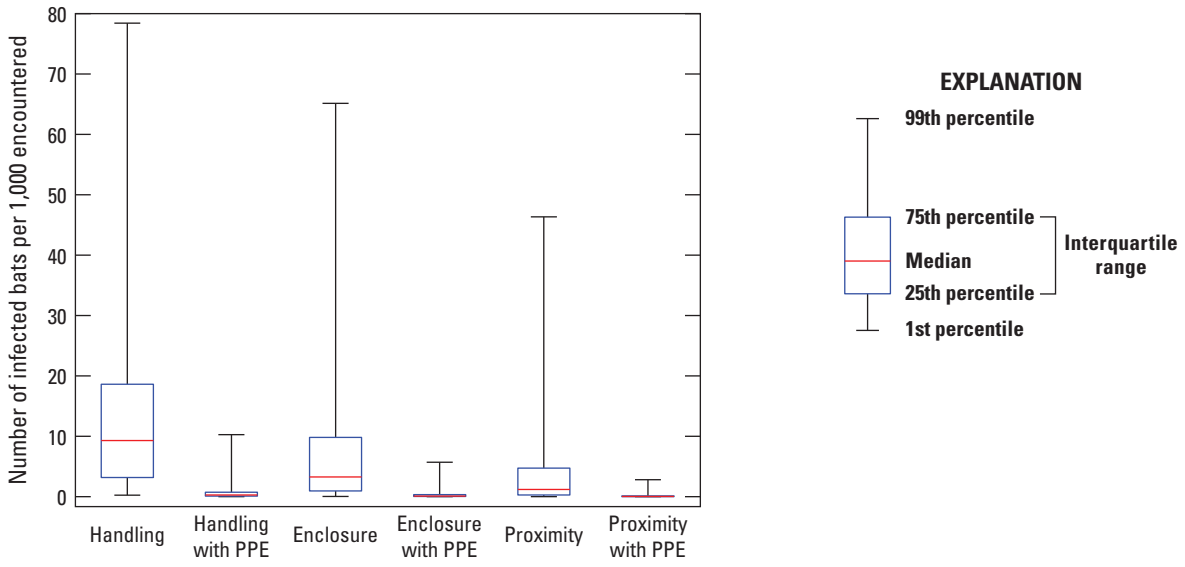

Figure 8. Number of bats per 1,000 exposed to and infected by SARS-CoV-2 from an average scientist in the RSM pathway, by encounter type, without and with proper use of personal protective equipment. (RSM, research, survey, monitoring, and management activities; PPE, personal protective equipment)

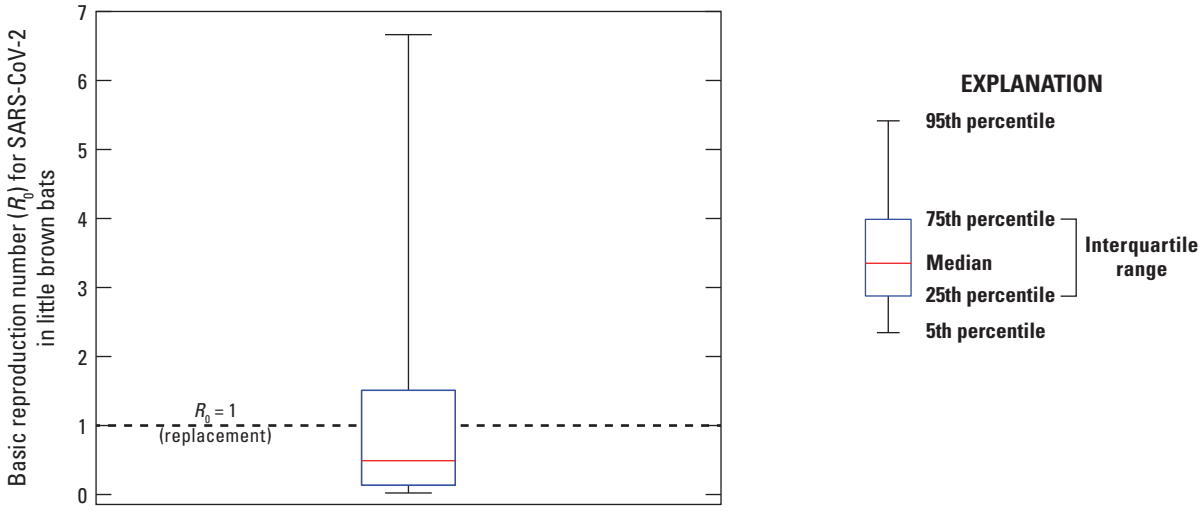

Figure 9. Basic reproduction number, R_0, for SARS-CoV-2 in little brown bats, as estimated by an expert panel.

Discussion

This risk assessment was a response to the concern that the novel β-coronavirus, SARS-CoV-2, could be transmitted to naïve North American bat populations through human contact, and once infected, bats could experience mortality and become a reservoir for the virus with the potential to re-infect people in the future. The goal of this assessment is to provide timely scientific information to guide State and Federal wildlife management agency response to this potential risk. The rapid emergence of SARS-CoV-2 in human populations created significant uncertainty in forecasting the risk of transmission to native bat populations. Along with decision makers from State and Federal agencies, we framed the management decision using principles of decision analysis, identified important objectives, and articulated potential mitigation actions. By framing the decision explicitly, we were able to provide information specifically useful for risk mitigation.

The World Organisation for Animal Health (OIE) Aquatic Animal Health Code defines a risk analysis as being composed of four parts: hazard identification, risk assessment, risk management, and risk communication (World Organisation for Animal Health, 2019, Chapter 2.1). The first step is the identification of a pathogen which may pose a hazard to wildlife. The second step, which is the aim of this report, provides decision makers with an objective and defensible method of assessing the risk associated with the pathogen. The third step is the implementation of risk management actions to mitigate the identified risk. Communication occurs throughout the process.

Uncertainty is the central challenge of risk management for decision makers—how to estimate the uncertainty and how to understand risk tolerance in choosing an action in the face of uncertainty. A quantification of risk combines the uncertainty in the range of outcomes and some measure of the potential harm under those outcomes. By framing the mitigation decisions with wildlife management agencies, we identified the outcomes that agencies wanted to avoid (the objectives articulated in the "Decision Framework" section). The task described in this report was to estimate the probability of several early steps in the causal chains that lead to those undesirable outcomes. Because of uncertainties about the distribution of the SARS-CoV-2 pathogen in the human population, the likelihood of transmission to bats, and the probability of infection given exposure, we combined expert elicitation and a model for the number of infected bats to estimate the current risk of transmission and the potential level of mitigation provided by the expanded use of PPE for individuals that conduct work with bats. Here, we considered risk as the combined probability of an event happening (that is, the transmission of SARS-CoV-2 from an infected human to a bat) and the magnitude of the undesired outcome (that is, persistence of the coronavirus within bat populations). The level of risk mitigated by a management intervention is determined by the reduction in likelihood of an undesired event and in the reduction of magnitude of the effect of the undesired event. Our aim was to provide decision makers with a risk assessment that could inform their risk management decisions in the near term, for activities that could affect bats over the next 6 months (April–November 2020).

Summary of Results

Our analysis finds a non-negligible risk of transmission of SARS-CoV-2 to bats from humans conducting research, survey, management, rehabilitation, and wildlife control activities. For example, our expert panel estimated that if a research scientist is shedding virus while handling bats under status quo protocols, 50 percent (15–84 percent) of those bats will be exposed to virus, and 17 percent (3–51 percent) will become infected. Although there were differences in exposure potential among the three transmission pathways (RSM, WR, and WC) and the three encounter types, without additional protective measures the probability of transmission resulting in infected bats cannot be ruled out. We found that the type of work being conducted changed the underlying risk; as expected, conducting work in proximity to bats (but in an unenclosed space) had a much lower risk of exposure than direct handling of bats.

We found that the use of PPE is expected to significantly reduce the exposure probabilities for all three modes of encounter with bats. The expert panel estimated that exposure risk from research scientists could be reduced by 94–96 percent (uncertainty, 86–99 percent) through proper use of appropriate N95 respirators and dedicated clothing and gloves.

Finally, we estimate that the median likelihood of bat-to-bat transmission is lower than the value for sustained transmission (that is, the median R_0 value is less than 1.0). However, there was significant uncertainty for this rate, and there remains a reasonable probability (approximately 33 percent) that sustained bat-to-bat transmission will be possible should SARS-CoV-2 be introduced into a wild free-ranging bat population. Further research to better understand bat-to-bat SARS-CoV-2 transmission is warranted.

Scope of Inference

There are some potential limitations to our assessment. We used the little brown bat as a surrogate species for all North American bats for this risk assessment. The little brown bat is one of the most widespread species of *Myotis*, a genus which is diverse and widespread in North America (O'Shea and Bogan, 2003). This species frequently inhabits buildings (Fenton and Barclay, 1980; Kunz and Reynolds, 2003) and is commonly captured for scientific field work (for example, Frick and others, 2010), which leads to a potential for virus transmission from humans to bats. We asked the expert panel to think specifically of little brown bats while they were responding to the elicitation. Our ability to extend the conclusions of this study to other North American species of

bats depends on the similarity of behavior, ecology, physiology, cellular biology, and genetics of those species to little brown bats.

The scope of inference for this analysis was limited to the active period for little brown bats, which we defined as the period from April 15 (when the bats leave hibernacula for maternal roost sites) through November 15 (when individuals return to hibernacula). This is when we expected the greatest contact rates with humans to occur. Because the active season for bat research, wildlife rehabilitation, and wildlife control activities was imminent, our assessment was designed to provide information to management agencies to update interim guidance to these groups. The expert panel and the modeling included herein focused on the active season. It is reasonable to think that the dynamics of exposure, infection, and subsequent transmission may be different during the hibernation season. Subsequent work may be needed to assess the risks for winter bat field work.

For PPE, we considered proper training, oversight, and use of dedicated clothing, gloves, and N95-type respirators. We expected use of PPE to have the largest effect on reducing bat exposure probability. In the elicitation, we did not make a distinction between vented and non-vented respirators, but from the discussion we assumed the experts were thinking about N95 respirators designed to filter exhaled particles. We did not specifically ask the expert panel about the use of alternative face coverings (like surgical masks), nor did we ask the experts to estimate the difference in efficacy of PPE among RSM, WR, and WC workers. In an open-ended question, some members of the expert panel did expect that proper and consistent use of appropriate N95 respirators might vary among groups. Note that other face coverings, including surgical masks, may be effective for reducing the transmission of SARS-CoV-2 because they have been found to be effective for human coronaviruses (Leung and others, 2020), but we do not know whether they will mitigate the transmission risk to the same level as expected for N95 respirators.

Key Assumptions

The inference in this report extends to regions with populations of little brown bats. The analysis contains an assumption that the number and modes of exposure reported by the 7 states, 3 agencies, and the WNS surveillance program represent the proportional encounter rates across the range of the little brown bat. Estimates of human exposure, shedding duration, and the basic reproduction number for SARS-CoV-2 in humans are all currently uncertain. We used estimates of cumulative incidence in humans from the emerging literature, assuming that the cumulative incidence over 7 months (April–November 2020) will be between 0.17 and 0.71 with 80-percent confidence. The forecasts of Moghadas and others (2020) that form the upper end of this interval assume no self-isolation of symptomatic individuals and an infectious period of 4.6 days, although their forecasts including self-isolation have little effect on reducing the epidemic size and peak timing. We thus assume that the current practices of stay-at-home, quarantine, and social distancing may reduce the duration of the epidemic but do not affect the cumulative incidence; given the current uncertainty in the ability to enforce or maintain such social distancing we believe this to be a reasonable baseline estimate to include in the risk assessment. Further, the reported cases do not include the asymptomatic individuals, and the estimated reporting rate (Bommer and Vollmer, 2020) is for actual cases attributed to COVID-19, so if the (adjusted) reported cases represent approximately 50 percent of the total infections (including mildly symptomatic and asymptomatic individuals; Nishiura and others, 2020; Li and others, 2020; World Health Organization, 2020; Ferguson and others, 2020; Mizumoto and others, 2020), then we believe this estimate to be reasonable for this risk assessment. We note that the asymptomatic portion of the population is a critical uncertainty, discussed in the section “Critical Uncertainties.” The experts were asked to assume that a worker who is infected (positive for SARS-CoV-2) is not showing symptoms. We used an estimated median shedding duration of 33 days—asymptomatic individuals would shed virus for the entire period and would still contribute to bat exposure; we assumed that symptomatic individuals would cease work within 1 day of symptom onset, and would not return to work until 14 days after symptoms resolved. This means that symptomatic individuals would expose bats for 3–4 days before stopping work because they are infectious before symptom onset (He and others 2020).

Experts were asked about their belief in the compliance of the different groups for proper use of PPE. We assume for this analysis that the average effect of PPE was identical across all individuals regardless of profession. Experts were uncertain whether the proportional change in the handling and proximity exposure probabilities for wildlife rehabilitators and wildlife control operators, owing to the same protocol guidance, would be different than for scientists.

Critical Uncertainties

Critical uncertainties are those uncertainties which, if resolved, would change the selection of a mitigation strategy. Because we framed this problem as a decision—identifying the management agencies, authorities, objectives, and potential interventions, and developing a model to link actions with the risk of bat infection—we can identify those uncertainties in the analysis that we would expect to change the risk assessment. At this stage, we have not conducted a value-of-information analysis (Runge and others, 2011) to verify that these uncertainties are critical to the decisions, in part because we have not yet evaluated the full causal pathways. Instead, we discuss below (1) uncertainties we evaluated, which strongly affected the probabilities of the early steps in the causal chains, and (2) uncertainties we have not yet evaluated, but which we judge could have a strong effect on the long-term outcomes and bear future examination.

Bat infection probability and sustained bat-to-bat transmission. These rates are related, and the probability a North American bat could become infected with SARS-CoV-2 was a significant uncertainty. Bats are known to maintain coronavirus infections, and experts expressed the opinion that North American bats were undertested for coronaviruses. New World bats from the Americas are known to host α-coronaviruses (Osborne and others, 2011; Dominguez and others, 2007), but β-coronaviruses may be relatively rare (Anthony and others, 2013; Góes and others, 2013). For the infection rate, σ_{ML}, there is some evidence that the probability of infection may be low (based on sequence matching of the ACE2 receptor; Damas and others, 2020; Luan and others, 2020) but possible; at this time we do not have results from experimental virus challenge trials in bats that would provide the most useful information. SARS-CoV-2 is a member of a group of viruses that is prone to host switching and recombination (Woo and others 2009), so transmission among species may be possible if it establishes in a population of a single species.

Species and regional differences. We also considered in our discussions *Eptesicus fuscus* (big brown bats) and *Tadarida brasiliensis* (Brazilian free-tailed bats), which also have widespread distributions but may have different human contact rates, infection probabilities, basic reproduction numbers, and transmission rates. The important questions to ask in extending this analysis to other species will be which parameters might differ and whether those differences might affect the baseline risk or the effect of proposed mitigation strategies. Species, communities, roost sites, availability, adherence to PPE guidelines, and the modes of interaction between bats and humans may all differ regionally.

The human probability of infection, shedding, and the amount of viral particles shed. The probability of transmission from humans to bats increases with both the duration of exposure and the quantity of viral particles shed. Shedding of viral particles changes over the course of infection and may peak even before symptoms manifest (He and others, 2020). It is unknown whether asymptomatic infected individuals shed virus in the same manner (duration and amount) as symptomatic individuals.

The asymptomatic frequency and shedding rate. A key uncertainty in estimating the exposure risk is the number of truly infected people that will encounter bats. We assumed for this analysis that individuals who are symptomatic are not conducting work with or near bats. Emerging evidence indicates that individuals may be infected with SARS-CoV-2 without showing symptoms. Estimates of the fraction of infections that are asymptomatic range from an average of 30.8 percent (Nishiura and others, 2020) to 86 percent (Li and others, 2020; also see World Health Organization, 2020; Ferguson and others, 2020; Mizumoto and others, 2020).

General public as a source of SARS-CoV-2. We did not estimate the potential transmission from the public at large to bats. Bats in the living spaces of houses may constitute a large fraction of the submissions for rabies testing, and it is estimated that many bats that are exposed to human spaces are released by the public rather than sent for testing. Further, people may not be aware of bats in their attics or barns and may expose bats to aerosols containing SARS-CoV-2. We assumed that contact from wildlife researchers, surveyors, managers, rehabilitators, and control operators would occur only when individuals were asymptomatic, but people recovering from infection in their homes may also expose bats roosting or trapped in homes.

Future Steps

From a rapid initial risk assessment associated with a subset of the parameters in the full influence diagram (fig. 1), we aim to provide information to decision makers that they can apply in their specific settings. Ultimately, how agencies use this decision framing and risk assessment may differ across agencies, taking into account their specific mandates. Different decision makers may tolerate varying amounts of risk (that is, agencies may have different acceptable levels of protection) and, thus, may choose to implement different sets of mitigation actions.

Future work may take several forms. First, we may improve upon the risk assessment presented here with updated parameter estimates from empirical data. There is ongoing research of human and bat systems that can update our parameter estimates (for example, challenge trials for the R_0 and σ parameters for bats, and the components of the p^{+}_{RSM} parameter in humans). Second, we considered probability of exposure and infection for the active field season only; different kinds of work, with potentially different exposure and infection risks, are conducted during the winter hibernation period. Guidelines developed from this risk analysis for wildlife scientists, rehabilitators, and control operators may differ for winter work. Third, we focused on a subset of State and Federal agencies. We may expand the scope of future assessments to include a larger number of State, Federal, and tribal agencies. Fourth, we focused only on the initial transmission stages (fig. 2) and did not evaluate the remaining steps in the causal diagram (fig. 1). Work on the remainder of the system diagram would include re-transmission to humans, domesticated animals, and other wildlife, and may reveal other management actions that could reduce the risk to the full set of objectives that are important to management agencies. In addition, there are more complex dynamics within the causal diagram that might be important to study, like the interplay between WNS and coronavirus shedding in bats (Davy and others, 2018). Fifth, we consider risks to bat populations from human exposure, but there are other human-animal interactions that may present risk to wildlife populations. A node was included in the influence diagram for feral and domestic cat infection because there is increasing evidence that felids may sustain infections (Shi and others, 2020). Given that feral and free-ranging cats already pose a significant risk to wildlife populations, including zoonotic disease (Medina and others, 2014), it may be important to expand the influence diagram and estimate the probabilities along this exposure route.

Summary

This report describes a risk assessment led by the U.S. Geological Survey, in cooperation with the U.S. Fish and Wildlife Service, to examine the possibility of reverse zoonotic transmission of SARS-CoV-2, the coronavirus that causes the human disease COVID-19, from humans to bats in North America. The study was undertaken to inform State, Federal, and tribal wildlife management agencies in the United States that manage some aspects of the interactions between humans and bats and are in the process of developing guidance.

The study was designed by first framing the decisions that concern State and Federal wildlife agencies, with a focus on the long-term outcomes the agencies desire and the near-term mitigation actions that are within their authority to implement. From these components, a causal diagram was developed to trace the linkages from the potential actions through intermediate steps to the desired outcomes. The subsequent risk analysis focused on the early steps of three transmission pathways, namely the exposure and infection of bats from research, survey, monitoring, and management activities; wildlife rehabilitation; and nuisance wildlife control operations. The assessment focused on the immediate field season, from April to November 2020, and used little brown bats as a case study and as a surrogate species for other North American bats.

From the causal diagram, a quantitative model was developed to forecast the number of infected bats using estimates of the number of bats handled through the three transmission pathways, the probability of exposure through various modes of encounter, the probability of infection conditional on exposure, and the probability that a worker is actively shedding the SARS-CoV-2 virus. The parameters in this model were estimated primarily through a formal process of expert judgment.

The expert panel estimated that, if a research scientist were shedding virus while handling bats under the protocols in use prior to the COVID-19 pandemic, 50 percent (15–84 percent) of those bats would be exposed to virus, and 17 percent (3–51 percent) would become infected. Although there were differences in exposure potential among the transmission pathways and encounter types, without additional protective measures, the probability of transmission resulting in infected bats cannot be ruled out. The expert panel expected that proper use of personal protective equipment would significantly reduce the exposure probabilities for all modes of encounter with bats. For example, the panel estimated that exposure risk from research scientists could be reduced by 94–96 percent (uncertainty, 86–99 percent) through proper use of appropriate personal protective equipment (such as N95 respirators and dedicated clothing and gloves). Regarding the possibility of sustained bat-to-bat transmission of SARS-CoV-2 in a wild population of little brown bats, the expert panel estimated a median basic reproduction number (R_0) of 0.45, but expressed considerable uncertainty, such that there was a 33-percent chance that R_0 could be greater than 1; these results indicate that sustained transmission within bat populations is a possibility, if SARS-CoV-2 is introduced.

This research was conducted at a time when there were few empirical studies of SARS-CoV-2 in North American bats, so there was considerable uncertainty in the results. As new information becomes available, the risk model can be updated with data concerning human infection rates, bat infection rates, and other parameters. Future work could look at the risks posed by field work after November 2020 (that is, during the hibernation season), as well as later steps in the causal diagram.

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Appendix 1. Instructions for the Expert Panel

This appendix contains that exact documents that were provided to the experts during the expert elicitation process. The contents of this Appendix have not been edited to conform to USGS editorial standards.

Introduction to Expert Elicitation for an Expert Panel

Justification for an Expert Elicitation

Ideally, we would obtain parameter estimates from empirical data and associated mathematical models. Because these information are unavailable and time is of the essence for decision makers, we aim to use an expert panel to elicit parameter values with associated uncertainty, using techniques of expert judgment that utilize best available scientific information, account for uncertainty, and reduce bias (Morgan, 2014; Sutherland and Burgman, 2015).

Expert elicitation is a formal, structured process of obtaining expert judgment for specific questions. An expert is someone who possesses substantive information on a particular topic that is not widely known by others. We know that experts have knowledge, often privileged knowledge, that accrues as a result of their research and experience, even about processes for which data have not been collected. The question is how to extract that knowledge accurately and precisely. Expert judgment is a quantitative expression of an expert's belief based on knowledge and experience; it is an informed belief. Expert elicitation can provide improved information over single-expert inquiry when a diverse group of experts is asked to provide estimates, using a facilitated approach with discrete opportunities for information sharing, provision of estimates, and review of summarized information (Martin and others, 2012). Expert elicitation, when conducted with the same level of rigor as the collection and use of empirical data, can result in reliable predictions (for example, O'Hagan and others, 2006; Speirs-Bridge and others, 2010; Runge and others, 2011; Martin and others, 2012; Adams-Hosking and others, 2016).

An expert elicitation is governed by specific protocols to avoid inherent biases resulting from cognitive traps. These cognitive traps are shortcuts, or heuristics, that serve us well for simple decisions but result in biased estimates for more complex tasks (O'Hagan, 2019). These biases include

- Availability bias (experts will be influenced by evidence or events that are easily recalled),
- Anchoring bias (experts fail to consider possible values far from an initial estimate),
- Overconfidence (experts tend to underestimate their uncertainty, and make forecasts that are too narrow),
- Representativeness bias (a tendency to think of probabilities related to readily available examples), and
- Motivational bias (an innate desire to further our own interests).

When the number of experts is limited, we would additionally be concerned about small-sample bias.

There are additional biases that arise through the behavior of groups. To some extent, these can be collectively referred to as "groupthink," the tendency for groups to converge too quickly on consensus estimates or decisions and to ignore or forget divergent views that are held by members of the group. In this way, groups of experts can be collectively overconfident, or even biased.

So, the methodological challenge of expert judgment is to reliably extract the desired information from each member of a group of experts, without falling into the cognitive and behavioral biases that can undermine such an exercise. The best practices in an expert judgment approach have evolved by considering this challenge, testing approaches via experiments, and recommending a set of protocols for conducting an expert elicitation.

Steps in an Elicitation

We are using a protocol based on a modified Delphi method called the IDEA protocol (Hanea and others, 2017), with the four-point elicitation method (Speirs-Bridge and others, 2010). There are six steps in the process:

1. Select experts;
2. Calibrate experts (seed questions and sharing available information);
3. Elicitation of parameter values (4-point method);
4. Summary, review, and discussion (aimed at reducing linguistic uncertainty—relating to the instructions—and sharing insights, not to reach consensus);
5. Experts revise their initial values (if desired); and
6. Aggregate information across experts.

Steps 3–6 comprise a modified Delphi approach (described below).

Selection of Experts

Experts are individuals with specific subject-matter experience and knowledge. Experts should have relevant expertise which may come from formal training and be demonstrated by professional accomplishments such as peer-reviewed publications, familiarity with and knowledge of the system or related systems, willingness to participate fully and impartially in an

elicitation process, and good interpersonal and communication skills (Ayyub, 2001; Fazey and others, 2006).

Groups of experts have been found to perform as well (in terms of providing information close to the true empirically observed data) as more specific experts (for example, Burgman and others, 2011). The expert panel should be diverse—possessing knowledge of North American bats, zoonotic disease, and possible mitigation strategies; representing multiple institutions, specialization, and gender. The optimal number of experts for a structured elicitation is between 5 and 12, with decreasing marginal benefit after 12 experts (Hogarth, 1978; Hemming and others, 2018).

Training Questions

Before starting the elicitation concerning the questions of interest, we will provide the expert panel a chance to practice the elicitation methods. We will provide questions that are known (that is, we have identified values from the literature, but are unlikely to be known precisely by experts). We use these questions to ensure that the instructions are understood by experts, and to allow experts a chance to calibrate their estimates of uncertainty.

Three questions are listed below (see accompanying spreadsheet <BatEE Practice Questions v2.xlsx> [not included with this report]). For each question, we ask experts to provide four responses: an estimate that represents your view of the lowest reasonable value; an estimate of the highest reasonable value; an estimate that represents the best central value; and your confidence that the true value lies within the low and high values that you have provided. We have attached a spreadsheet in which you can enter these values; the spreadsheet automatically calculates a probability distribution that represents your uncertainty, as immediate feedback about whether your responses reflect your expert belief. This is a "closed book" exercise (we ask that you do not check this information in books or online). Please return your answers to us; we will use them to provide feedback to the group about your individual and collective accuracy and precision; as a means of allowing you to calibrate your thinking process prior to the elicitation for the questions of central importance.

The calibration questions are

1. What is the mean forearm length (in centimeters) of an adult little brown bat (*Myotis lucifugus*)?

2. What is the average number of subsequent white-nose syndrome infections resulting from a single infected little brown bat (that is, R_0)?

3. In a population that has already experienced decline due to WNS, out of 100 adult female little brown bats, how many would you expect to breed in a given year?

Elicitation of Parameters Using a Modified Delphi Approach

To generate empirical estimates of each parameter, we use a "4-point" elicitation method. This approach has been shown to reduce overconfidence in experts (Speirs-Bridge and others, 2010) and can generate a quantitative estimate from experts who may be uncomfortable providing estimates. We derive a median and credible interval for each parameter from the following four questions:

1. Realistically, what is the lowest reasonable value for the parameter?

2. Realistically, what is the highest reasonable value for the parameter?

3. Realistically, what is the most likely reasonable value (that is, your best estimate) for the parameter?

4. How confident are you that the true value is between the lowest and highest values you provided?

We then assume that the most likely value is the median value, and combine the upper and lower estimates and the reported confidence to generate a credible interval.

Experts provide their estimates anonymously, and summaries are provided that maintain anonymity, to avoid biases associated with group thinking and dominant personalities. Experts are encouraged to discuss the information during a facilitated discussion of the summarized data, after which experts have the opportunity to revise any of their estimates.

The modified Delphi sequence (independent-group-independent) is important to preserve the unique insights held by individuals while at the same time allowing the benefit of wisdom to be shared. By asking experts to perform the first estimate independently, their own personal views are captured. By allowing the expert to share and discuss their initial estimates, we can explore whether there is residual linguistic uncertainty that needs to be corrected and we can allow insights to be shared across experts. By allowing the final estimates to be made independently, we guard against dominant voices in the group and retain the diversity of insights among the experts.

Aggregation of Information Across Experts

Following the elicitation, we will aggregate the results to produce a single probability distribution that represents an estimate, with uncertainty, for each parameter. To do this, we will first transform the four-point elicitation results into a probability distribution for each expert. We will then average these probability distributions across experts, with equal weighting. (There are involved methods for weighting experts based on sets of calibration questions, but we are both skeptical of these methods and limited on time).

Questions for the Expert Panel

For each of the questions that ask for a quantitative response, we are asking you to provide a low estimate, a high estimate, a central estimate, and a degree of confidence that the true value is between your low and high estimates. Please see the document that provides instructions on expert elicitation that was sent by Evan Grant on April 9 [see "Introduction to Expert Elicitation for an Expert Panel"]. Please record your responses in the accompanying spreadsheet, which also provides graphical feedback.

In all the questions below, unless otherwise noted, we are thinking specifically about little brown bats (*Myotis lucifugus*) throughout their range in North America, with a focus on the time period between now and the initiation of hibernation in the autumn of 2020.

Questions 1–7 all involve estimation of an exposure probability in the absence of any new restrictions, regulations, or protocols, that is, under the status quo conditions for contact with bats that existed before the arrival of SARS-CoV-2 in North America. In the past, concern about biological agents has been primarily focused on rabies virus and the fungus *P. destructans*; typical protocols involve decontamination of clothing and footwear between sites, wearing nitrile gloves (with disposal or decontamination between bats), but use of face masks or respirators has not been typical.

Note that we are separating the processes of exposure and infection. By **exposure probability**, we mean the likelihood that a particular interaction between an average bat and a biologist who is actively shedding SARS-CoV-2 virus will result in exposure of the bat to a sufficient viral dose to cause infection. By **infection probability**, we mean the probability that the virus replicates in the host (bat) tissue, conditional on that bat having been exposed to a sufficient viral dose. That is, the exposure process is about whether enough virus was transferred to make an infection possible; it is a property of the interaction between the biologist and that bat. The infection process is about the molecular, cellular, immunological, and physiological conditions that allow replication in the bat; it is a property of the interaction of the bat and the pathogen. Questions 1–7 only ask if the bat will be exposed to a sufficient viral dose; Question 8 asks about the probability of developing an infection, conditional on exposure.

Questions 1–7 differ from each other in two respects: the exposure pathway (the types of work being conducted), and the degree of interaction. We consider three exposure pathways: through activities related to research, survey, monitoring, and management (RSM); through wildlife rehabilitation (WR); and through wildlife control operations (WC). We consider three degrees of interaction: handling; proximity in an enclosed spaced without handling; and proximity in an unenclosed space without handling.

1. Consider a wildlife biologist engaged in research, survey, monitoring, or management (RSM) who is actively shedding SARS-CoV-2 virus (CoV+), performing their routine activities in the absence of any new restrictions, regulations, or protocols. If that biologist **directly handles** 100 average little brown bats, how many of those bats do you estimate will be exposed to a sufficient viral dose of SARS-CoV-2 that they could become infected? (This relates to the parameter β_H^{RSM} in equation 1).

2. Same setting as question 1, a CoV+ biologist conducting RSM under status quo protocols. If that biologist is **in an enclosed space and within 6 feet** of 100 average little brown bats (but does not handle them), how many of those bats will be exposed to a sufficient viral dose that they could become infected? (This relates to the parameter β_E^{RSM} in equation 1).

3. Same setting as question 1. If the RSM biologist is ***not* in an enclosed space but is within a 6-foot proximity** of 100 little brown bats (and does not handle them), how many of those bats will be exposed to a sufficient viral dose that they could become infected? (This relates to the parameter β_P^{RSM} in equation 1).

4. Now consider a wildlife rehabilitator (WR) who is actively shedding SARS-CoV-2 virus (CoV+), performing their routine activities in the absence of any new restrictions, regulations, or protocols. If that rehabilitator **directly handles** 100 average little brown bats, how many of those bats do you estimate will be exposed to a sufficient viral dose of SARS-CoV-2 that they could become infected? (This relates to the parameter β_H^{WR} in equation 2).

5. Same setting as question 4, a CoV+ wildlife rehabilitator (WR) conducting their work under status quo protocols. If that rehabilitator **is within a 6-foot proximity** (whether enclosed or unenclosed) of 100 average little brown bats but does not handle them, how many of those bats will be exposed to a sufficient viral dose that they could become infected? (This relates to the parameter β_P^{WR} in equation 2).

6. Now consider a wildlife control operator (WC) who is actively shedding SARS-CoV-2 virus (CoV+), **performing their routine activities that involve handling bats**, in the absence of any new restrictions, regulations, or protocols. For example, a typical activity might involve capturing bats in a home or trapping and transporting bats from an attic. If that WC operator directly handles 100 average little brown bats, how many of those bats do you estimate will be exposed to a sufficient viral dose of SARS-CoV-2 that they could become infected? (This relates to the parameter β_H^{WC} in equation 3).

7. Same setting as question 6, a CoV+ wildlife control operator (WC) conducting their routine work under status quo protocols, but **without handling the bats**. For example, a typical activity might involve working in an attic to set up an exclusion device, or trapping bats without handling

them. If that WC operator is within a 6-foot proximity (whether enclosed or unenclosed) of 100 average little brown bats but does not handle them, how many of those bats will be exposed to a sufficient viral dose that they could become infected? (This relates to the parameter β_P^{WC} in equation 3).

The next question focuses on the probability of infection, conditional on exposure. (This relates to the parameter σ_{ML} in equations 1, 2, and 3.)

8. What is the probability that a little brown bat exposed to a sufficient viral dose of SARS-CoV-2 would actually become infected by the virus (that is, sustained viral replication would occur in their tissue)?

The next three questions focus on the efficacy of guidance and protocols to reduce the exposure rate. In all of these questions, the new guidance and protocols consist of: restriction of fieldwork to people without symptoms and without contact with someone who had symptoms of COVID-19 in the last 14 days; proper training and compliance protocols for the use of PPE; proper use of Tyvek or other dedicated clothing; proper use of an N95 respirator; and proper use of gloves for handling bats. In these questions, please assume that the biologists have proper training, have access to PPE, and are using it appropriately.

9. Consider your response to question 1, regarding exposure through handling by RSM scientists. By what proportion should this exposure probability be multiplied if the new guidance and protocols are put into place? (Note that a proportion of 1 means there would be no change in exposure probability; a proportion of less than 1 would indicate a reduction in exposure probability; and a proportion of greater than 1 would indicate an increase in exposure probability as a result of such guidance.)

10. Consider your response to question 2, regarding exposure through proximity in an enclosed space by RSM scientists. By what proportion should this exposure probability be multiplied if the new guidance and protocols are put into place?

11. Consider your response to question 3, regarding exposure through proximity in an unenclosed space by RSM scientists. By what proportion should this exposure probability be multiplied if the new guidance and protocols are put into place?

12. **Open-ended response**. Are there reasons to believe that the proportional change in the handling and proximity exposure probabilities for wildlife rehabilitators (WR) and wildlife control operators (WC), owing to the same protocol guidance, would be different than for scientists involved in research, survey, and management (RSM)? Explain.

The last question addresses the risk of sustained bat-to-bat transmission of SARS-CoV-2.

13. What is R_0 for SARS-CoV-2 in little brown bats during the active season? That is, for each infected little brown bat, how many other little brown bats would become infected with the virus? Note that R_0 can be less than 1, in which case you can think of it as the probability that an infected bat will infect one other bat, or it can be greater than 1, in which case each infected bat infects more than one other bat. Note that the spreadsheet [not included in this report] calculates from your responses the probability that R_0 is greater than 1.

We are grateful for your time and expertise. Thank you for your thoughtful participation in this elicitation.

Clarification Provided Between Rounds of Elicitation

During the discussion with the experts between Rounds 1 and 2 of the elicitation, the experts raised some questions about the typical activities of RSM, WR, and WC workers when encountering bats. The following clarifications were provided before the second round of elicitation was completed.

Because research on bats typically involves more than one scientist, we consider the number encountered by each member of a research team; the β parameters in equation 1 describe the exposure probability per scientist while conducting each of the activities. The description of typical handling procedures for researchers working with bats includes: 1–2 minutes of contact per bat, holding a bat within 12 inches of the face, taking morphometrics, and blowing on a bat to aid in determining reproductive condition or to discourage biting. Some research and management activities may involve longer holding periods for collection of metabolic measurements, attachment of radiotransmitters and other sampling, but these interactions are less common. The definition of enclosed space includes caves and mines with various sizes and morphologies that may result in variation in airflow among sites. We assumed that activity in enclosed space may be greater than 1 hour, and bats in these spaces may be a mixture of stationary (roosting) and in flight. Typical activities near bats but in an unenclosed space include a management agency conducting emergence counts outside a cave or mine entrance or under a bridge.

Typical activities of wildlife rehabilitators were assumed to include repeated contact with a small number of bats, involving hand feeding (especially for little brown bats), medical management of injuries, with a contact duration of weeks to months. We assumed that most rehabilitators typically dedicate an enclosed room for rehabilitation activities, with facilities that may range from a shed or garage to a purpose-built structure.

The definition of enclosed space includes attics of various sizes and dimensions that may result in variation in airflow among sites. Wildlife control operators typically do not enter enclosed spaces during the summer season, so as not to disturb bats who may be rearing pups. For bats within a home's living space, a wildlife control operator may catch a bat for release. We assumed that activity in enclosed space may be greater than 1 hour, and bats in these spaces may be a mixture of stationary (roosting) and in flight. Typical activities near bats but in an unenclosed space include a wildlife control operator working to exclude bats from a home (that is, installing an excluder device near soffits or eaves after young bats are flying and not likely to be trapped inside when their mothers go out to forage).

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Sutherland, W.J., and Burgman, M., 2015, Policy advice—Use experts wisely: Nature, v. 526, no. 7573, p. 317–318, accessed May 19, 2020, at https://doi.org/10.1038/526317a.

Appendix 2. Expert Elicitation Results

Results of responses to Questions 1–13 are shown in illustrations.

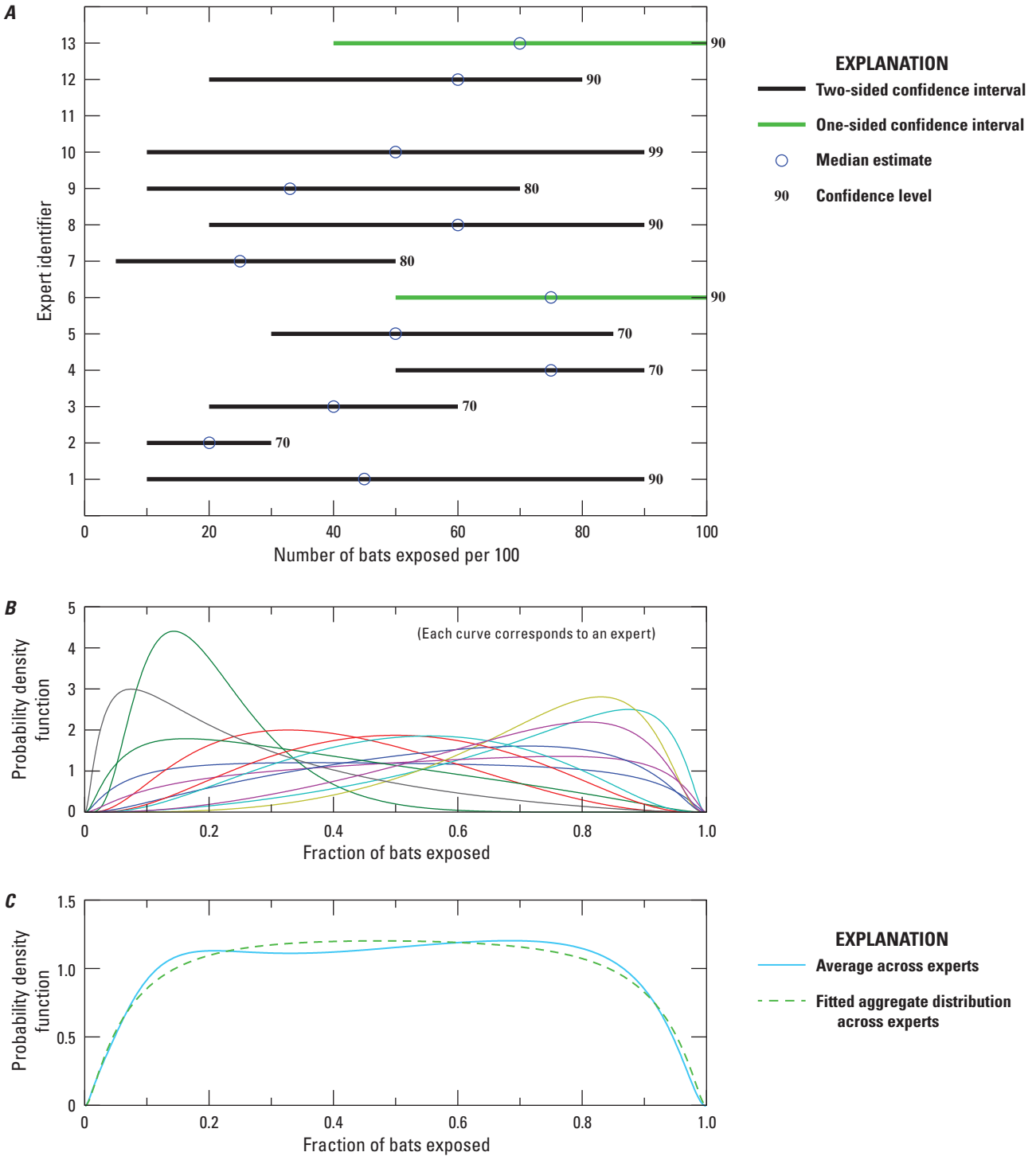

Figure 2.1. Expert panel responses to Question 1—number of bats exposed to virus by a SARS-CoV-2-positive scientist handling bats. *A,* Four-point-elicitation responses from the individual experts, *B,* fitted probability distributions for individual experts, and *C,* average and fitted distributions across experts. The aggregate distribution has a median of 49.7 bats and an 80-percent confidence interval of (15.3, 84.3).

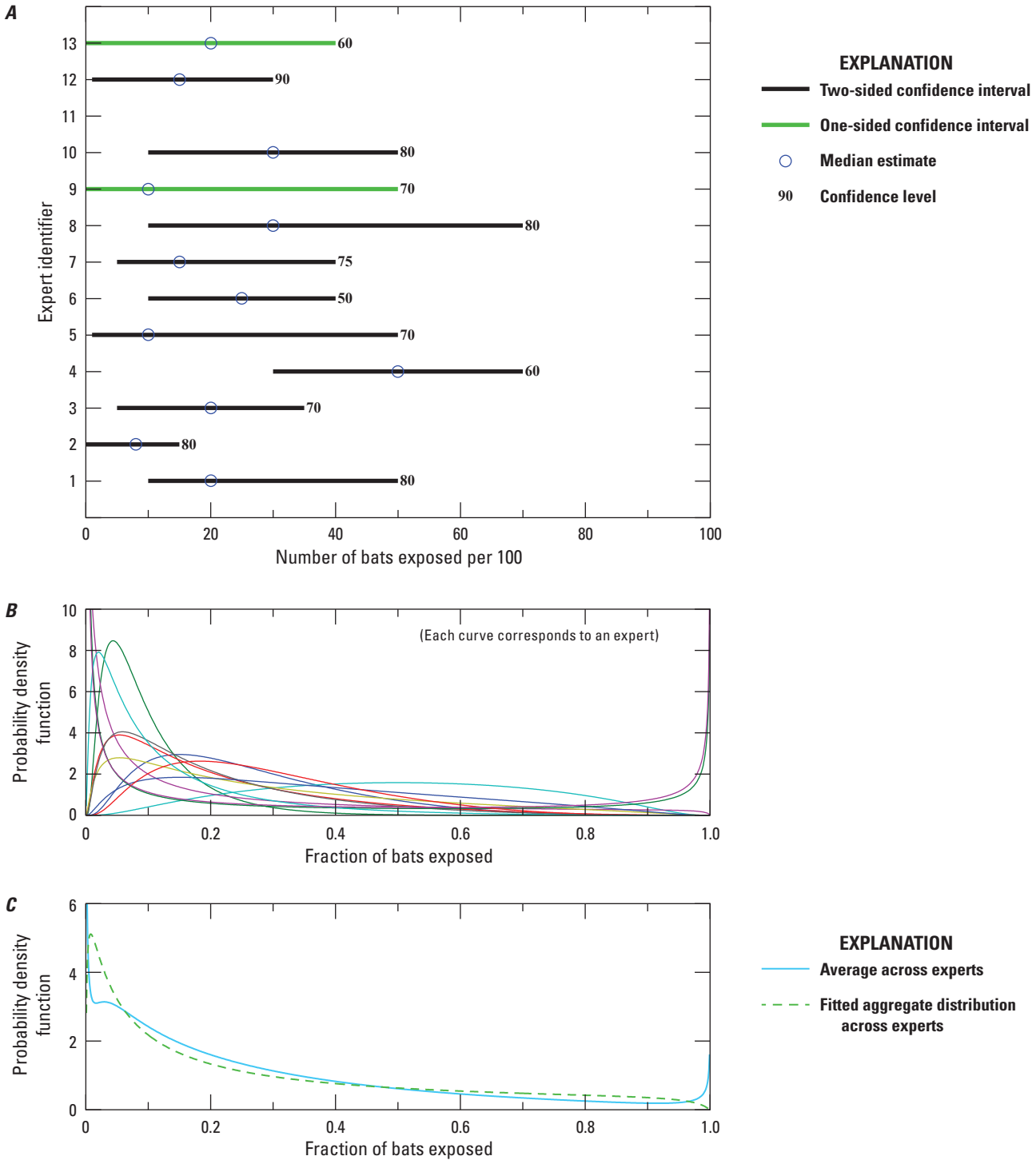

Figure 2.2. Expert panel responses to Question 2—number of bats exposed to virus by a SARS-CoV-2-positive scientist in an enclosed space within 6 feet of bats. *A*, Four-point-elicitation responses from the individual experts, *B*, fitted probability distributions for individual experts, and *C*, average and fitted distributions across experts. The aggregate distribution has a median of 19.4 bats and an 80-percent confidence interval of (2.2, 72.4).

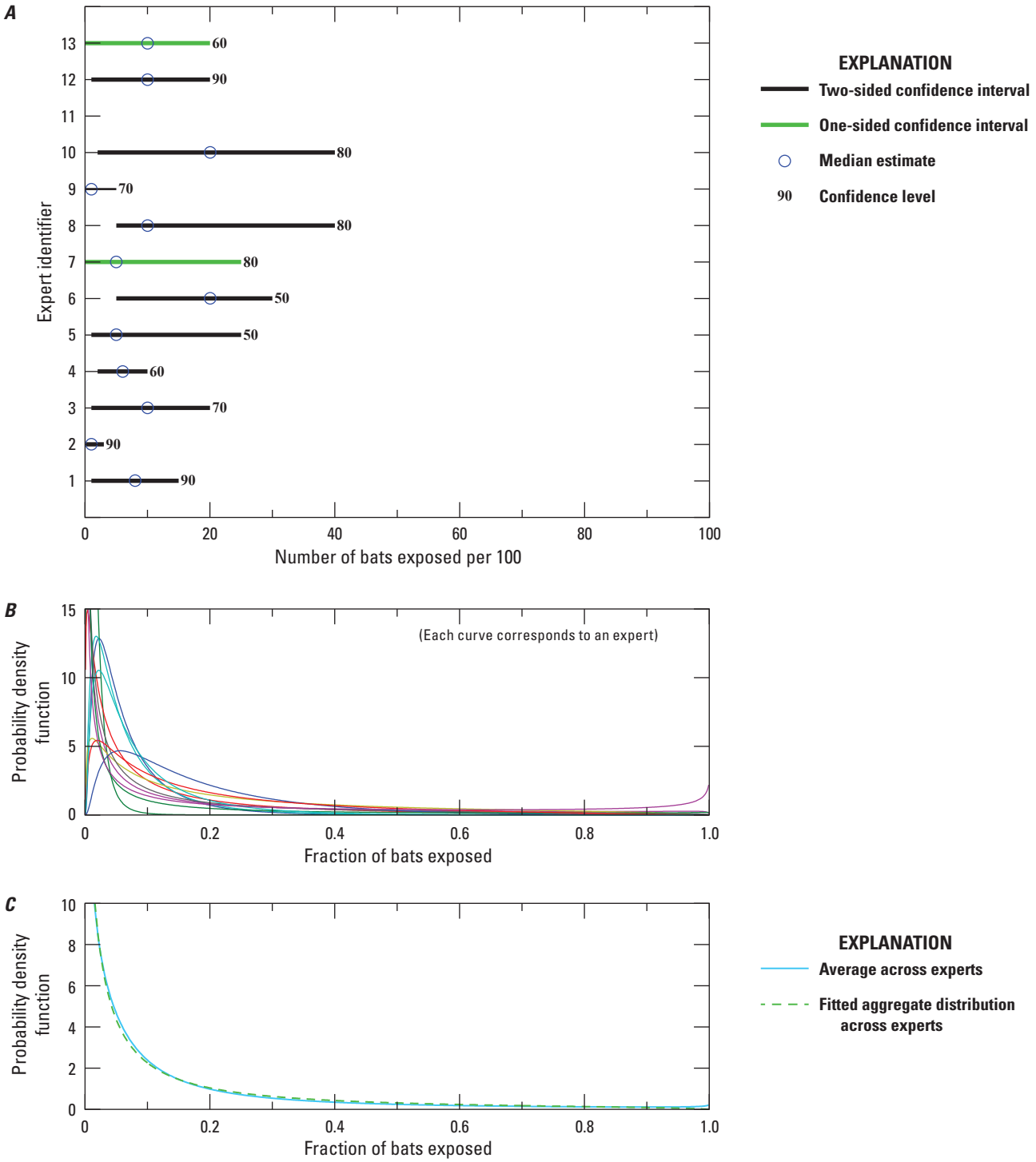

Figure 2.3. Expert panel responses to Question 3—number of bats exposed to virus by a SARS-CoV-2-positive scientist in an unenclosed space within 6 feet of bats. *A*, Four-point-elicitation responses from the individual experts, *B*, fitted probability distributions for individual experts, and *C*, average and fitted distributions across experts. The aggregate distribution has a median of 6.4 bats and an 80-percent confidence interval of (0.6, 43.8).

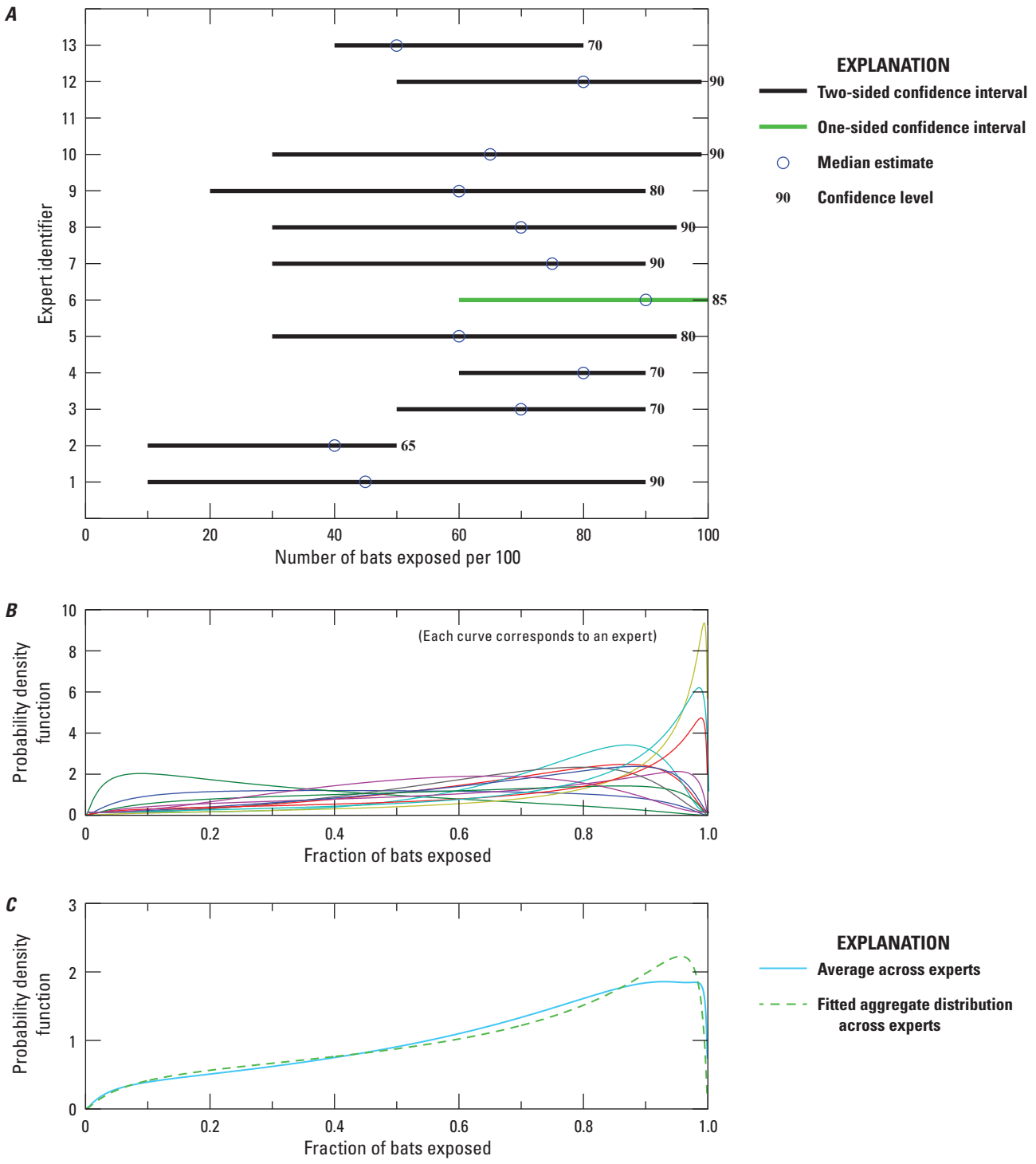

Figure 2.4. Expert panel responses to Question 4—number of bats exposed to virus by a SARS-CoV-2-positive wildlife rehabilitator handling bats. *A*, Four-point-elicitation responses from the individual experts, *B*, fitted probability distributions for individual experts, and *C*, average and fitted distributions across experts. The aggregate distribution has a median of 70.4 bats and an 80-percent confidence interval of (24.4, 94.6).

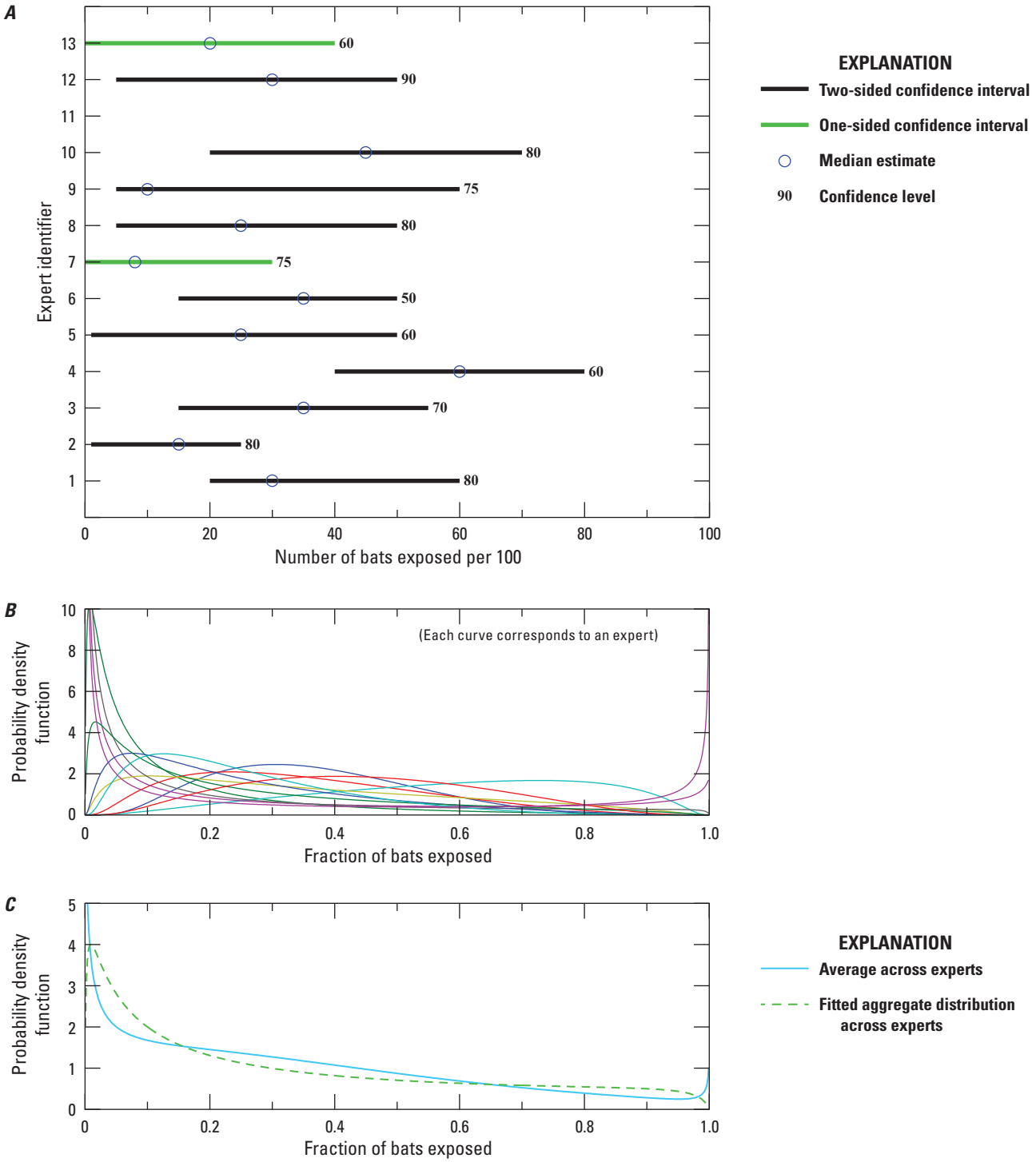

Figure 2.5. Expert panel responses to Question 5—number of bats exposed to virus by a SARS-CoV-2-positive wildlife rehabilitator within 6 feet of bats. *A*, Four-point-elicitation responses from the individual experts, *B*, fitted probability distributions for individual experts, and *C*, average and fitted distributions across experts. The aggregate distribution has a median of 24.3 bats and an 80-percent confidence interval of (2.8, 78.4).

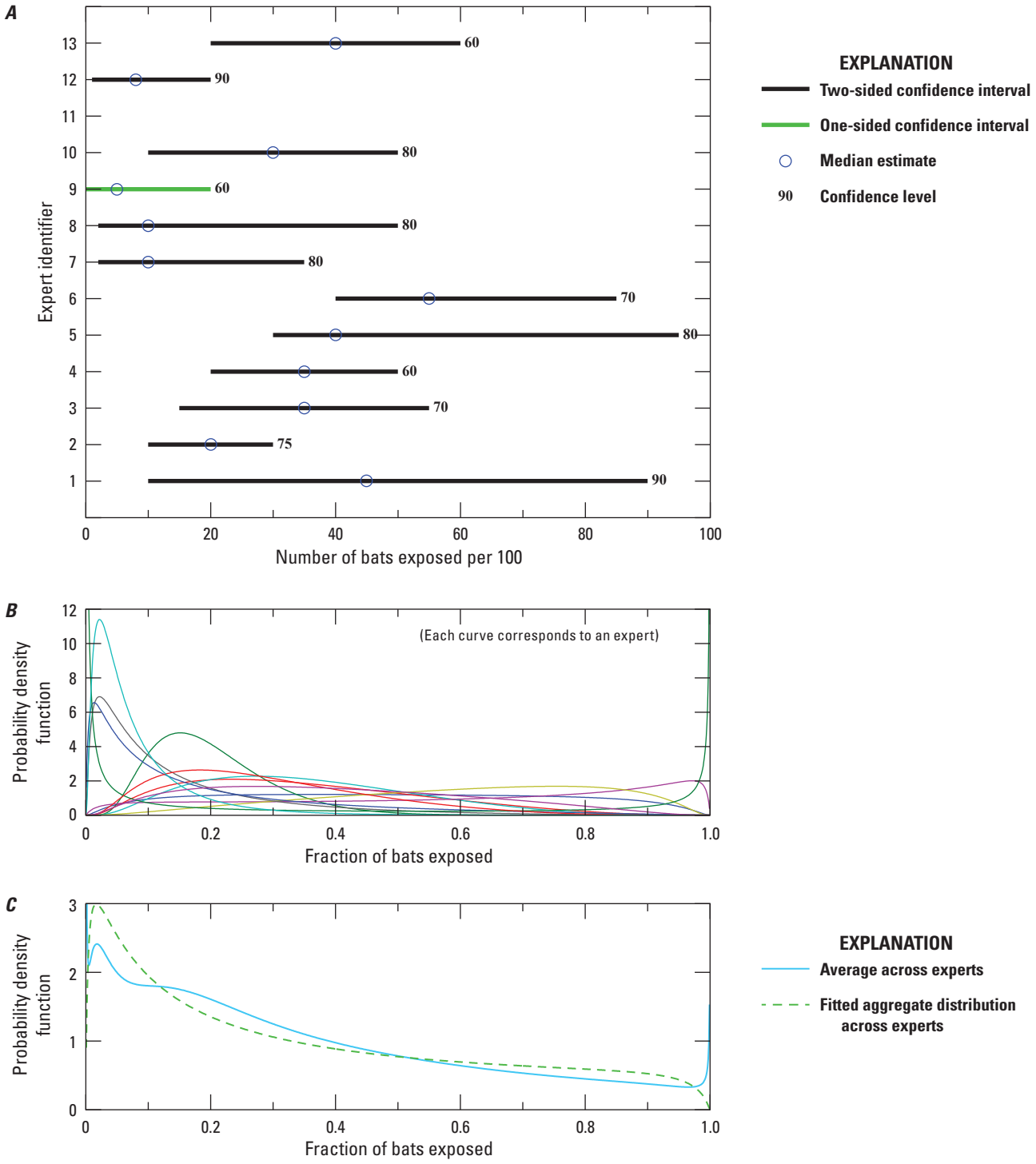

Figure 2.6. Expert panel responses to Question 6—number of bats exposed to virus by a SARS-CoV-2-positive wildlife control operator handling bats. *A*, Four-point-elicitation responses from the individual experts, *B*, fitted probability distributions for individual experts, and *C*, average and fitted distributions across experts. The aggregate distribution has a median of 27.7 bats and an 80-percent confidence interval of (3.7, 79.2).

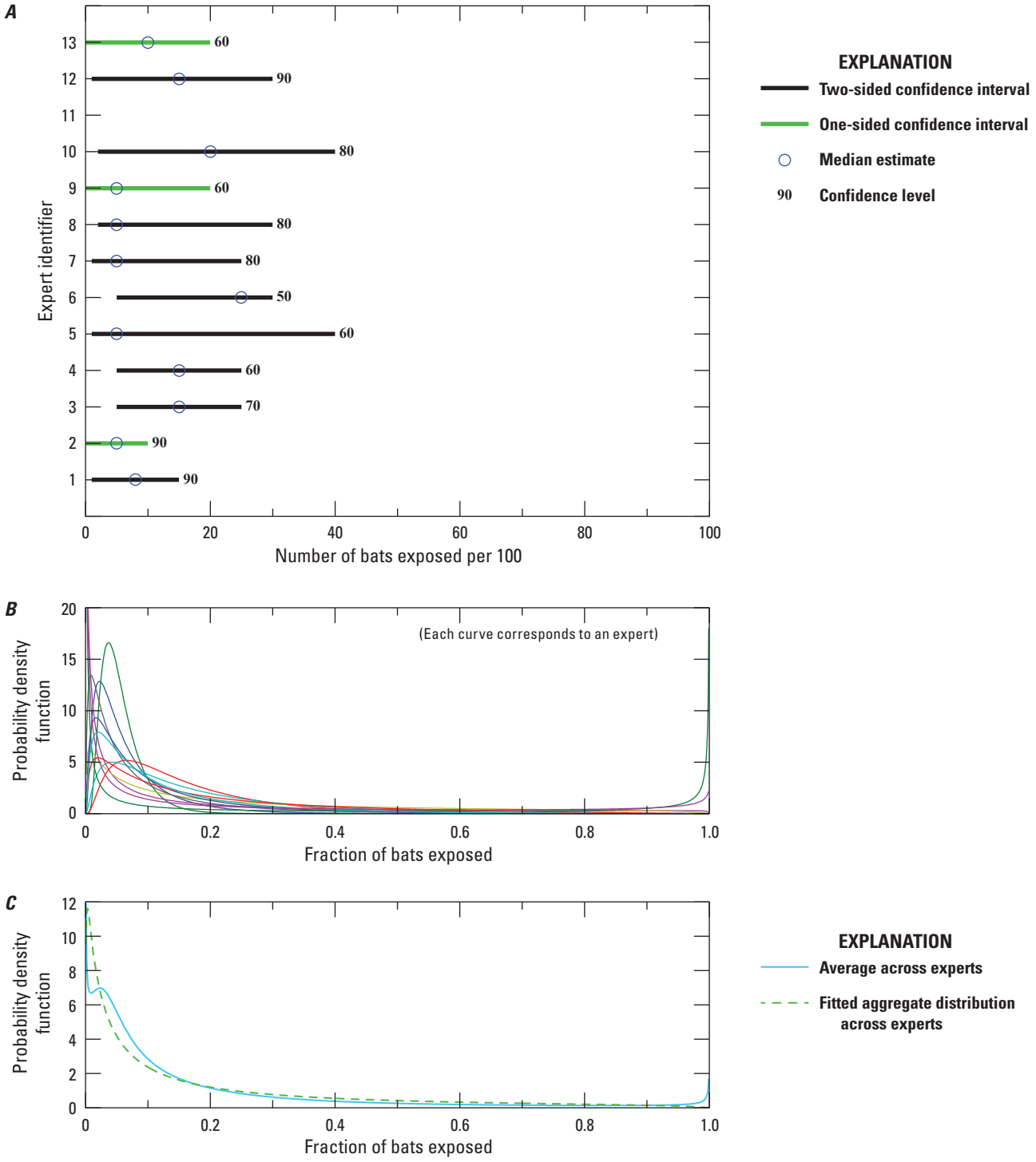

Figure 2.7. Expert panel responses to Question 7—number of bats exposed to virus by a SARS-CoV-2-positive wildlife control operator within 6 feet of bats. *A*, Four-point-elicitation responses from the individual experts, *B*, fitted probability distributions for individual experts, and *C*, average and fitted distributions across experts. The aggregate distribution has a median of 9.6 bats and an 80-percent confidence interval of (1.0, 53.9).

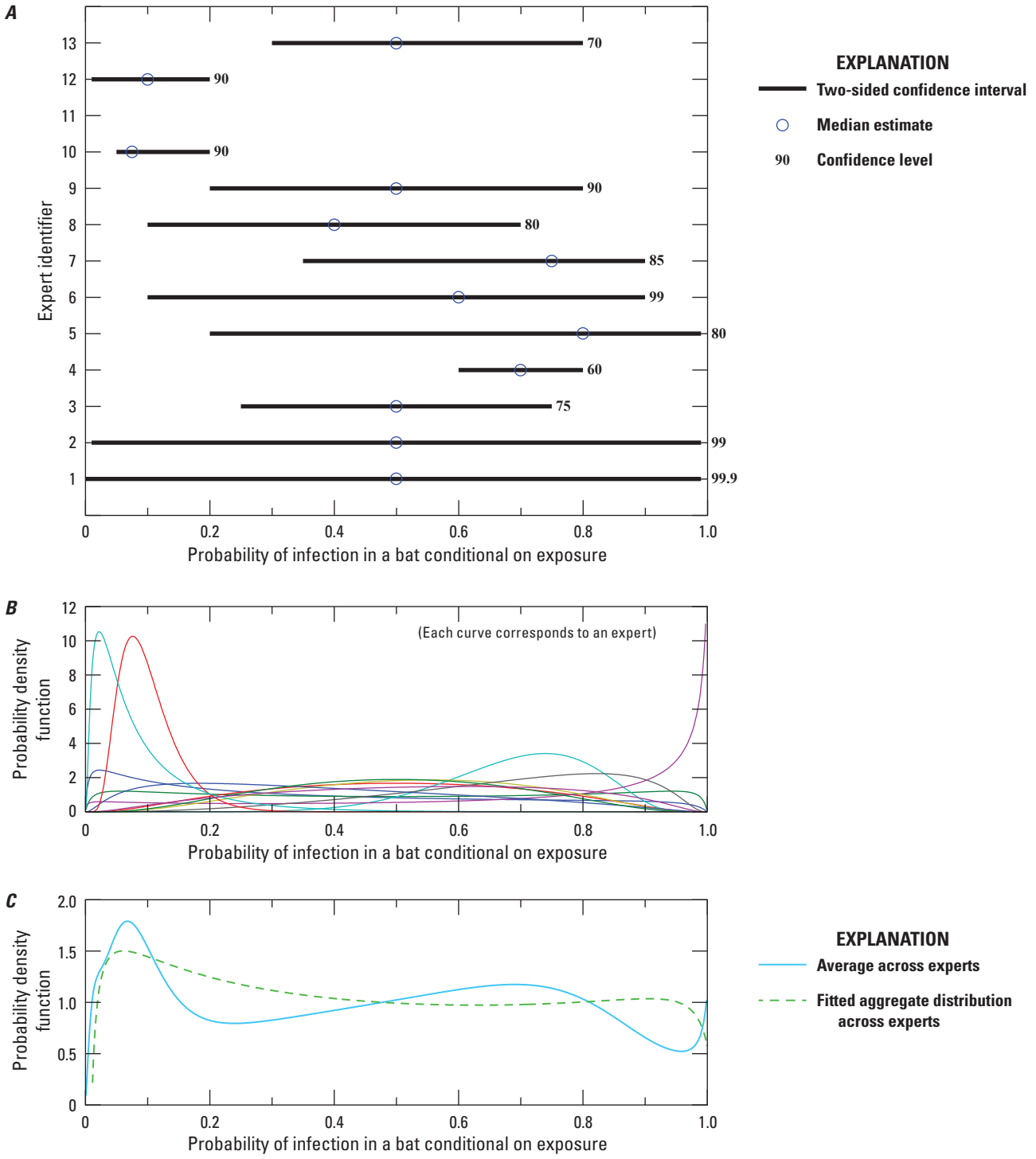

Figure 2.8. Expert panel responses to Question 8—probability of infection in a bat conditional on exposure. *A*, Four-point-elicitation responses from the individual experts, *B*, fitted probability distributions for individual experts, and *C*, average and fitted distributions across experts. The aggregate distribution has a median of 0.44 and an 80-percent confidence interval of (0.08, 0.88).

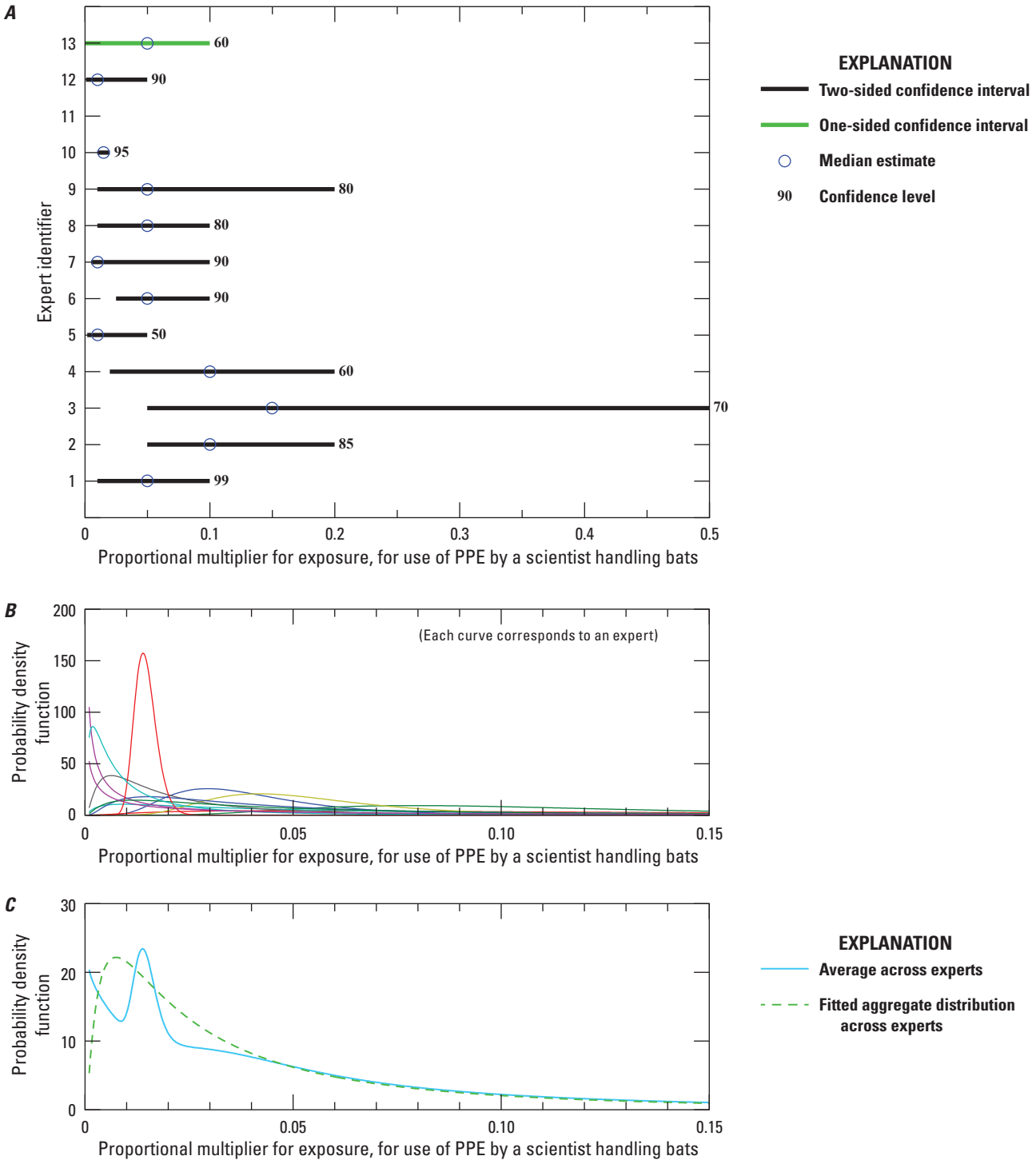

Figure 2.9. Expert panel responses to Question 9—multiplier for exposure, when using personal protective equipment, for a research scientist handling bats. *A*, Four-point-elicitation responses from the individual experts, *B*, fitted probability distributions for individual experts, and *C*, average and fitted distributions across experts. The aggregate distribution has a median of 0.031 and an 80-percent confidence interval of (0.007, 0.141). PPE, personal protective equipment.

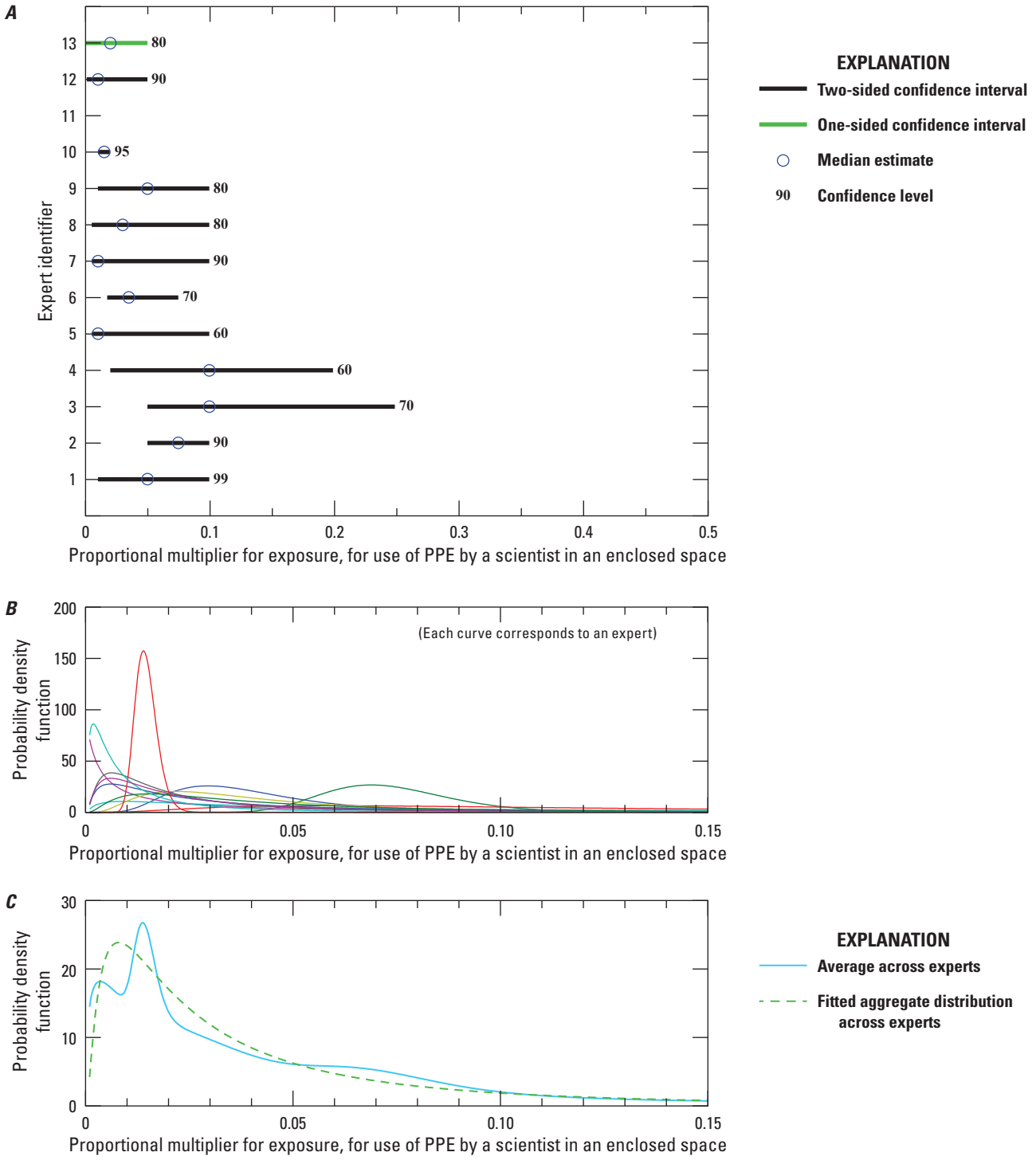

Figure 2.10. Expert panel responses to Question 10—multiplier for exposure, when using personal protective equipment, for a research scientist in an enclosed space within 6 feet of bats. *A*, Four-point-elicitation responses from the individual experts, *B*, fitted probability distributions for individual experts, and *C*, average and fitted distributions across experts. The aggregate distribution has a median of 0.028 and an 80-percent confidence interval of (0.007, 0.117). PPE, personal protective equipment.

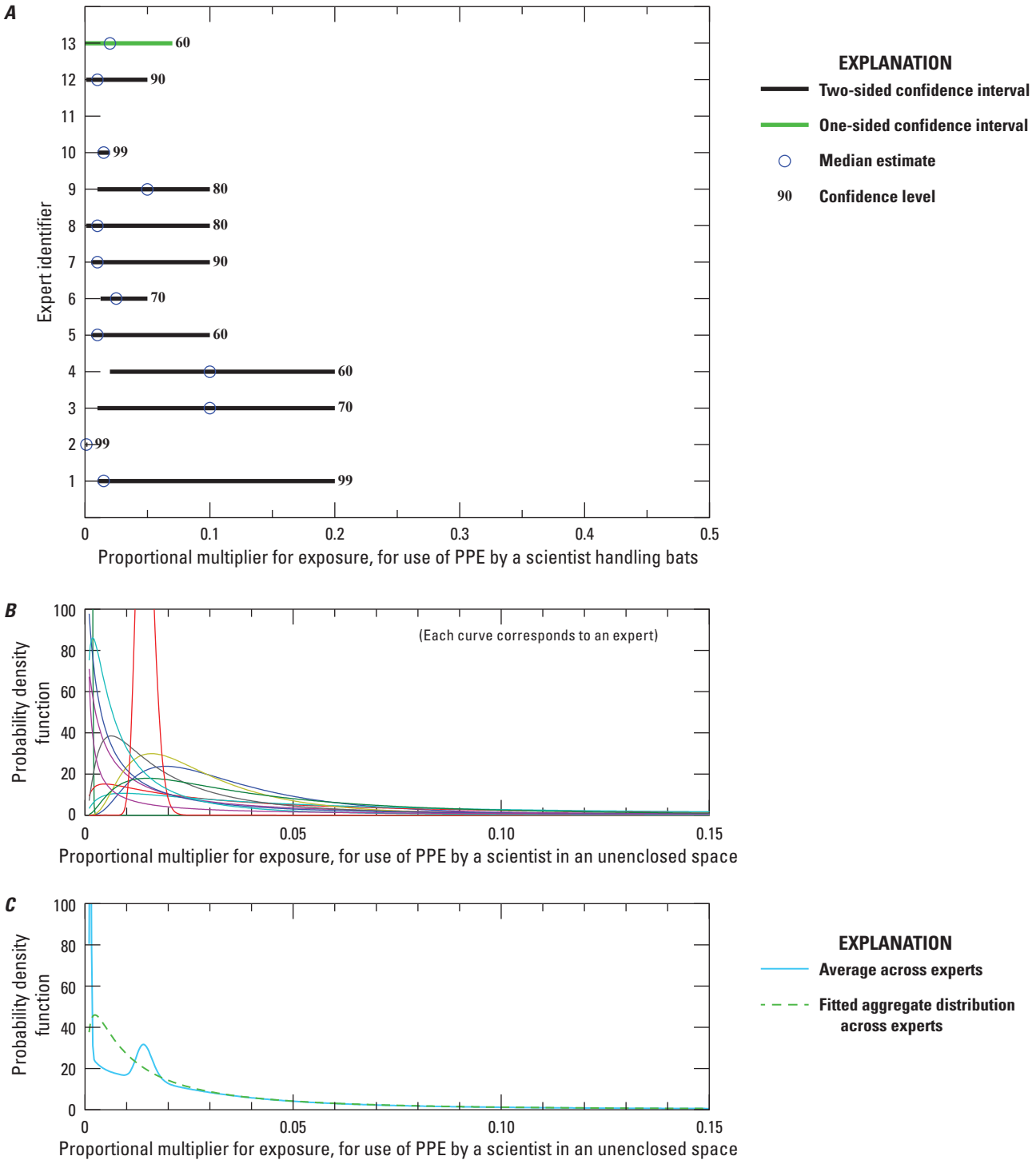

Figure 2.11. Expert panel responses to Question 11—multiplier for exposure, when using personal protective equipment, for a research scientist in an unenclosed space within 6 feet of bats. *A*, Four-point-elicitation responses from the individual experts, *B*, fitted probability distributions for individual experts, and *C*, average and fitted distributions across experts. The aggregate distribution has a median of 0.016 and an 80-percent confidence interval of (0.003, 0.096). PPE, personal protective equipment.

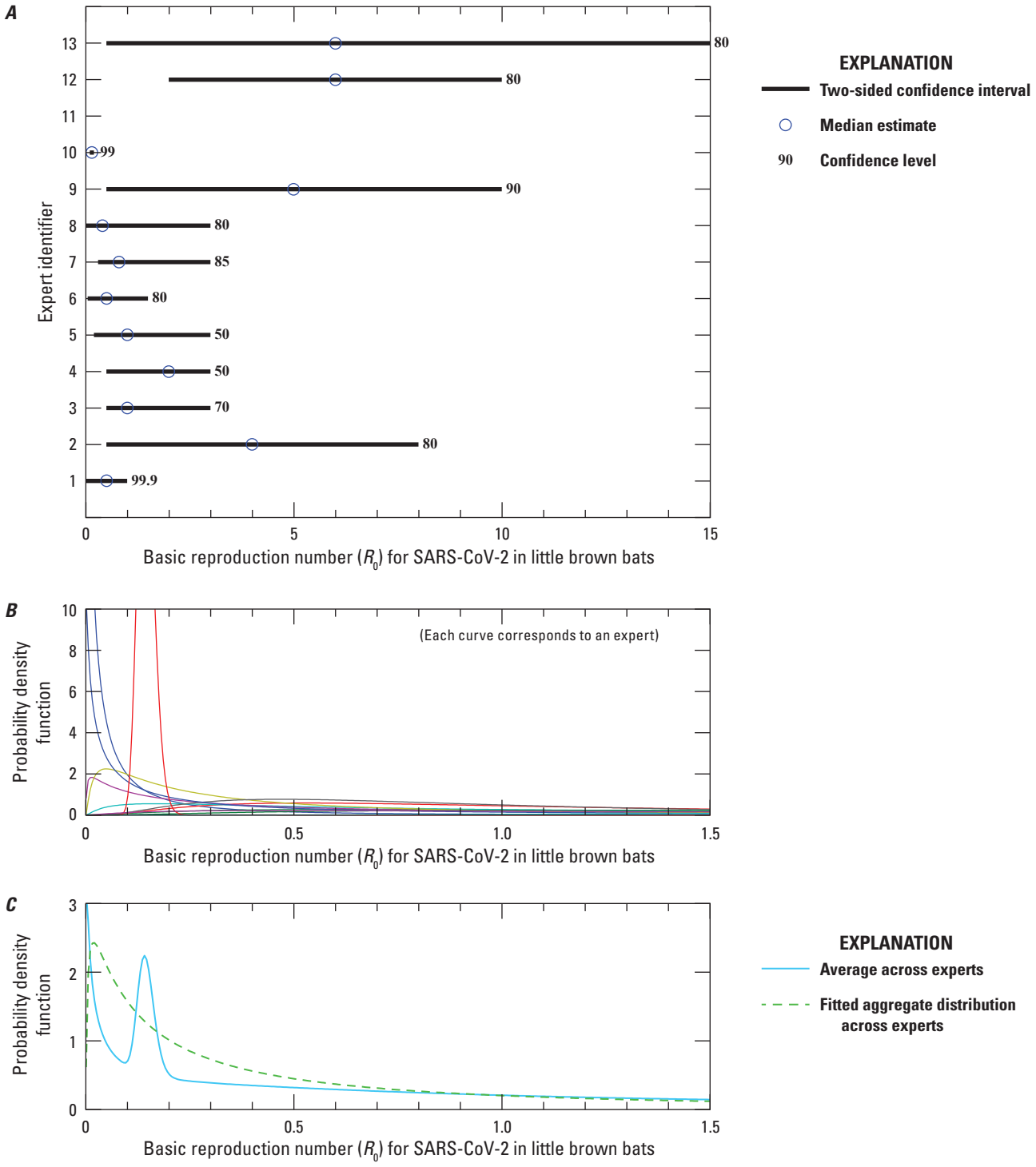

Figure 2.12. Expert panel responses to Question 13—SARS-CoV-2 R_0 in little brown bats. *A*, Four-point-elicitation responses from the individual experts, *B*, fitted probability distributions for individual experts, and *C*, average and fitted distributions across experts. The aggregate distribution has a median of 0.45 and an 80-percent confidence interval of (0.05, 4.38). In the aggregate distribution, the probability that R_0 is greater than 1.0 is 0.326.

For additional information, contact:
Director, Patuxent Wildlife Research Center
U.S. Geological Survey
12100 Beech Forest Road
Laurel, MD 20708

or visit our website at:
https://www.usgs.gov/centers/pwrc

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ISSN 2331-1258 (online)
https://doi.org/10.3133/ofr20201060

From: Cryan, Paul
Sent: Tuesday, April 14, 2020 6:08 PM EDT
To: Kading,Rebekah
CC: olival ecohealthalliance.org>
Subject: SARS-CoV-2 spillback risk in North American bats

Hi Rebekah,

I got your email yesterday and will reply soon on that more-fun front, but here's a semi-spam message about the other stuff...

Sorry for the silence since my call for help about the risks of humans potentially infecting bats in North America with the SARS-CoV-2 virus. Thanks for your patience and willingness to get involved in what we're hoping can be another disease response where scientists coming at disparate aspects of bats and pathogens can help each other. Those of us in the bat research world that focused most of our past efforts in the U.S. only on conservation and management of bat populations can certainly use your expertise and help adjusting to the new situation.

A lot has happened during my silence. As you know by now, the USGS group led by Evan Grant and Mike Runge has been working at the behest of decision makers across federal and state natural resource management agencies to pull off a formal risk assessment by querying a subset of the experts we've reached out to. You were one of the dozen or so experts chosen for and actively participating in that exercise, so thanks for helping with that. I know from experience it can be a lot of work on an inconveniently compressed timeline, but think the immediate results will be very helpful to decision-makers faced with impending decisions about people interacting closely with bats. We may bug you about sources of state rabies lab data summaries at some point soon, so be forewarned and start flagging your emails from us as spam if you've already done your time! ☺

The other thing keeping me silent over the past couple of weeks is a short manuscript (currently 5 pages single spaced) that Kevin and I drafted to articulate the potential risks of humans infecting North American temperate-zone bats with SARS-CoV-2, potentially relevant patterns we observed in bat-CoV distributions at a global scale, and the likely benefits of disease and bat researchers working together to draw on the strengths of our various disciplines. You've seen the long, rambling, unfocused version with the expert elicitation package, but its much more focused and concise now. We hope to have a draft to circulate by tomorrow and would appreciate input and feedback from any of you willing to read it and help us stress test the concepts and assertions therein. Please let me know if you are interested.

Thanks again for your help and patience.

Talk soon,
Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Kevin Olival ecohealthalliance.org>
Sent: Tuesday, May 12, 2020 10:13 AM EDT
To: Paul Cryan < >; Brian R. Amman ; Ralph S. Baric ; David S Blehert Cara Brook >; Charles H Calisher Kevin Castle Jeremy Coleman >; Peter Daszak ecohealthalliance.org>; epstein ecohealthalliance.org>; Hume Field ecohealthalliance.org>; Winifred F Frick, Ph.D. < >; Gilbert, Amy T - APHIS >; David Hayman >; Hon S Ip ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah ; Tigga Kingston >; Lorch, Jeffrey M ; Ian MENDENHALL PhD ; alisonpeel >; Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; DeeAnn Reeder Jonathan D Reichard ; Jonathan M Sleeman ; Daniel Streicker ; Jonathan S. Towner >; Wang Linfa
Subject: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PNAS (new plan)
Attachment(s): "smime.p7m"

Dear Co-authors,

Attached is the latest, submission ready version of our paper"**Possible risks of SARS-CoV-2 spillover to free-ranging wildlife: a case study of bats**". Thank you all for the last round of invaluable edits and comments. Paul and I have now gone through multiple revisions since you last saw the paper in an attempt to include everyone's feedback; so apologize for the delay in turning this around and moving towards submission.

We started a submission to *Lancet Infectious Diseases*, but after thinking more about the journal's scope and reading other recent reviews that have been published in the journal, Paul and I decided it was not the best fit after all. We instead plan to submit this as a Perspectives article to *PNAS* (https://www.pnas.org/page/authors/purpose-scope). We think *PNAS* is a better fit all around, especially given the US focus of our review. We are currently following up some leads for "sponsorship" of our paper with PNAS which would make it an invited piece. If you have any specific suggestions in this regard, please let me know.

As before, the plan is once we submit (hopefully this week) to *PNAS* we will also post as a pre-print on BioRxiv so it can be viewed and used immediately. **If there are any objections to this plan or to submit to *PNAS*, please let me know.** Also, for those that have secured USG approval already, please let me know if these needs to be updated or if you need any more information.

This has been a fantastic exercise in group writing! Big thank you to everyone.

Cheers,
Kevin

Dear Co-authors,

Attached is the latest, submission ready version of our paper "**Possible risks of SARS-CoV-2 spillover to free-ranging wildlife: a case study of bats**". Thank you all for the last round of invaluable edits and comments. Paul and I have now gone through multiple revisions since you last saw the paper in an attempt to include everyone's feedback; so apologize for the delay in turning this around and moving towards submission.

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Also, for those that have secured USG approval already, please let me know if these needs to be updated or if you need any more information.

This has been a fantastic exercise in group writing! Big thank you to everyone.

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
460 West 34th Street, Suite 1701
New York, NY 10001

www.ecohealthalliance.org

From: Caitlin Devaney
Sent: Tuesday, March 10, 2020 2:30 PM EDT
To: kityrob ; abelwade
epstein >; Tigga.Kingston ;
Kading,Rebekah ; spwa ; ian.mendenhall

CC: Stokes, Martha M CIV (USA) ; Jamechia Hoyle ; Katie Leahy
>; Megan Hudson ; Aleman, Nicki D CTR DTRA
COOP THRT REDUCT (USA)
Subject: World One Health Congress and BTRP TRN Side Meeting - BOHRN
Attachment(s): "WOHC and BTRP Side Meeting Schedule.pdf"

Dear BOHRN TRN Steering Committee Members,

On behalf of Dr. Martha Stokes, please accept this Save the Date to attend the World One Health Congress in Edinburgh, Scotland 15-17 June 2020 and participate in side meetings on BTRP's Threat Reduction Networks and planning for BOHRN.

Tentatively, we plan to hold two sessions at the end of the week: Thursday, 18 June - an afternoon TRN session that will include a wide group of BTRP-funded participants from its other research networks to discuss network metrics for sustainability; Friday, 19 June - a side meeting for BOHRN to map out its schedule and strategy, aligning with funding opportunities from BTRP and other entities. Attached is a tentative schedule for the week, for your reference. Due to travel and budgetary constraints we are unable to invite the entire steering committee, but intend to have productive discussions and meet objectives with the smaller group on this Save the Date email.

Please let us know if you will be able to attend the WOHC and side meetings on 18-19 June. Official invitation with travel instructions, details on arrangements, and more formal agenda will be forthcoming. Please note that there is a potential for the WOHC and BTRP side meetings to be postponed, given the current travel uncertainties related to COVID-19. We will be monitoring the status of the conference, and will keep you apprised of any cancellations should they occur. As always, let us know if you have any questions!

We hope to see you in Edinburgh!!

V/r,
Caitlin Devaney

CAITLIN DEVANEY | ***Program Manager***
Global Systems Engineering, LLC
A Certified HUBZone Company
www.globalsyseng.com
(

World One Health Congress & BTRP Side Meetings

**located at Edinburgh International Conference Centre (EICC), for more info: https://www.eicc.co.uk/organising/the-venue*

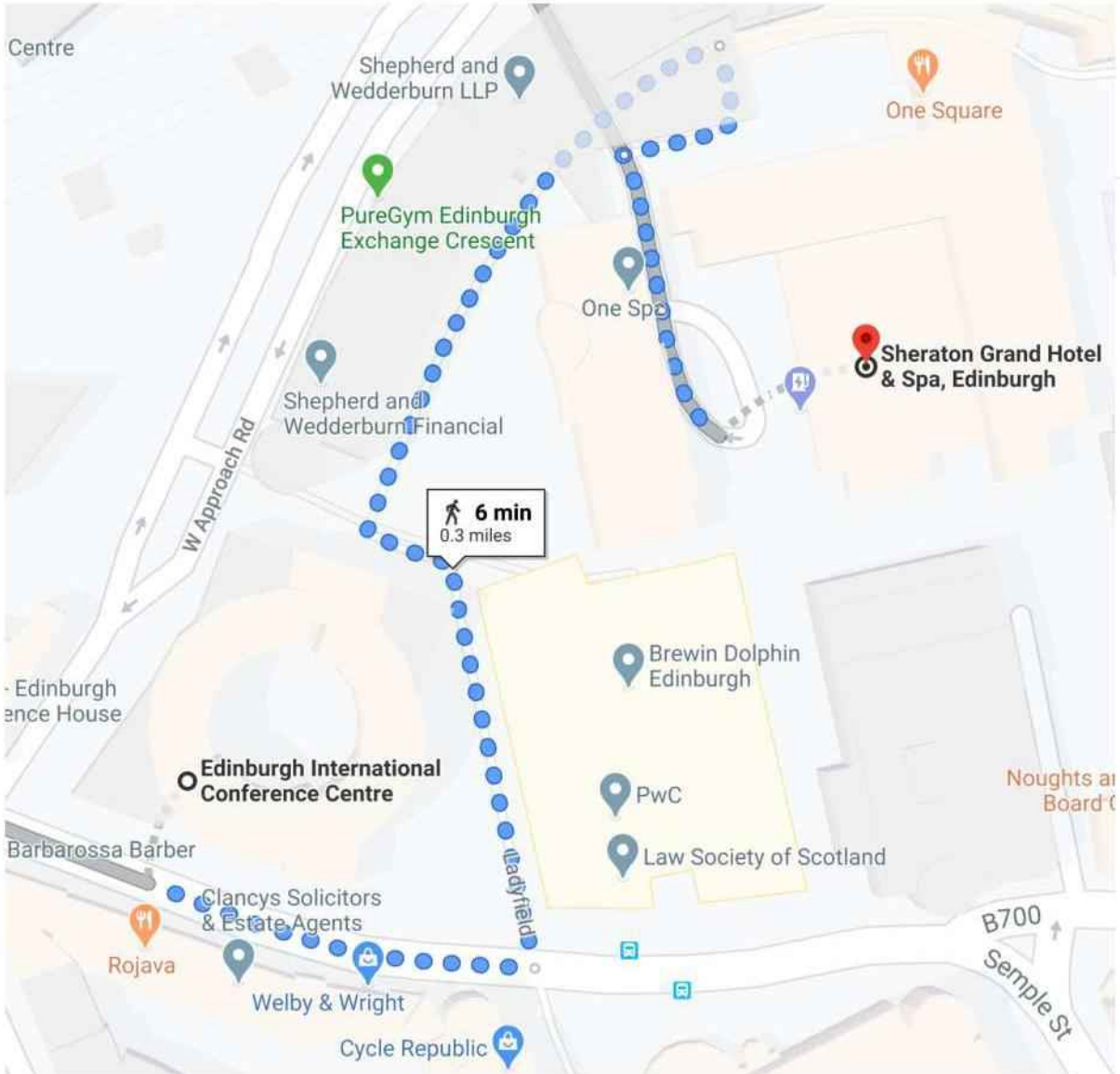
Galloway Suite Garrick I & II* | Plenary Room* | Sheraton Grand Hotel & Spa

Galloway Suite Harris II* | National Museum of Scotland | TBD: WOHC EICC*

	JUNE 14	JUNE 15	JUNE 16	JUNE 17	JUNE 18	JUNE 19
0700			0730-0900 Special Plenary Session BMJ/VET RECORD	0730-0900 Special Plenary Session	0730-0830 Keynote Lectures	
0800					0830-1015 PARALLEL SESSIONS worldonehealthcongress.org	0800-1200 CANARIES Working Group Meeting
0900	*The meetings below are TBD:*		0915-1015 Keynote Lectures	0915-1015 Keynote Lectures		
1000	1000-1800 US DTRA BTRP 101 Seminar	1000-1330 Special Plenary Session University of Edinburgh	1045-1800 PARALLEL SESSIONS See agenda at: worldonehealthcongress.org	1045-1800 PARALLEL SESSIONS See agenda at: worldonehealthcongress.org		
1100						
1200						1200-1300 Lunch
1300	1000-1330 US DTRA AOHC Steering Committee				1300-1430 COVID-19	1300-1700 BOHRN Working Group Meeting
1400		1400-1530 Asclepius One Health				
1500					1500-1700 TRNs: Prevention & Detection Integration	
1600		1600-1730 Health Security Interface				
1700					1730-1930 TRN Networking Dinner	
1800		1830-2000 Opening Ceremony	1800-1930 Bavarian Nordic	1800-1930 Vaccination		
1900				1930-2100 Poster Networking Session		
2000			2000-2300 Congress Networking Dinner			
2100						

Directions from the EICC to the Sheraton Grand Hotel & Spa

Walking



6 min (0.3 mile)

via Morrison St/B700

Mostly flat

⚠ Use caution–walking directions may not always reflect real-world conditions

Edinburgh International Conference Centre

The Exchange, 150 Morrison St, Edinburgh EH3 8EE, United Kingdom

1. Head east on Morrison St/B700 toward Ladyfield
   269 ft
2. Turn left onto Ladyfield
   0.1 mi
3. Turn right
   Take the stairs
   128 ft
4. Turn left
   108 ft
5. Turn left
   Destination will be on the left
   95 ft

Sheraton Grand Hotel & Spa, Edinburgh

1 Festival Square, Edinburgh EH3 9SR, United Kingdom

From: Kading,Rebekah
Sent: Monday, September 14, 2020 6:30 PM EDT
To: Kading,Rebekah
CC: Guzal Masharipova
BCC:

(

Subject: Bat One Health Research Network Directory - request to join!

Dear BOHRN colleagues,

Oh my goodness, what a year it has been! We hope this message finds you all healthy and safe. While the pandemic has taken many of us on various detours from our usual routine and research over the past six months, we all have been very busy responding to this pandemic in myriad ways. In many cases, BOHRN network members have found ourselves working together on various initiatives, which has been exciting. We are looking forward to the time when we can interact in person again at conferences and at future BOHRN meetings. Thank you SO MUCH for all your efforts during this challenging time!

Tigga and I are writing to you today with a BOHRN-related update and a **specific action request to participate in a BOHRN membership directory (more details below)**.

The context: One of the positive outcomes of months of quarantine in Texas (Tigga) and Colorado (Rebekah) -- is that we followed up in a tangible way on one of the key challenges identified during our BORHN meetings: addressing the polarization of the bat ecology and infectious disease research communities. We have written a Perspectives piece, currently in review at PLOS Biology, which reports the results of a bibliometric analysis of co-author relationships among bat researchers between 1950 and 2019. This analysis identified a division between ecology- and infectious disease disciplines from the perspective of co-authored interdisciplinary journal articles (no surprise there!). However, our fields have done a good job at converging over issues that have presented a common mission, such as white nose syndrome. SARS-CoV-2 has provided a similar common ground for us to rally around as far as the risk this virus poses to both human and bat health. The editors and reviewers have challenged us to take steps that will actually lead to productive outcomes and interdisciplinary collaborations. Hence, we are very excited to engage directly with BOHRN and build on the infrastructure that has already been put into place by DTRA-BTRP.

Action item: In the immediate-term, **our goal is build a searchable membership directory housed within the BOHRN website.** This will enable members to connect with each other, learn more about what others are doing, and recruit people to the various working groups that BOHRN has established. DTRA and Global Systems Engineering have graciously and expeditiously revamped the website to enable this specific functionality. **How this works**: interested stakeholders will set up a member login on the BOHRN website as well as a member profile that will be visible to other members after logging in. **Members will benefit** from being able to search the directory for colleagues in complementary research areas, and receive information disseminated by BOHRN regarding opportunities and meetings. All of the information you enter will be accessible only to other members.

Steps we're asking you to take:

1. Go to https://www.bohrn.net
2. Click on "Join"
3. Create an account, fill out your profile
4. Check the boxes to affirm that you agree with having your information visible to others within the member page, and with the BOHRN mission statement (provided)
5. Click "Continue" to be brought to the Members page.
6. Your profile will automatically be entered into the directory, butthis may take a few hours to sync and be visible on the website.
7. From the Members page you should be able to view other member profiles as well as search the directory.

Thanks so much, and please don't hesitate to reach out to us if you have any questions. We look forward staying in contact and growing the BOHRN network together.

Kind regards,

Rebekah and Tigga

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kading,Rebekah
Sent: Wednesday, September 16, 2020 12:24 PM EDT
To: Kading,Rebekah
CC: Kingston, Tigga Stokes, Martha M CIV (USA) ; Katie Leahy

BCC:

Subject: Bat One Health Research Network directory

Dear colleagues,

I hope this message finds you all healthy and safe. While the pandemic has taken many of us on various detours from our usual routine and research over the past six months, we all have been very busy responding to this pandemic in myriad ways. Thank you SO MUCH for all your efforts during this challenging time!

I'm writing to invite you to join the Bat One Health Research Network (BOHRN). BOHRN was formed in 2017 by the Defense Threat Reduction Agency Biological Threats Reduction Program (DTRA-BTRP) with the mission:

To convene a multidisciplinary consortium of disease researchers, conservationists, policy makers, and medical / veterinary practitioners into a network to characterize global threats of bat-borne pathogens and formalize community standards and conservation-conscientious practices for One Health disease research.

Tigga Kingston and I have been working with BOHRN to faciliate connecting researchers and other stakeholder groups with diverse, complementary expertise. O**ur goal is build a searchable membership directory housed within the BOHRN website.** This will enable members to connect with each other, learn more about what others are doing, and recruit people to the various working groups that BOHRN has established. DTRA and Global Systems Engineering have graciously and expeditiously revamped the website to enable this specific functionality (thank you!!). **How this works**: interested stakeholders will set up a member login on the BOHRN website as well as a member profile that will be visible to other members after logging in. **Members will benefit** from being able to search the directory for colleagues in complementary research areas, and receive information disseminated by BOHRN regarding opportunities and meetings. All of the information you enter will be accessible only to other members

If you're interested, please:

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2. Click on “Join”
3. Create an account, fill out your profile
4. Check the boxes to affirm that you agree with having your information visible to others within the member page, and with the BOHRN mission statement (above)
5. Click “Continue” to be brought to the Members page.
6. Your profile will automatically be entered into the directory, butthis may take a few hours to sync and be visible on the website.
7. From the Members page you should be able to view other member profiles as well as search the directory.

Please feel free to spread the word, and encourage trainees/students/post-doctoral researchers on your teams to join!!

Thanks so much, and please don’t hesitate to reach out to us if you have any questions. We look forward staying in contact and growing the BOHRN network together.

Kind regards,

Rebekah

Rebekah C. Kading, PhD

Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kading,Rebekah on behalf of Kading,Rebekah <
Sent: Thursday, June 25, 2020 1:54 PM EDT
To: Kendra Phelps ecohealthalliance.org>
Subject: contact

Dear Kendra,

I hope this message finds you hanging in there ok during all of this! Thank you also for all your hard work on this North American bat paper! I've been interacting regularly with Tigga through the IUCN Bat Specialist Group and working on another paper; it's been nice keeping up with her outside of BOHRN. With everything going on with the bat research community and SARS-CoV-2 though, lots of BOHRN members are involved in various initiatives and and keeping pretty busy...someday when we are on the other side of this, I hope DTRA revitalizes a BOHRN meeting in person so we can all reconnect, debrief, and move some ideas forward that we had been discussing. I don't think anyone would accept another Zoom meeting at this point though!

Anyway, I'm writing to ask if I can put you in touch with a DVM/PhD student in my lab, Anna Fagre. Anna is outstanding, and interested in applying for one of the open positions at EcoHealth and just wants to do due diligence in finding out more about the position, expectations, etc. I thought of you as being a good person to provide some inside perspective, but wanted to reach out first to make sure that wouldn't put you in an awkward position, like if you're on the hiring committee or something.

Thanks so much!

Best regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kendra Phelps ecohealthalliance.org>
Sent: Tuesday, June 16, 2020 8:59 AM
To: Raina Plowright
Cc: Paul Cryan ; Wang Linfa ; oliva < >; dreeder < ; Hume Field ecohealthalliance.org>; Charles H Calisher ; Brian R. Amman ; Ralph S. Baric ; Blehert, David S ; Cara Brook ; Kevin Castle >; Coleman, Jeremy T ; Peter Daszak ecohealthalliance.org>; epstein ecohealthalliance.org>; wfrick ; Gilbert, Amy T - APHIS ; David Hayman ; Ip, Hon S ; William B. Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah ; Tigga Kingston >; Lorch, Jeffrey M Ian Mendenhall alisonpee Reichard, Jonathan D >; Sleeman, Jonathan M >; Daniel Streicker ; Jonathan S. Towner
Subject: Re: [EXTERNAL] SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Agreed, great job Kevin and Paul for the quick turnaround.

The CNN special can be viewed on www.cnn.com/go, click on “Shows” to the left-side of the screen and the special should be an option at the top of the screen (or one scroll to the right). I think you need a cable subscription to log-in to view though.

Cheers,
Kendra

Kendra Phelps, PhD
Research Scientist

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200
New York, NY 10018

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

> On Jun 16, 2020, at 10:48 AM, Raina Plowright > wrote:
>
> Thanks for doing the record turn-around! Well done everyone and great leadership Paul and Kevin!
> Does anyone have a link to the full CNN documentary? I heard it was great.
> Raina

> > On Jun 16, 2020, at 8:40 AM, Cryan, Paul > wrote:
> >
> > That was one of those unforgettable moments for me watching many of you on the CNN special...in my opinion you all came off very well! Congrats!
> >
> > Paul
> >
> > Paul Cryan
> > Research Biologist
> > USGS Fort Collins Science Center
> >
> > Web Page and Contact Info

From: Wang Linfa
Sent: Monday, June 15, 2020 11:22 PM
To: oliva ecohealthalliance.org>; dreeder >; Hume Field ecohealthalliance.org>; Charles H Calisher ; Brian R. Amman ; Ralph S. Baric >; Blehert, David S >; Cara Brook < ; Kevin Castle ; Coleman, Jeremy T ; Peter Daszak ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; wfrick ; Gilbert, Amy T - APHIS >; David Hayman >; Ip, Hon S ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah ; Tigga Kingston ; Lorch, Jeffrey M ; Ian Mendenhall alisonpee ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; Reichard, Jonathan D >; Sleeman, Jonathan M >; Daniel Streicker < >; Jonathan S. Towner
Cc: Cryan, Paul
Subject: [EXTERNAL] RE: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Thanks Kevin and Paul for doing a great job so quickly.

I guess the CNN documentary yesterday also made this a hot (hotter) topic now and the editor may want to have “a ride on the bat wings” to get it out asap!

Fingers crossed.

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,

8 College Road, Singapore 169857
Tel: +65 6516 8397

From: Kevin Olival ecohealthalliance.org>
Sent: Tuesday, 16 June 2020 1:19 PM
To: DeeAnn Reeder ; Hume Field cohealthalliance.org>; Charles H Calisher >; Brian R. Amman Wang Linfa >; Ralph S. Baric >; David S Blehert >; Cara Brook >; Kevin Castle Jeremy Coleman >; Peter Daszak ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Winifred F Frick, Ph.D. < g>; Gilbert, Amy T - APHIS ; David Hayman Hon S Ip < >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson >; Kading,Rebekah ; Tigga Kingston ; Lorch, Jeffrey M >; Ian Mendenhall ; alisonpee Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; Jonathan D Reichard Jonathan M Sleeman >; Daniel Streicker ; Jonathan S. Towner >
Cc: Paul Cryan >
Subject: Re: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

- External Email -

Hi Team,

Funny thing, bioRxiv actually rejected us! Apparently they don't take "reviews".

In any case we got **very positive reviews back from *PLoS Pathogens*** today, and the revised ms was just resubmitted (<24 hour turnaround). Woohooo! Finger's crossed that the editors turn it around again quickly and we can see this published soon.

Attached is the cover letter, response to reviewers, and the resubmitted version of ms.

Cheers,
Kevin and Paul

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org
EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

> On Jun 12, 2020, at 10:43 AM, Kevin Oliva ecohealthalliance.org> wrote:
>
> Dear all,
>
> We successfully submitted to bioRxiv yesterday and it's currently in "review" with the editorial staff and should be posted within 48 hours. Big thanks to Paul for getting the final USGS approvals and ms formatting in place.
>
> Hume and Charlie, I understand your very valid and "traditional" concerns here, there's a lot of riff-raff out there on pre-print servers and hence why we have the peer-review system. Nonetheless, given that there are other similar reviews being posted at the moment and the timeliness of this given the USGS/USFW Risk Assessment out last week, etc., would be best to get this out there while we're still in review at PLOS.
>
> Best,
> Kevin
>
> **Kevin J. Olival, PhD**
> *Vice President for Research*
>
> EcoHealth Alliance
> 520 Eighth Avenue, Suite 1201
> New York, NY 10018
>
> www.ecohealthalliance.org
> *EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.*
>
> > On Jun 12, 2020, at 8:24 AM, DeeAnn Reeder wrote:
> >
> > Thanks all - I am in support of bioRxrv for this paper (although I don't systematically use it - in this fast moving CoV environment, for some papers I think it is a very good option).
> >
> > Cheers - DeeAnn
> >
> > On Thu, Jun 11, 2020 at 7:22 PM Hume Field @ecohealthalliance.org> wrote:
> >
> > > Thanks Kevin.. no prob, tho philosophically I'm with Charlie!
> > >
> > > Hume
> > >
> > > On Fri., 12 Jun. 2020, 1:23 am , <calisher wrote:
> > >
> > > > No significant objections about the manuscript but I am not crazy about pre-print servers or their purpose. I am not only old, I am a traditionalist. Lots of crap being sent out as pre-print servers that wind up not being acceptable – or withdrawn.
> > > >
> > > > Charlie
> > > >
> > > > ---
> > > > **From:** Amman, Brian R. (CDC/DDID/NCEZID/DHCPP)
> > > > **Sent:** Thursday, June 11, 2020 8:05 AM
> > > > **To:** Kevin Oliva ecohealthalliance.org>; Wang Linfa >; Paul Cryan ; Ralph S. Baric ; David S Blehert Cara Brook >; Charles H Calisher < ; Kevin Castle >; Jeremy Coleman ; Peter Daszak ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Hume Field @ecohealthalliance.org>; Winifred F Frick, Ph.D. < >; Gilbert, Amy T - APHIS ; David Hayman < ; Hon S Ip >; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah >; Tigga Kingston ; Lorch, Jeffrey M ; Ian MENDENHALL PhD >; alisonpee ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina < >; DeeAnn Reeder >; Jonathan D Reichard ; Jonathan M Sleeman < ; Daniel Streicker Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)
> > > > **Subject:** RE: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)
> > > >
> > > > Thanks Kevin!

From: Kevin Olival < ecohealthalliance.org>
Sent: Thursday, June 11, 2020 9:43 AM
To: Wang Linfa >; Paul Cryan < >; Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) >; Ralph S. Baric David S Blehert ; Cara Brook >; Charles H Calisher >; Kevin Castle >; Jeremy Coleman >; Peter Daszak ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Hume Field ecohealthalliance.org>; Winifred F Frick, Ph.D. >; Gilbert, Amy T - APHIS >; David Hayman >; Hon S Ip ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah >; Tigga Kingston >; Lorch, Jeffrey M ; Ian MENDENHALL PhD >;alisonpeel ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina >; DeeAnn Reeder ; Jonathan D Reichard Jonathan M Sleeman >; Daniel Streicker >; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)

Subject: Re: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Dear all,

Update on our ms. It was submitted to PLOS Pathogens on June 2nd (you should have all received an email from the journal confirming this) and it is currently under review.

We are in the final stages of USGS approval to also submit to bioRxiv (pre-print server), and expect to finalize that and post it on bioRxiv in the next 24 hours. *Please let me know if there are any objections.*

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eight Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org
EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

> On May 28, 2020, at 4:38 PM, Kevin Olival < cohealthalliance.org> wrote:
>
> Hi Folks,
>
> Quick update on our paper — unfortunately got news yesterday that *PNAS* was not interested in this as a Perspectives piece, and rejected our proposal. We are currently pursuing options with editors at *PLOS Pathogens* to see if they want it as a review. Will keep you all posted.
>
> Latest version attached that has cleared CDC and USGS review. We will still aim to get this on BioRxiv, but wanted to wait until we had it cleared first and ideally in review at a journal.
>
> Cheers,
> Kevin
>
> <Olival et al. bat CoVs 20200520_v11.3.docx>
>
> **Kevin J. Olival, PhD**
> *Vice President for Research*
>
> EcoHealth Alliance
> 520 Eight Avenue, Suite 1201
> New York, NY 10018
>
> www.ecohealthalliance.org
> *EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.*
>
> > On 12 May 2020, at 10:13 PM, Kevin Olival < .org> wrote:
> >
> > Dear Co-authors,
> >
> > **Attached is the latest, submission ready version of our paper** "**Possible risks of SARS-CoV-2 spillover to free-ranging wildlife: a case study of bats**". Thank you all for the last round of invaluable edits and comments. Paul and I have now gone through multiple revisions since you last saw the paper in an attempt to include everyone's feedback; so apologize for the delay in turning this around and moving towards submission.
> >
> > We started a submission to *Lancet Infectious Diseases*, but after thinking more about the journal's scope and reading other recent reviews that have been published in the journal, Paul and I decided it was not the best fit after all. We instead plan to submit this as a Perspectives article to *PNAS*(https://www.pnas.org/page/authors/purpose-scope). We think *PNAS* is a better fit all around, especially given the US focus of our review. We are currently following up some leads for "sponsorship" of our paper with PNAS which would make it an invited piece. If you have any specific suggestions in this regard, please let me know.
> >
> > As before, the plan is once we submit (hopefully this week) to *PNAS* we will also post as a pre-print on BioRxiv so it can be viewed and used immediately. **If there are any objections to this plan or to submit to *PNAS*, please let me know.**
> > Also, for those that have secured USG approval already, please let me know if these needs to be updated or if you need any more information.
> >
> > This has been a fantastic exercise in group writing! Big thank you to everyone.
> >
> > Cheers,
> > Kevin
> >
> > <Olival et al. bat CoVs 20200511_V9.1.docx>
> >
> > **Kevin J. Olival, PhD**
> > *Vice President for Research*
> >
> > EcoHealth Alliance
> > 460 West 34th Street, Suite 1701
> > New York, NY 10001
> >
> > www.ecohealthalliance.org
> > EcoHealth Alliance develops science-based solutions to prevent pandemics *and* promote conservation

--
DeeAnn M. Reeder, PhD
Professor
Department of Biology
Bucknell University
Lewisburg, PA 17837

http://deeannreeder.scholar.bucknell.edu

Important: This email is confidential and may be privileged. If you are not the intended recipient, please delete it and notify us immediately; you should not copy or use it for any purpose, nor disclose its contents to any other person. Thank you.

From: Kading,Rebekah
Sent: Wednesday, February 07, 2018 11:01 AM EST
To: Kevin Olival, PhD ecohealthalliance.org>
Subject: field trip pic
Attachment(s): "DSC_0810.JPG"

Hi Kevin,

I hope this message finds you well, and that your travel home was smooth! The trip to the Chonburi field site was fantastic; thank you for sharing with the group about the PREDICT research there. It was a perfect example of One Health. I thought you'd enjoy having this picture. Take care and see you at our next gathering -

Best regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University


PMAC
PRINCE MAHIDOL AWARD CONFERENCE 2018
KU
KASETSART
Wild life disease surveillance research for EID
D
STATION
Field Trip Site No.4
USAID
PREDICT


PMAC
2018
KU
Wild life disease surveillance research for EID
D
STATION
Field Trip Site No.4


PMAC
PRINCE MAHIDOL AWARD CONFERENCE 2018
KU
Wild life disease surveillance research for EID
D
STATION
Field Trip Site No.4
USAID
USAID PREDICT

From: Kading,Rebekah
Sent: Monday, June 22, 2020 6:14 PM EDT
To: Joy O'Keefe ; Diana Hews < >; Fagre,Anna ; Kevin Castle ; Paul Cryan <c >; Bowen,Richard ; Schountz,Tony >; olival >; epstein ecohealthalliance.org>; Jonathan Towner >; Brian Amman ; raina.plowright >; Karen Fox - DNR ; Stokes, Martha M CIV (USA) >; Robert Kityo ; abelwade >; Tony Goldberg ; Christine Kreuder Johnson ; dreeder ; Brian H Bird ; Piaggio, Antoinette J - APHIS ; Gilbert, Amy T - APHIS >; David Hayman >; Grant, Evan H ; Stoner,Kathryn < >; Baric, Ralph S < ; Bowen,Richard >; Bosco-Lauth,Angela >; Robert Aruho >; Patrick Atimnedi >; Luke Nyakarahuka ; Julian Kerbis >; Margaret Driciru ; Clif McKee ; spwa < ; Charles Calisher >; kosoy >; Franklin, Alan B - APHIS Root, Jeff - APHIS >; Bevins, Sarah N - APHIS ; ksidamonidze ; lelincdc ; c demetria >; wanda.markotter >; Julius Lutwama >; VandeWoude,Susan >; Webb,Colleen >; nisreen.hmoud >; Schuh, Amy (CDC/OID/NCEZID) >; Sealy, Tara K. (CDC/DDID/NCEZID/DHCPP)
CC: Kingston, Tigga
Subject: IUCN guidelines
Attachment(s): "IUCN infographic FINAL 062220.pdf"

Dear colleagues,

Hot off the press! The IUCN Species Survival Commission Bat Specialist Group has released guidelines for researchers, to prevent the human-to-bat transmission of SARS-CoV-2. Our infographic is attached, and full guidelines available through either link below. Additional products are to follow shortly, tailored for other stakeholder groups. Please feel free to distribute as you see fit.

Best regards,
Rebekah

https://www.iucnbsg.org/publications.html
https://tinyurl.com/mapforbats

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

Preventing human-to-bat transmission of SARS-CoV-2

Exposure Risks

Contact exposure
Bats coming into contact with contaminated hands or equipment

Aerosol exposure
Infectious droplets from handlers holding bats in close proximity

Environmental exposure
Sharing enclosed, poorly-ventilated spaces with bats, where virus may persist in the air or on surfaces

MAP your plan to prevent transmission to bats!

Mitigation Strategies

Minimize

Delay, prioritize, or avoid handling bats when possible, i.e. implement acoustic surveys

Assess

Postpone handling bats if there is a probability that you have been exposed to SARS-CoV-2 or if you have symptoms

Protect

Adopt practices that reduce exposure, i.e. face covering, gloves, disinfection procedures

IUCN SSC Bat Specialist Group

www.iucnbsg.org

Full recommendations @ https://tinyurl.com/mapforbats

From: Kading,Rebekah on behalf of Kading,Rebekah
Sent: Tuesday, August 25, 2020 3:03 PM EDT
To: Katie Leahy >; Kingston, Tigga < ; martha.m.stokes

CC: jamechia.d.hoyle.ctr ; Guzal Masharipova < ;
epstein ecohealthalliance.org>
Subject: Re: [External Sender] RE: BOHRN Status, publication

Hi Katie, Marty, and Guzal -

Just chiming in to say hello and THANK YOU for the quick response and support for this effort! This is all great to hear, and I think we have a fantastic opportunity with this paper to provide another way to invigorate and draw attention to BOHRN. As Tigga and I were discussing the reviewer's suggestion, we basically converged on "Hey, BOHRN has already done all of this!" So it is wonderful to hear that we can move forward together to use this paper to direct people to BOHRN, which is where the rubber will hit the road. Looking forward to moving this forward, and we'll keep in touch with the revised manuscript. Thanks!

Best,
Rebekah :-)

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Katie Leahy
Sent: Tuesday, August 25, 2020 11:54 AM
To: Kingston, Tigga ; martha.m.stokes >
Cc: jamechia.d.hoyle l>; Guzal Masharipova >;
Kading,Rebekah >; epstein ecohealthalliance.org>
Subject: Re: [External Sender] RE: BOHRN Status, publication

Hi, Tigga. Guzal (copied) should be able to help. I can make sure she has all the passwords; give us a day to make sure all the links are active. I talked with her today about it and she is ready to support in any way.

V/r,

Katie Leahy

KATIE LEAHY | ***Director, Science Engagement***
Global Systems Engineering, LLC
A Certified HUBZone Company
www.globalsyseng.com

From: "Kingston, Tigga"
Date: Tuesday, August 25, 2020 at 1:51 PM
To: "martha.m.stokes.civ"
Cc: Katie Leahy , "jamechia.d.hoyle >, Guzal
Masharipova ,Rebekah" , Jon Epstein
ecohealthalliance.org>
Subject: [External Sender] RE: BOHRN Status, publication

Dear Marty
Thanks for the speedy response and support! Great to hear of the documentation efforts and continued commitment.

The lynchpin to everything that we'd like to do is the BOHRN website – is there a webmaster, or can one be allocated, so that we can host content, build membership, post some of the materials that have been developed.

Best
Tigga

From: Stokes, Martha M CIV (USA)
Sent: Tuesday, August 25, 2020 8:45 AM
To: Kingston, Tigga
Cc: Katie Leahy >; Hoyle, Jamechia D CTR (USA) ; Guzal Masharipova Kading,Rebekah Jon Epstein ecohealthalliance.org>
Subject: RE: BOHRN Status, publication

Hi Tigga,

Congratulations on having your piece accepted (with revisions, as always)! I would really appreciate you adding detail about BOHRN and highlighting the network's efforts. All of the positive outcomes you mention are well noted and align with our goals and objectives, which remain steadfast.

The current situation has certainly created unexpected challenges for all our work, but we're adapting, and want to ensure that we continue moving forward and position the network to pick up where it left off last summer, once things return to a more normal environment. In the meantime, we'll do what we are able virtually.

Let us know what you need to support this. Katie and I, along with our teams, recently updated a huge amount of documentation, reports, participant lists, etc. for BOHRN and other our TRNs for the incoming BTRP Director, in order to deposit it on our internal database, so it should be very easy to provide whatever you need. Just let us know how we can help.

Thanks so much!

Best,
Marty

Martha M Stokes, PhD
Southeast Asia Regional Science Manager
Biological Threat Reduction Program (BTRP)

From: "Kingston, Tigga"
Date: Monday, August 24, 2020 at 5:09 PM
To: "martha.m.stokes.civ"
Cc: Katie Leahy >, "jamechia.d.hoyle.ctr" , Guzal Masharipova >, "Kading,Rebekah" >, Jon Epstein ecohealthalliance.org>
Subject: [External Sender] BOHRN Status, publication

Dear Marty,

Rebekah Kading and I wrote a perspectives piece that is in revision for PLOS Biology. It calls for greater integration of ecologists/virologists (hmm, sounds familiar) and builds on analysis of a publication coauthor network. We conceptualized this at BORHN meetings and consider it a true BOHRN output, supporting BOHRN's message.

One of the reviewers specified some simple, but concrete actions that they would like to see in the revision. These actions closely ally with things we've begun at BOHRN (e.g., mission statement, contact lists of researchers). We would really like to be able to respond using BOHRN's infrastructure as it would be a good fit and would draw substantial attention to BOHRN and help boost the distributed membership and get us more on the map. The reviewer called for a mission statement, a list of who is doing what, and other simple things that could easily be integrated into the BOHRN website.

Currently, we refer to BOHRN in the acknowledgements, but have been reluctant to feature the network too centrally because we are unsure of its status and stability. It would be great to move forward with BOHRN featured more prominently, but we could do with some clarity of where things are heading. At minimum we need support of the website as that is where we will be directing people. Currently people can't join, or reset passwords etc, and we would need to work with someone on updates supporting these simple collations of information.

We have a bit less than a month to turn this around and get our revision in, so it would be great to hear your thoughts. I hope we can talk soon. I am now free fairly consistently between 10 am-Noon Mo-Thursday. I have other windows here and there as well.

All the best

Tigga

From: Kading,Rebekah on behalf of Kading,Rebekah
Sent: Thursday, April 30, 2020 1:35 PM EDT
To: Cryan, Paul >; olival <
Subject: Re: [EXTERNAL] Re: Final version of North American bat/SARS2 ms - PLEASE REVIEW
Attachment(s): "FB_IMG_1588182632839.jpg"

Yeah, exactly! Might be Thursday, but it might also be Saturday. :-) This made me laugh yesterday so I thought I'd pass it along.
Take care -
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Cryan, Paul
Sent: Thursday, April 30, 2020 10:17 AM
To: Kading,Rebekah olival
Subject: Re: [EXTERNAL] Re: Final version of North American bat/SARS2 ms - PLEASE REVIEW

What, there's a difference between weeks and weekends?!?!? □

Thanks Rebekah!

P

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Kading,Rebekah
Sent: Wednesday, April 29, 2020 5:07 PM
To: olival ecohealthalliance.org>; Cryan, Paul >
Subject: [EXTERNAL] Re: Final version of North American bat/SARS2 ms - PLEASE REVIEW

p.s. Kevin AND Paul, I mean to say in my previous email. Sorry, it's been a long week already! □ Thanks to both of you!!
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kading,Rebekah
Sent: Wednesday, April 29, 2020 5:05 PM
To: Kevin Olival ecohealthalliance.org>; 'Paul Cryan' >
Subject: Re: Final version of North American bat/SARS2 ms - PLEASE REVIEW

Hi Kevin,

Very nice job on this! Only spotted a couple small things.
1) "highlights" is misspelled on line 128.
2) looks like a ref is still needed in line 342 regarding PPE usage in the field. This ref might fit...it's more broadly on wildlife professionals though (PMID: 31993824)
3) don't forget to delete the [...] on line 421

Yes, I would be delighted to be a co-author.

My ORCID is 0000-0002-4996-915X.

Thanks so much!
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology

From: Kevin Olival ecohealthalliance.org>
Sent: Sunday, April 26, 2020 10:11 PM
To: Paul Cryan >; Brian R. Amman >; Ralph S. Baric ; David S Blehert >; Cara Brook Charles H Calisher < ; Kevin Castle ; Jeremy Coleman ; Peter Daszak ecohealthalliance.org>; epstein ecohealthalliance.org>; Hume Field ecohealthalliance.org>; Winifred F Frick, Ph.D. ; Gilbert, Amy T - APHIS ; David Hayman >; Hon S Ip ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah ; Tigga Kingston ; Lorch, Jeffrey M ; Ian Mendenhall >; alisonpee < Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; DeeAnn Reeder < ; Jonathan D Reichard ; Jonathan M Sleeman >; Daniel Streicker ; Jonathan S. Towner >
Subject: Final version of North American bat/SARS2 ms - PLEASE REVIEW

Dear Esteemed Colleagues,

Please review the attached penultimate draft of our manuscript (now entitled: **"Possible risks of SARS-CoV-2 spillover to free-ranging wildlife: a case study of bats")**, together with the supplementary table and refs. Our plan is to submit to *Lancet Infectious Diseases* as a review article (correct length and they allow 150 refs) in the next week - references are currently formatted for that journal. We would also like to post it on bioRxiv as a pre-print once we get it submitted to *Lancet ID*. Please let me know if you have any concerns with that plan.

Thank you all for your excellent comments and edits on the previous draft. Paul and I have gone back and forth on several rounds of revisions since then (and multiple late night texts), aiming to take each and every suggestion into account, and we believe it's a much better manuscript now! Very excited about this one, and looking forward to getting it published!

By Thursday April 30th (or ASAP), could you each please:

1. Confirm that you agree to be a co-author.
2. Double check your name and affiliation, and send me your ORCID number if you have one.
3. Read through the ms and send any important, last minute changes or edits you feel are necessary. Please use track changes. If you're okay with the ms as is, please just confirm so.
4. For my Federal US Gov't friends (USFWS, USGS, CDC, USDA) - please let us know what we need to do for approval on your end. I know Paul is working with USGS now to hopefully get rapid clearance.

No need to cc all if you don't want, but please include both me and Paul on your response.

Looking forward to hearing from you all soon!

Cheers,
Kevin and Paul

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
460 West 34th Street, Suite 1701
New York, NY 10001

AVIRUS

HARRIS COUNTY MASK ORDER

FACE COVERINGS REQUIRED IN PUBLIC

- Face masks required starting Monday April 27th through 30 days
- 10 years and older must wear face coverings
- Homemade masks, scarfs, bananas
- Possible $1,000 fine for not wearing face covering

5:05 | 84°

From: Kading,Rebekah on behalf of Kading,Rebekah
Sent: Monday, April 20, 2020 11:40 AM EDT
To: Cryan, Paul ; Kingston, Tigga
CC: olival >
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats
Attachment(s): "Olival et al. Table S1_20200417_rck.xlsx"

Hi everyone -

Kevin and Paul - this manuscript is very good - thank you for putting it together!! I'll follow up later today with a few comments on the text. I want to read it again but have to go take care of our mosquito colonies at the moment...the one essential duty we have ongoing! I'm attaching the table in the meantime...very comprehensive, wow! I thought it might be helpful for readers to have a column with the broad geographic region of the coronavirus detection in each of the bats, so I added a column to cover this. In instances where the range of the bat species was fairly extensive, I went with where the sampling occurred in the paper. See if you like it...no worries if you don't think its necessary. A couple details/questions came up while I was working on that though:

- excel line 13 - *Nyctalus leisleri* is a European species but Tao and Tong sampled in Kenya...did they mis-identify or maybe there's an accidental reference error?
- excel line 22 - *Hipposideros pratti* looks like an Asian species but the Tao and Tong reference just sampled from Kenya
- excel line 49 - I changed this to Yinterochiroptera and colored it yellow

Question: Is it worth denoting on the table somehow where there is evidence of cross-species sharing of coronavirus strains? For example lines 44-45 the notes have "Eidolon_CoV" but the virus detections being reported were from *Scotophilus* and *Triaenops*...my interpretation is that the virus detected from those latter two bats was the same strain as was detected in *Eidolon* previously? Is there enough evidence to say anything about viral sharing (i.e. are full genomes available) or do we just leave that go for now? I was just thinking that it might be worthwhile to point out any propensity for transfer of strains between/among bat species because that would have relevance to NA bats too.

More later - thanks again - this is a very nice paper and impressive you put it together so quickly!

Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Cryan, Paul >
Sent: Friday, April 17, 2020 11:14 AM
To: Kading,Rebekah Kingston, Tigga
Cc: oliva ecohealthalliance.org>
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Hi Rebekah and Tigga,

Without further adieu, I'm attaching the manuscript draft that Kevin and I put together over the past week and would very much like your input on. Its much leaner and meaner than the rambling draft that went out to the decision-making group last week.

Please take a look if you have the time and consider joining us in trying to get it published somewhere fairly high profile in the coming weeks.

All the best,
Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Kading,Rebekah
Sent: Wednesday, April 15, 2020 8:27 PM

To: Cryan, Paul >; Kingston, Tigga
Cc: olival ecohealthalliance.org>
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Oh my goodness Paul! LOL!
Hang in there - you're doing great.

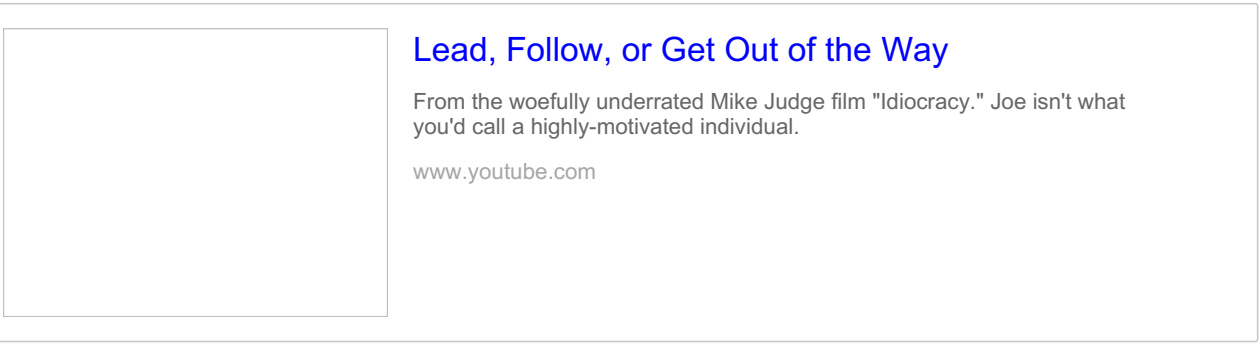
Rebekah
😂

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Cryan, Paul >
Sent: Wednesday, April 15, 2020 7:11 PM
To: Kading,Rebekah >; Kingston, Tigga
Cc: olival ecohealthalliance.org>
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Great to know we're on the same path! I'm finding that coordinating and obsessively researching/writing/getting-up-to-speed on a issue are difficult to pull off at the same time!

https://www.youtube.com/watch?v=onoaKEEyNEI



Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Kading,Rebekah
Sent: Wednesday, April 15, 2020 8:43 AM
To: Kingston, Tigga ; Cryan, Paul
Cc: olival >
Subject: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Hi Paul, Kevin, Tigga,

I'll just reply to this thread. □ Yes, I'd be happy to take a look at the paper as well -- thank you very much for spearheading that effort! As Tigga mentioned we're working on something as well that we'll reach out to you guys separately about. Seems like BOHRN is mobilizing on multiple fronts, which is great to see.

Take care and talk to you soon -
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kingston, Tigga
Sent: Wednesday, April 15, 2020 7:52 AM
To: Cryan, Paul ; Kading,Rebekah >
Cc: olival ecohealthalliance.org>
Subject: RE: SARS-CoV-2 spillback risk to North American bats

Hi Paul
Very interested to see the MS. Rebekah and I have been working on something that arose out of BOHRN that would be very complementary and might be worth trying to coordinate dissemination in some way. We are meeting today and will take stock of where we are at.

I just started an email to you and Kevin about the state of affairs as we Rodrigo and I are getting quite a bit of push-back on the IUCN BSG recommendation to suspend field studies while further data are gathered (primarily from western scientists with access to PPE). It would be good to hear what those committees are finding sooner rather than later.

Best wishes
Tigga

From: Cryan, Paul >
Sent: Tuesday, April 14, 2020 2:16 PM
To: Kingston, Tigga
Cc: ecohealthalliance.org
Subject: SARS-CoV-2 spillback risk to North American bats

Hi Tigga,

Sorry for the silence since my call for help about the risks of humans potentially infecting bats in North America with the SARS-CoV-2 virus. Thanks for your patience and willingness to get involved in what we're hoping can be another disease response where scientists coming at disparate aspects of bats and pathogens can help each other. Those of us in the bat research world that focused most of our past efforts in the U.S. on conservation and management of bat populations can certainly use your expertise and help adjusting to the new situation.

A lot happened during my silence. Another group in USGS has been working at the behest of decision makers across federal and state natural resource management agencies to pull off a formal risk assessment by querying a subset of the experts we've reached out to. You lucked out and were not chosen for that exercise (yet), but we will keep you posted on the outcomes of that rapid assessment.

The other thing keeping me silent over the past couple of weeks is a short manuscript (currently 5 pages single spaced) that Kevin Olival and I drafted to articulate the potential risks of humans infecting North American temperate-zone bats with SARS-CoV-2, potentially relevant patterns we observed in bat-CoV distributions at a global scale, and the likely benefits of disease and bat researchers working together to draw on the strengths of our various disciplines. We hope to have a draft to circulate by tomorrow and would appreciate input and feedback from any of you willing to read it and help us stress test the concepts and assertions therein. Please let me know if you are interested.

Thanks again for your help and patience.

All the best,
Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

Table S1. Global patterns of β-CoV associations in bats. Bat species in which β-CoVs were detected, organized by viral subgenera, bat family, and bat suborder. Bats of the suborder Yinpterochiroptera highlighted in yellow and Yangochiroptera in blue.

β-CoV SUBGENERA	BAT SPECIES	BAT FAMILY	GEOGRAPHIC REGION	REFERENCE	BAT SUBORDER
Sarbecoviruses	*Rhinolophus ferrumequinum*	Rhinolophidae	Africa	Anthony et al. 2017	Yinpterochiroptera
Clade 3	*Rhinolophus sinicus*	Rhinolophidae	Africa	Anthony et al. 2017	Yinpterochiroptera
	Rhinolophus macrotis	Rhinolophidae	Asia	Tao and Tong 2019	Yinpterochiroptera
	Rhinolophus pearsonii	Rhinolophidae	Asia	Tao and Tong 2019	Yinpterochiroptera
	Aselliscus stoliczkanus	Hipposideridae	Asia	Tao and Tong 2019	Yinpterochiroptera
	Chaerephon plicatus	Molossidae	Asia	Tao and Tong 2019	Yangochiroptera
Clade 2	*Rhinolophus pusillus*	Rhinolophidae	Asia	Tao and Tong 2019	Yinpterochiroptera
	Rhinolophus rex	Rhinolophidae	Asia	Wong et al. 2019	Yinpterochiroptera
Clade 1	*Rhinolophus blasii*	Rhinolophidae	Africa	Tao and Tong 2019	Yinpterochiroptera
	Rhinolophus sp. Kenya	Rhinolophidae	Africa	Tao and Tong 2019	Yinpterochiroptera
	Nyctalus leisleri	Vespertilionidae		Tao and Tong 2019	Yangochiroptera
Hibecoviruses	*Hipposideros armiger*	Hipposideridae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Hipposideros caffer	Hipposideridae	Africa	Anthony et al. 2017	Yinpterochiroptera
	Rhinolophus clivosis	Rhinolophidae	Africa	Anthony et al. 2017	Yinpterochiroptera
	Hipposideros commersoni	Hipposideridae	Africa	Tao and Tong 2019	Yinpterochiroptera
	Rhinolophus creaghi	Rhinolophidae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Hipposideros galeritus	Hipposideridae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Hipposideros larvatus	Hipposideridae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Hipposideros lekaguli	Hipposideridae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Hipposideros pratti	Hipposideridae	Asia	Tao and Tong 2019	Yinpterochiroptera
	Hipposideros ruber	Hipposideridae	Africa	Anthony et al. 2017	Yinpterochiroptera
	Rhinonicteris aurantia	Hipposideridae	Australia	Smith et al. 2016	Yinpterochiroptera
β-CoV SUBGENERA	BAT SPECIES	BAT FAMILY		REFERENCE	BAT SUBORDER
Nobecoviruses	*Cynopterus brachyotis*	Pteropodidae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Cynopterus horsfieldi	Pteropodidae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Cynopterus sphinx	Pteropodidae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Dyacopterus spadiceus	Pteropodidae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Megaerops niphanae	Pteropodidae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Eidolon helvum	Pteropodidae	Africa	Anthony et al. 2017	Yinpterochiroptera
	Pteropus alecto	Pteropodidae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Pteropus giganteus	Pteropodidae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Epomopohorous gambianus	Pteropodidae	Africa	Anthony et al. 2017	Yinpterochiroptera
	Epomops franqueti	Pteropodidae	Africa	Anthony et al. 2017	Yinpterochiroptera
	Eonycteris spalaea	Pteropodidae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Lissonycteris angolensis	Pteropodidae	Africa	Anthony et al. 2017	Yinpterochiroptera
	Megaloglossus woermanni	Pteropodidae	Africa	Anthony et al. 2017	Yinpterochiroptera
	Micropteropus pusillus	Pteropodidae	Africa	Anthony et al. 2017	Yinpterochiroptera
	Rousettus aegyptiacus	Pteropodidae	Africa	Anthony et al. 2017	Yinpterochiroptera
	Rousettus amplexicaudatus	Pteropodidae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Rousettus leschenaulti	Pteropodidae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Hipposideros lekaguli	Hipposideridae	Asia	Anthony et al. 2017	Yinpterochiroptera
	Triaenops persicus	Hipposideridae	Africa	Anthony et al. 2017	Yinpterochiroptera
	Scotophilus dinganii	Vespertilionidae	Africa	Anthony et al. 2017	Yangochiroptera
	Scotophilus leucogaster	Vespertilionidae	Africa	Anthony et al. 2017	Yangochiroptera
	Mops condylurus	Molossidae	Africa	Anthony et al. 2017	Yangochiroptera

	J	K	L	M	N	O
1						
2	cross-ref					
3	SARS_related_beta_CoV					
4	SARS_related_beta_CoV					
5						
6						
7						
8						
9						
10						
11						
12						
13						
14	SARS_related_betaCoV					
15	Beta_corona_Gabon, Predict_CoV_32, Predict_CoV_43, Predict_CoV_44					
16	Predict_CoV_43					
17						
18	Predict_CoV_51					
19	Predict_CoV_51					
20	BtCoV_hip_KT_Thai					
21	Predict_CoV_22, Predict_CoV_24	put this one in Nobe...see entry in Nobecorviruses				
22						
23	Predict_CoV_20					
24						
25	cross-ref					
26	Predict_CoV_24					
27	Predict_CoV_24					
28	Predict_CoV_24					
29	Phil_Dil1525G2					
30	Predict_CoV_24					
31	Bat_CoV_HKU9, Eidolon_bat_CoV, Kenya_CoV_BtKY56					
32	Betacoronavirus_1, Predict_CoV_67, Predict_CoV_68					
33	Predict_CoV_16, Predict_CoV_17, Betacoronavirus_1					
34	Kenya_CoV_BtKY55, Kenya_CoV_BtKY56					
35	Eidolon_bat_CoV					
36	Bat_CoV_HKU9, Predict_CoV_22					
37	Predict_CoV_30, Predict_CoV_66, Kenya_CoV_BtKY55					
38	Eidolon_bat_CoV, Predict_CoV_2					
39	Kenya_CoV_BtKY55, Kenya_CoV_BtKY56					
40	Bat_CoV_HKU9, Predict_CoV_30, Kenya_CoV_BtKY55, Kenya_CoV_BtKY56, Eidolon_bat_CoV					
41	Bat_CoV_HKU9					
42	Bat_CoV_HKU9					
43	Predict_CoV_22, Predict_CoV_24					
44	Eidolon_bat_CoV					
45	Eidolon_bat_CoV					
46	Kenya_CoV_BtKY56					
47	Predict_CoV_30, Kenya_CoV_BtKY55					

	A	B	C	D	E	F	G	H	I
48	β-CoV SUBGENERA		BAT SPECIES		BAT FAMILY			REFERENCE	BAT SUBORDER
49	*Merbecoviruses*		*Hipposideros armiger*		Hipposideridae	Asia		Anthony et al. 2017	Yinpterochiroptera
50			*Myotis pilosus [ricketti]*		Vespertilionidae	Asia		Anthony et al. 2017	Yangochiroptera
51			*Eptesicus isabellinus*		Vespertilionidae	Iberian Peninsula		Falcón et al. 2011	Yangochiroptera
52			*Hypsugo savii*		Vespertilionidae	Iberian Peninsula		Falcón et al. 2011	Yangochiroptera
53			*Neoromicia zuluensis*		Vespertilionidae	Africa		Ithete et al. 2013	Yangochiroptera
54			*Pipistrellus abramus*		Vespertilionidae	Asia		Tao and Tong 2019	Yangochiroptera
55			*Pipistrellus coromandra*		Vespertilionidae	Asia		Anthony et al. 2017	Yangochiroptera
56			*Pipistrellus hesperidus*		Vespertilionidae	Africa		Anthony et al. 2017	Yangochiroptera
57			*Pipistrellus nathusii*		Vespertilionidae	Europe		Annan et al. 2013	Yangochiroptera
58			*Pipistrellus pipistrellus*		Vespertilionidae	Asia		Anthony et al. 2017	Yangochiroptera
59			*Pipistrellus pygmaeus*		Vespertilionidae	Europe		Annan et al. 2013	Yangochiroptera
60			*Tylonycteris pachypus*		Vespertilionidae	Asia		Anthony et al. 2017	Yangochiroptera
61			*Vespertilio sinensis [superans]*		Vespertilionidae	Asia		Anthony et al. 2017	Yangochiroptera
62			*Ia io*		Vespertilionidae	Asia		Anthony et al. 2017	Yangochiroptera
63			*Nyctinomops laticaudatus*		Molossidae	Latin America		Anthony et al. 2017	Yangochiroptera
64			*Taphozous perforatus*		Emballonuridae	Arabian Peninsula		Memish et al. 2013	Yangochiroptera
65			*Nycteris gambiensis*		Nycteridae	Africa		Annan et al. 2013	Yangochiroptera
66			*Pteronotus parnelii*		Mormoopidae	Latin America		Anthony et al. 2017	Yangochiroptera
67			*Pteronotus personatus*		Mormoopidae	Latin America		Anthony et al. 2017	Yangochiroptera
68			*Artibeus literatus*		Phyllostomidae	Latin America		Anthony et al. 2017	Yangochiroptera
69			*Artibeus obscurus*		Phyllostomidae	Latin America		Anthony et al. 2017	Yangochiroptera
70			*Dermaneura phaeotis*		Phyllostomidae	Latin America		Anthony et al. 2017	Yangochiroptera

	J	K	L	M	N	O
48	cross-ref					
49	Vesper_betaCoV					
50	Predict_CoV_57					
51						
52						
53						
54				á		
55	Predict_CoV_34			ñ		
56	MERS_like_CoV			í		
57						
58	Bat_CoV_HKU5, Predict_CoV_57					
59						
60	Bat_CoV_HKU4					
61	BtVs_betaCoV_SC2013					
62	Vesper_betaCoV					
63	Predict_CoV_9					
64						
65						
66	Predict_CoV_10					
67	Predict_CoV_11					
68	Predict_CoV_11					
69	Predict_CoV_11					
70	Predict_CoV_11					

From: Kading,Rebekah on behalf of Kading,Rebekah >
Sent: Monday, April 20, 2020 5:27 PM EDT
To: Cryan, Paul ; Kingston, Tigga
CC: olival >
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats
Attachment(s): "Olival et al. bat CoVs 20200417_REVIEW_rck.docx"

Hi Paul,

That's very kind of you to offer authorship - its unexpected and very generous of you, but I do appreciate being included! I'm attaching the text with some minor edits/suggests tracked for your consideration. Tigga's comments are great, and I'm glad to hear DeeAnn is involved as well.

Thanks!
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Cryan, Paul >
Sent: Monday, April 20, 2020 2:04 PM
To: Kingston, Tigga >; Kading,Rebekah
Cc: olival
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Hi Rebekah and Tigga,

Thanks for the awesome and quick improvements to the manuscript. I'm assuming you're okay with being co-authors, cause you are now. ☺

I'm working through the comments from everyone now and will get back to you with thoughts about the more strategic and substantive ideas after I've had some time to think about them and catch up with myself.

In the meantime, one easy answer is that I see I created some confusion by citing Tao and Tong for Nyctalus leisleri and Hipposideros pratti in the supplemental table, which were actually reported by Drexler et al. 2010 (attached)...oops, good catch! I'll add country of origin to that table and flesh out the cross-referencing a little better for the next iteration.

And Tigga, thanks for those taxonomy updates! I didn't know about those changes, so thanks for that. DeeAnn is also looking at this and said she'd send a new table of the African pteropodid names, so I'm learning a lot.

Stay tuned and thanks again,
Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Kingston, Tigga
Sent: Monday, April 20, 2020 11:30 AM
To: Kading,Rebekah >; Cryan, Paul
Cc: olival
Subject: RE: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

P.S. I looked at the table, and also spotted some things to check in addition to those high-lighted by Rebekah. Perhaps “Region” needs some clarification if it is where the bat was sampled – in the cases below it isn’t very representative of the distribution or was impossible

- *Rhinolophus ferrumequinum* is a Eurasian species, just tips into N. Africa
- https://en.wikipedia.org/wiki/Greater_horseshoe_bat

R. sinicus – predominantly Chinese bat -- doesn’t get in to Africa

https://en.wikipedia.org/wiki/Chinese_rufous_horseshoe_bat

Taxonomic updates:

FYI *Pteropus giganteus* is no more, it is currently recognized as *P. medius*

Eonycteris spalaea – spelling sp**e**laea

Note that the Hipposiderids have been broken with Rhinonycteridae elevated to family…

family **Rhinonycteridae**. elevated by Foley, *et al*, 2014.[2]
- genus *Cloeotis*
- genus *Brevipalatus*
- genus *Brachipposideros*
- genus *Paratriaenops*
- genus *Rhinonicteris* J.E. Gray, 1847
- genus *Triaenops*

So you might want to update the relevant species.

Best
Tigga

From: Kingston, Tigga
Sent: Monday, April 20, 2020 12:01 PM
To: Kading,Rebekah ; Cryan, Paul >
Cc: ecohealthalliance.org
Subject: RE: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Hi Paul and Kevin

Great job, as Rebekah said.

I thought I'd give holistic feedback of possible gaps, inevitably based on commenting on the influence of ecology or at least species variability in possible risk. Despite the fact that you mention there are 40+ species at the beginning, this gets a bit lost and so we end up of perceiving "north American bats" as a single species. This is a trend that I've seen elsewhere in disease papers, in fact I read a risk perception paper recently that managed to get although way through without identifying a single species. It is relevant because, as we've seen with WNS, species have exhibited different responses and we could anticipate different spillback and transmission probabilities among species. This may be a function of differences in species-specific physiology but critically aspects of ecology (especially sociality/roosting ecology) and human-bat interface. So perhaps in the paragraph about interdisciplinary research you could highlight the diversity of bats and their ecology (not just numbers) and the consequences for interspecific differences in risk. (for eg. do you think Lasiurines are as at risk as Myotis?). The implications are essentially that there will never be a simple model system, and we must be very wary of extrapolating from single-species studies, but perhaps current knowledge of bat ecology in N Am (a pretty well known fauna compared to some parts of the world) in combination with virological, genomic and disease ecology expertise could be used to prioritize research.

This leads into whether there could be more strategic research recommendations to close out with. I like the suggestions in the final paragraph on how to implement research and useful contributions that could be made in the study of "north american bats". Closing out with possible priorities or a suggested strategy would make the document even more useful. For example, ensuring surveillance/discovery of the more synanthropic species, colonial species, or species already compromised by WNS, surveil widely across the N. Am phylogeny. Are there particular regions or contexts of N. America that should be the focus of efforts (species-rich caves, peri-urban and urban settings, species-rich geographic areas?). If that all seems too much to be definitive on, perhaps calling for cooperative development of a strategy with these as some suggested areas for consideration could be the way to go.

I think some consideration of the above would improve the MS and position it better in the research community as a springboard for more cohesive collaborative work. You want to guard against "we need more surveillance so give us funding" criticisms. Happy to help on that although my knowledge of N. Am bats is limited as you know, but could work on something about priority setting if you wish.

Minor point.. the SEABCRU link – that goes with the sentence below is actually a good example of how PPE guidance can be developed for ecologists/field researchers. It was based on a decision tree that reflects different contexts, and hence risks, that field biologists might find themselves. (great job Kevin…..) So it better illustrates that this can be done.

Hope this helps
Tigga
Xx

From: Kading,Rebekah >
Sent: Monday, April 20, 2020 10:40 AM
To: Cryan, Paul >; Kingston, Tigga >
Cc: ecohealthalliance.org
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Hi everyone -

Kevin and Paul - this manuscript is very good - thank you for putting it together!! I'll follow up later today with a few comments on the text. I want to read it again but have to go take care of our mosquito colonies at the moment...the one essential duty we have ongoing! I'm attaching the table in the meantime...very comprehensive, wow! I thought it might be helpful for readers to have a column with the broad geographic region of the coronavirus detection in each of the bats, so I added a column to cover this. In instances where the range of the bat species was fairly extensive, I went with where the sampling occurred in the paper. See if you like it...no worries if you don't think its necessary. A couple details/questions came up while I was working on that though:

- excel line 13 - *Nyctalus leisleri* is a European species but Tao and Tong sampled in Kenya...did they mis-identify or maybe there's an accidental reference error?
- excel line 22 - *Hipposideros pratti* looks like an Asian species but the Tao and Tong reference just sampled from Kenya
- excel line 49 - I changed this to Yinterochiroptera and colored it yellow

Question: Is it worth denoting on the table somehow where there is evidence of cross-species sharing of coronavirus strains? For example lines 44-45 the notes have "Eidolon_CoV" but the virus detections being reported were from *Scotophilus* and *Triaenops*...my interpretation is that the virus detected from those latter two bats was the same strain as was detected in *Eidolon* previously? Is there enough evidence to say anything about viral sharing (i.e. are full genomes available) or do we just leave that go for now? I was just thinking that it might be worthwhile to point out any propensity for transfer of strains between/among bat species because that would have relevance to NA bats too.

More later - thanks again - this is a very nice paper and impressive you put it together so quickly!

Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Cryan, Paul >
Sent: Friday, April 17, 2020 11:14 AM
To: Kading,Rebekah ; Kingston, Tigga
Cc: olival ecohealthalliance.org>
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Hi Rebekah and Tigga,

Without further adieu, I'm attaching the manuscript draft that Kevin and I put together over the past week and would very much like your input on. Its much leaner and meaner than the rambling draft that went out to the decision-making group last week.

Please take a look if you have the time and consider joining us in trying to get it published somewhere fairly high profile in the coming weeks.

All the best,
Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Kading,Rebekah >
Sent: Wednesday, April 15, 2020 8:27 PM
To: Cryan, Paul ; Kingston, Tigga
Cc: olival ecohealthalliance.org>
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Oh my goodness Paul! LOL!
Hang in there - you're doing great.

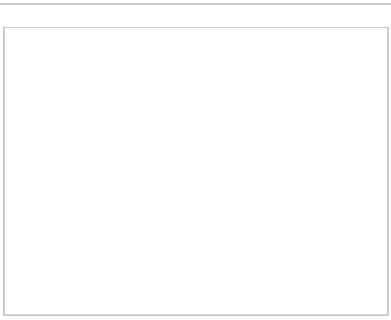
Rebekah
😂

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Cryan, Paul >
Sent: Wednesday, April 15, 2020 7:11 PM
To: Kading,Rebekah ; Kingston, Tigga >
Cc: olival ecohealthalliance.org>
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Great to know we're on the same path! I'm finding that coordinating and obsessively researching/writing/getting-up-to-speed on a issue are difficult to pull off at the same time!

https://www.youtube.com/watch?v=onoaKEEyNEI



Lead, Follow, or Get Out of the Way

From the woefully underrated Mike Judge film "Idiocracy." Joe isn't what you'd call a highly-motivated individual.

www.youtube.com

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Kading,Rebekah >
Sent: Wednesday, April 15, 2020 8:43 AM
To: Kingston, Tigga >; Cryan, Paul >
Cc: olival ecohealthalliance.org>
Subject: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Hi Paul, Kevin, Tigga,

I'll just reply to this thread. Yes, I'd be happy to take a look at the paper as well -- thank you very much for spearheading that effort! As Tigga mentioned we're working on something as well that we'll reach out to you guys separately about. Seems like BOHRN is mobilizing on multiple fronts, which is great to see.

Take care and talk to you soon -
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kingston, Tigga >
Sent: Wednesday, April 15, 2020 7:52 AM
To: Cryan, Paul <>; Kading,Rebekah <>
Cc: olival ecohealthalliance.org>
Subject: RE: SARS-CoV-2 spillback risk to North American bats

Hi Paul
Very interested to see the MS. Rebekah and I have been working on something that arose out of BOHRN that would be very complementary and might be worth trying to coordinate dissemination in some way. We are meeting today and will take stock of where we are at.

I just started an email to you and Kevin about the state of affairs as we Rodrigo and I are getting quite a bit of push-back on the IUCN BSG recommendation to suspend field studies while further data are gathered (primarily from western scientists with access to PPE). It would be good to hear what those committees are finding sooner rather than later.

Best wishes
Tigga

From: Cryan, Paul >
Sent: Tuesday, April 14, 2020 2:16 PM
To: Kingston, Tigga >
Cc: ecohealthalliance.org
Subject: SARS-CoV-2 spillback risk to North American bats

Hi Tigga,

Sorry for the silence since my call for help about the risks of humans potentially infecting bats in North America with the SARS-CoV-2 virus. Thanks for your patience and willingness to get involved in what we're hoping can be another disease response where scientists coming at disparate aspects of bats and pathogens can help each other. Those of us in the bat research world that focused most of our past efforts in the U.S. on conservation and management of bat populations can certainly use your expertise and help adjusting to the new situation.

A lot happened during my silence. Another group in USGS has been working at the behest of decision makers across federal and state natural resource management agencies to pull off a formal risk assessment by querying a subset of the experts we've reached out to. You lucked out and were not chosen for that exercise (yet), but we will keep you posted on the outcomes of that rapid assessment.

The other thing keeping me silent over the past couple of weeks is a short manuscript (currently 5 pages single spaced) that Kevin Olival and I drafted to articulate the potential risks of humans infecting North American temperate-zone bats with SARS-CoV-2, potentially relevant patterns we observed in bat-CoV distributions at a global scale, and the likely benefits of disease and bat researchers working together to draw on the strengths of our various disciplines. We hope to have a draft to circulate by tomorrow and would appreciate input and feedback from any of you willing to read it and help us stress test the concepts and assertions therein. Please let me know if you are interested.

Thanks again for your help and patience.

All the best,
Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

Associated references available (for review only) ftp://ftpext.usgs.gov/pub/cr/co/fort.collins/Cryan/

Is there a risk of SARS-CoV-2 infection and transmission in North American bats?

Kevin J. Olival, Paul M. Cryan*, Kevin T. Castle, and multiple invited co-authors…*

*These authors contributed equally

Spillover and "spillback" of pandemic viruses

The threat of emerging infectious diseases (EIDs) to wildlife populations and biodiversity conservation is recognized (*1*), but cross-species transmission of novel pathogens, or spillover, is typically viewed in the narrow context of originating *from* a wildlife reservoir and transmitting *to* humans. Research assessing EID risk has focused on identifying geographic regions (*2, 3*) and wildlife species (*4-6*) where spillover of zoonotic diseases into human populations is most likely. Among recent pandemic viruses of zoonotic origin, some have no evidence of "spillback" to wildlife or domestic animal populations after they were established in people (e.g., HIV, which causes AIDS), and others cross species boundaries with fluidity (e.g. pandemic H1N1 Influenza A virus (*7, 8*)). Evidence of spillback, or reverse zoonosis, into wildlife and domestic animals is widespread (*9*), but viral spillback to wild bats has not been recorded. In December 2019, a novel coronavirus (now SARS-CoV-2) infected a cluster of humans in Wuhan, China and has since spread to become a global pandemic. The virus has reached over 185 countries, infected >2.1 M people, and killed >147,000. Phylogenetic evidence suggests that SARS-CoV-2, along with the entire clade of SARS-related coronaviruses (SARSr-CoVs), are zoonotic and evolved in Old-World bats from the family *Rhinolophidae* (*10-13*). The closest known virus to SARS-CoV-2 was discovered in *Rhinolophus affinis* from Yunnan province in China with 96% sequence similarity across the virus' genome (*14*), yet which proximate species led to human spillover remains unclear (*15*). The United States (US) is currently the epicenter of the largest recognized outbreak of COVID-19, with community transmission in all 50 states. The unintended consequences of this pandemic are many and include the possibility of SARS-CoV-2 spillback to free-ranging wildlife populations. Here we assess the possibility of SARS-CoV-2 spillback from humans to North American (NA) bats and discuss possible consequences of the virus becoming endemic in bats outside its natural host range.

The triple threat of SARS-CoV-2 to North American bats

The pandemic human spread of SARS-CoV-2 may threaten NA bat populations in three different ways. First, SARS-CoV-2 might infect and cause disease among the diverse and historically isolated 40+ species of temperate-zone NA bats. Second, SARS-CoV-2 might be able to infect and become established in one or more of these NA species, creating a diverse new suite of temperate-zone wildlife disease reservoirs. Third, if SARS-CoV-2 can persistently infect one or more species of NA bats, it could potentially evolve, or recombine with other endemic viruses, to become more pathogenic to humans and other mammals. The latter outcomes would undoubtedly shift public perception of bats from mostly beneficial wildlife with manageable associated disease risks, to bats as harmful nuisance animals posing unacceptable disease risks to human health. In addition to new public health challenges, such shifts could undermine decades of concerted science, conservation, and education efforts aimed at these important animals.

Lessons from an epizootic -- susceptibility of North American bats to introduced pathogens

SARS-CoV-2 is not the first pathogen that humans could inadvertently spread to NA bats. The COVID-19 pandemic follows the arrival of a fungal pathogen (*Pseudogymnoascus destructans*) that in 2007 began infecting NA populations, crossing species barriers, spreading among, and altering the evolutionary trajectory of the continent's bats (*16-19*). The disease of hibernating bats caused by that fungus, White-Nose Syndrome (WNS), remains the first and only documented bat epizootic (*20, 21*). WNS has killed millions of NA bats, affected populations of at least 12 species of 3 genera, and has already spread across half of the United States (US) and Canada. Methods of mitigating WNS spread and impacts remain elusive. It took years of concerted international scientific effort to first identify the novel cold-growing fungus, determine that it probably originated somewhere in the temperate zones of Europe or Asia, understand its mechanisms of infection and pathogenicity, and to track its rapid spread through an immunologically naïve continental assemblage of hibernating bats that lacked many defenses against it (*22*). The devastating impact of WNS on a diverse group of NA bats likely resulted from evolutionary isolation of the continent's bat fauna from large parts of the world for millions of years. Bats in both Europe and Asia can become infected by *P. destructans*, but do not suffer mass mortality from WNS (*23, 24*). No extant species of bat that occurs in the Americas also occurs outside of the Americas (*25, 26*), and no bat species regularly migrates or likely survives flights across the Pacific or Atlantic oceans (*27, 28*). The bat fauna spanning the higher latitudes of NA (e.g., US and Canada) is composed almost entirely of species belonging to the world's largest bat family -- Vespertilionidae. Vespertilionid bats occur all over the world, but likely originated and diversified in NA tens of millions of years ago -- they are the only bat family to increase in diversity northward out of the tropics and consistently reach high latitudes (50ºN;(*29, 30*). The WNS epizootic taught us that a large proportion of this historically isolated bat fauna can be vulnerable to pathogens introduced from other continents. Additionally, bats already in a physiologically stressed condition due to WNS or other pressures may have increased susceptibility to viral infection, experience exacerabated disease outcome, and/or increased viral shedding (REFS). The COVID-19 pandemic invokes the specter of WNS and highlights deficits in our understanding of pathogens in NA bats.

Commented [K1]: https://www.nature.com/articles/s41598-018-33975-x¶ ¶ https://royalsocietypublishing.org/doi/10.1098/rspb.2007.1260¶ ¶ https://www.ncbi.nlm.nih.gov/pubmed/18198149¶ ¶

Gaps in understanding global patterns of bat-CoV diversity and evolution

Bats are among the most diverse mammals (approximately 1,400 species), and global distributions and diversity of CoVs in bats proportionally reflects that of their hosts (*31, 32*). Bats also rank among the most ecologically important but underappreciated mammals that play varied roles in most of Earth's ecosystems (*33, 34*). Coronaviruses appear to have ancient and ancestral relationships with bats, diversifying globally through a process of within-host evolution and cross-taxonomic host-switching events (*31, 35, 36*). Available evidence indicates that bats are natural reservoirs of CoVs with pre-emergent potential to cause diseases in humans, livestock, and other types of domestic animals and wildlife (*14, 31, 37-50*). Indeed, bats are the likely progenitor hosts of all alpha (α-) and beta (β-) CoVs (*51*) and potentially all *Coronaviridae* (*52-57*). Two recent human disease epidemics (Severe Acute Respiratory Syndrome [SARS], Middle East Respiratory Syndrome [MERS]) and now the COVID-19 pandemic were caused by

viruses that probably originated from CoVs circulating in populations of wild bats near the outbreak origins (*14, 38-43, 49, 50, 58, 59*). A similar CoV of likely bat origin also recently caused Swine Acute Diarrheal Syndrome (SADS) outbreaks and mass mortality of piglets on farms in Guangdong province, China (*46*). Emergence of diseases like SARS, SADS, and now COVID-19 from the same general region strongly indicates a close association between CoVs likely to evolve into pathogens and the wildlife reservoirs where they originate (*14, 38-43*). Bat CoVs show clear global patterns of geographic structure that reflect host distributions, and typically strong co-evolutionary patterns among related hosts (*31, 49, 60, 61*). These phylogeographic factors are also universal determinates of viral sharing among all mammals (*62*). However, predicting broad CoVs jumps (i.e., that lead to spillover and spillback) is difficult because of the wide potential host breadth for many CoVs (*13, 44, 45, 63-67*), and the fact that bats are often asymptomatic reservoirs capable of harboring a diversity of CoV lineages -- obscuring bat-virus association patterns (*31, 49, 50, 61, 68*). Bat-CoV associations remain woefully understudied in temperate-zone NA, despite the large number of bat biologists and virologists working in the US, Mexico, and Canada (*31, 68-70*).

Are viruses like SARS-CoV-2 already widespread in North American bats?

Our preliminary examination of CoV evolutionary lineages and global distribution patterns of the diverse bats they infect suggests that NA bats could be immunologically naïve to infection by viruses like SARS-CoV-2. Alpha and β-CoVs have been detected in bats on most continents, sometimes with both types occurring in the same bat species and individuals (*49, 50, 71*). However, a striking exception to this pattern is the apparent lack of evidence that β-CoVs infect bats of temperate-zone NA. Multiple novel α-CoVs have been detected and described in Nearctic vespertilionid bats of the US and Canada, infecting species living in close contact with humans and in remote wild areas (*68, 70, 72*). Alpha-CoVs ~~of~~ likely of bat origin can cause disease in humans and other animals including human α-CoVs NL63 and 229E (*73, 74*). However, emerging infectious diseases like MERS, SARS, SADS, and COVID-19 are caused by β-CoVs. Therefore, scientists have focused great effort on detecting, genotyping, studying the geographic distribution, and host-cell receptor binding of β-CoVs in bats (*49, 50*). SARSr-CoVs of the viral subgenus *Sarbecovirus* that can bind to angiotensin-converting enzyme 2 (ACE2) host-cell receptors of humans and other animals have thus far been detected mostly in species of the Old-World Chiropteran suborder Yinpterochiroptera (Table S1; Fig. 1A; (*11, 31, 49, 50, 75-79*). Two exceptions to this pattern were detection of novel Clade 3 and Clade 1 *Sarbecovirus* (*sensu* (*41*)) in the bat *Chaerephon plicata* (family Molossidae) in China (*80*) and the vespertilionid species *Nyctalus leisleri* cohabiting a Bulgarian cave during autumn with several species of *Rhinolophus* in which other SARS-related β-CoVs were concurrently detected (Fig. 1A; (*81*). β-CoVs of other distinct evolutionary lineages, such as viral subgenera *Hibecovirus* and *Nobecovirus*, also tend to occur mostly in Old-World bat families, with the exception of novel viruses of the latter subgenus detected in two species of *Scotophilus* in Africa (Fig 1B, C; (*31, 41, 49, 50, 77, 82*). Bat β-CoVs of the subgenus *Merbecovirus* (MERS-related lineage) occur in a greater diversity of bat families and across more global regions than others (Fig. 1D; (*49, 60*). These widely distributed viruses can evolve to cause disease in humans and animals (e.g., MERS) and notably appear to be the only bat β-CoVs to diversify among several families of the globally distributed suborder Yangochiroptera (Fig. 2; (*49, 50, 76-78, 83-87*). The several hundred species of extant bats spanning the Americas all belong to the suborder

Yangochiroptera, which likely diverged from the Old-World Yinpterochiroptera more than 50 million years ago (Fig. 2; (*88*)). In the Americas, a novel β-CoV of the subgenus *Merbecovirus* was detected in *Nyctinomops laticaudatus* (family Molossidae), and other distinct lineages in the subgenus *Merbecovirus* were described from *Pteronotus davyii* and *P. personatus* (family Mormoopidae), as well as species of *Artibeus* and *Dermaneura* (family Phyllostomidae) from tropical regions of Mexico (*31, 89, 90*); none of these bat species occur outside of the Neotropics. Successful *in vitro* infection of cells from the Neotropical bat *Artibeus jamaicensis* with MERS-CoV led to experimental infection trials that resulted in virus replication and shedding without obvious clinical signs of disease (*91*). Considering these laboratory findings and detection of only β-CoVs of the subgenus *Merbecovirus* in two exclusively Neotropical bat families (Phyllostomidae & Mormoopidae) and one that is globally distributed (Molossidae), available evidence suggests β-CoVs may have arrived to the New World through South America and have long been evolving in Neotropical bats. β-CoVs of the subgenus *Merbecovirus* are not known to target ACE2 cell receptors, instead using the dipeptidyl peptidase-4 (DPP4/CD26) or possibly other receptors (*41, 92*). Assessing SARS-CoV-2 host range using virus-host receptor binding assays *in silico* and *in vitro* (*14, 41, 92, 93*), together with future experimental infection studies for 'gold standard' confirmation, hold promise to better quantify the potential for NA bat infection. We are not aware of any published detections of β-CoVs in temperate-zone NA vespertilionid bats, although sampling has been limited. Overall, proportionally few studies have looked for CoVs in the approximately 1,400 species of bats occurring across six continents. This sampling deficit limits the inference obtainable by examining known patterns of bat-CoV occurrence and distribution. To our knowledge SARSr-CoVs (*Sarbecovirus spp*; (*41, 77*)) have only been detected in one species of vespertilionid bat in Bulgaria (*81*), a likely transmission from co-roosting *Rhinolophus* sp. bats. This absence of evidence for β-CoVs in temperate-zone bats of NA leaves important gaps in our ability to gauge threats posed by SARS-CoV-2 to bats in the US and Canada.

Figure 1. Global patterns of bats and associated beta-coronaviruses (β-CoVs). A) red-shaded distributions of bat species in which SARS-related β-CoVs of the viral subgenus *Sarbecovirus* were detected; B) pink-shaded distributions of bat species known to host β-CoVs of the subgenus *Hibecovirus*; C) brown-shaded distributions of bats in which β-CoVs of the *Nobecovirus* lineage have been detected; and D) green-shaded distributions of bats known to host MERS-related β-CoVs of the subgenus *Merbecovirus*. Different colors and shade styles within each panel represent different families of bats. See Table S1 for species lists. Maps created using ArcMap (ESRI, Redlands, California, USA) and bat ranges derived from spatial data on terrestrial mammals from the IUCN (https://www.iucnredlist.org/resources/spatial-data-download).

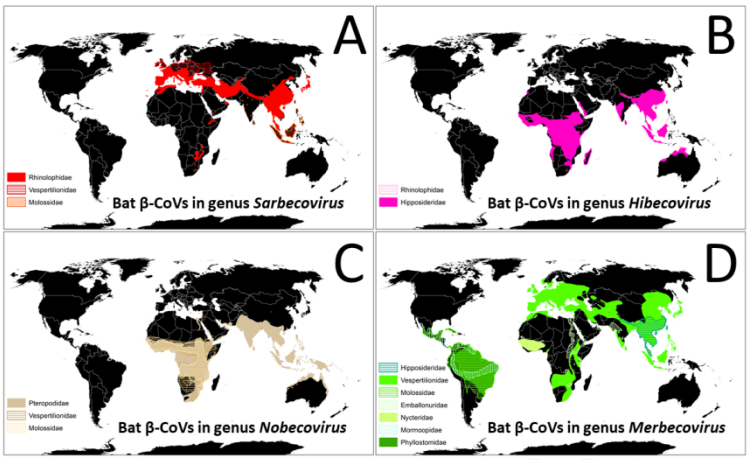
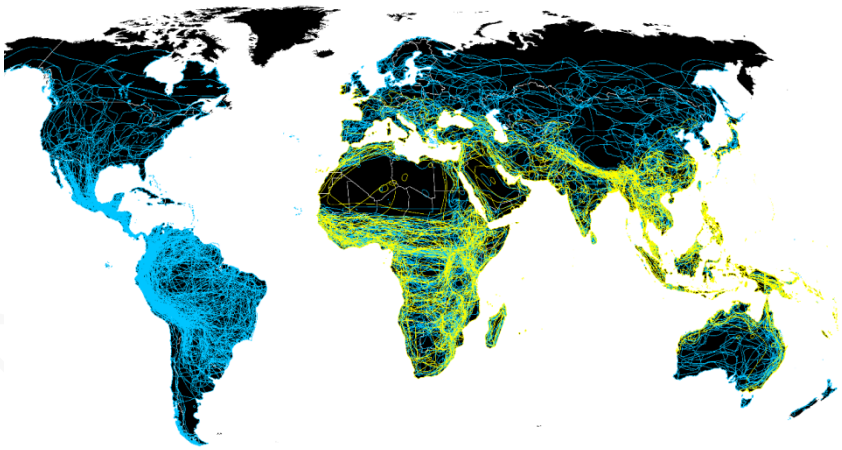


Figure 2. Old-world and new-world bats. Overlapping species distribution outlines of bats in the globally distributed suborder Yangochiroptera (blue) and Old-world Yinpterochiroptera (yellow). Maps created using ArcMap (ESRI, Redlands, California, USA) and bat ranges derived from spatial data on terrestrial mammals from the IUCN (https://www.iucnredlist.org/resources/spatial-data-download).



Proactively connecting the wellbeing of human and bat populations

Scientists have long recognized the risk of disease spillback from humans to bats (*94-96*), but bat researchers in NA did not systematically address such risk prior to WNS**.** Few bat

researchers studied infectious diseases ~~in~~ of bats before WNS emerged in 2007 (*69*) and proportionally few disease researchers studied bat pathogens before bats were retrospectively connected to the SARS epidemic (*12, 58, 97*). An often unstated duality of such disease responses is the seemingly contradictory facts that bats are unequivocally ecologically important (*33, 34*), yet also a diverse source of emerging infectious diseases (*6, 50, 97-101*). Factors driving the ecologic success of bats are often the same as those invoked for explaining why bats might host such a diversity of viruses. These factors include characteristics of bat life history (e.g., long-lived, slow reproducing, wide dispersal, multi-species aggregations, daily and seasonal torpor (*97*)), unique physiology for repairing damaged DNA (*102*), unique ability to regulate immune response (*103-105*), and unmatched metabolic range and high body temperatures during flight (*106*). Bats also cryptically come into closer contact with humans than many other types of wildlife, often daily crossing human-wildlife interfaces. An oft-overlooked flip side to abundant evidence that many dangerous human diseases originate from bats is the fact that bats rarely show signs of mass mortality and sickness from these same dangerous pathogens (*20*). Bats cope with viral infection in ways that we do not yet fully comprehend but learning how they do so may reveal important insights to develop therapeutics and ultimately protect human health. *In vitro* and laboratory studies demonstrate that bats can regulate immune response to effectively cope with MERS-CoV and SARS-CoV-2 infection, at least under experimental conditions (*104, 107*). Lack of clear signs of sickness in bats and the cryptic habits of many species also generally inhibit our ability to easily detect spillback of pathogens from human to bat populations, further adding to uncertainty about movement of CoVs among groups. Laboratory findings suggest human viruses like HCoV-NL63 may have historically moved back and forth between human and bat populations multiple times (*74*). SARS-CoV-2 and other CoVs are relatively long for RNA viruses, making them susceptible to recombination and copy errors with resulting functional adaptations (e.g., receptor binding ability, temperature adaptation enzymes)(*108*). CoVs can recombine with functional fragments of other virus families, such as when a bat-derived CoV gained a functional gene from a reovirus (*109*). If spillback of SARS-CoV-2 into NA bats led to the virus becoming more pathogenic to bats, domestic animals, or humans through genetic mixing in a NA bat reservoir host, the public-health and conservation consequences would be severe.

Need for an interdisciplinary disease response

Effectively managing risks of human disease caused by emerging zoonotic pathogens *and* ensuring the health and conservation of potential wildlife reservoirs of those disease agents are not mutually exclusive goals. Research has shown that spillover risk (and probably spillback risk) may be highest in disturbed ecosystems where there is a high frequency of human-wildlife interactions (*2, 110, 111*). Thus, effective bat conservation and management requires understanding both pathogens that cause disease in bats, as well as human activities that present health risks in environments we share with bats. Furthermore, seemingly intuitive reactions to disease risk from wildlife, such as culling infected bat populations, often have negative unintended consequences for the interconnected health of both human and bat populations (*112, 113*). Temperate-zone vespertilionid bats inhabiting human dwellings in US and Canada represent a particularly relevant human-wildlife interface where such actions and potential consequences for disease spillback and spillover may be particularly worth careful consideration. A growing field of 'One Health' or conservation-minded bat virus research studies

have demonstrated the potential for mutual benefit of collaboration between public health, disease, and conservation stakeholders (*95, 112, 114-119*). Disease-focused studies that integrate ecological principles into a rigorous study design provide the most ecologically-relevant context to the pathogen findings. ~~For example~~Additionally, proper use of personal protective equipment (PPE) including respiratory protection has been adopted by the bat virus research community but by few others studying bats. Assessing the risks of SARS-CoV-2 spillback into NA bats ~~seems like a perfect~~presents a timely opportunity to integrate and practically apply lessons learned from prior epizootic and pandemic disease responses, and to tap a growing field of CoV experts studying viral transmission, host range, and natural history. Free-ranging bats are notoriously difficult to study, so scientists researching EIDs can benefit from methods bat researchers have developed for observing, counting, and non-invasively sampling bats (*69, 120*). Bat researchers can learn important biosafety, health monitoring, and laboratory techniques from researchers with expertise in veterinary and medical sciences (*117, 118*).

SARS-CoV-2 alters the *status quo* of bat research, emphasizing the need to carefully weigh risks and benefits of wildlife research in the context of population-altering diseases (*121*). Adopting a precautionary approach in the face of widespread COVID-19 transmission, US and international wildlife organizations have begun advising limiting field research to minimize the risk of humans infecting bats with SARS-CoV-2 until further assessment can be made (*122, 123*). A rapid, quantitative risk assessment and analysis of various mitigation options is an urgent research priority and is currently underway (*122*). One key question is if the proper use of PPE and masks, together with other basic biosafety practices (*124*), during field work can significantly reduce the risk of transmission to bats. In the interim, until new guidelines are established for handling and near-proximity work with bats, important scientific inquiry could continue. Temporarily shifting to 'hands-off' bat research methods in temperate-zone NA seems prudent wherever possible. Examples of such methods applicable to both disease and conservation research include: monitoring echolocation calls to determine the occurrence, distributions, and seasonal/nightly activity patterns of bats (*125-128*); digital imaging methods for counting bats and studying physiology and behaviors in the context of disease and anthropogenic landscape change (*19, 129-134*); methods of safely attaching tracking tags and environmental sensors to bats for multi-month periods (*19, 135*); and sampling guano from below bat roosts to determine bat species and individual identity, population dynamics, and daily or seasonal patterns of bat occupancy and pathogen shedding (*68, 136-139*). Promising areas for innovation include making these 'hands off' field technologies more accessible to a broader global user base, less expensive, easier to use, and scientifically reproducible through open-source hardware, software, and laboratory methods (e.g., (*140-146*)). Assessing the risk of SARS-CoV-2 transmission to NA bats also raises critical gaps in knowledge about bat CoV diversity and distribution, particularly in the New World. Standardized field protocols and probabilistic sampling strategies for monitoring bats and their viruses at a continental scale are needed (www.nabatmonitoring.org; (*147-149*). The currently unknown but potentially high-consequence risk of SARS-CoV-2 transmission and establishment in NA bats warrants precaution. We are at a critical nexus of biosecurity and natural resource conservation. Our actions during this current pandemic could profoundly influence the health of both human and bat populations.

Acknowledgements

We thank Jonathan Sleeman, Tom O'Shea, Jonathan Reichard, Chip Clark, and […] for helpful comments on earlier drafts of this manuscript.

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From: Kading,Rebekah on behalf of Kading,Rebekah
Sent: Wednesday, April 15, 2020 10:27 PM EDT
To: Cryan, Paul ; Kingston, Tigga >
CC: olival ecohealthalliance.org>
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Oh my goodness Paul! LOL!
Hang in there - you're doing great.

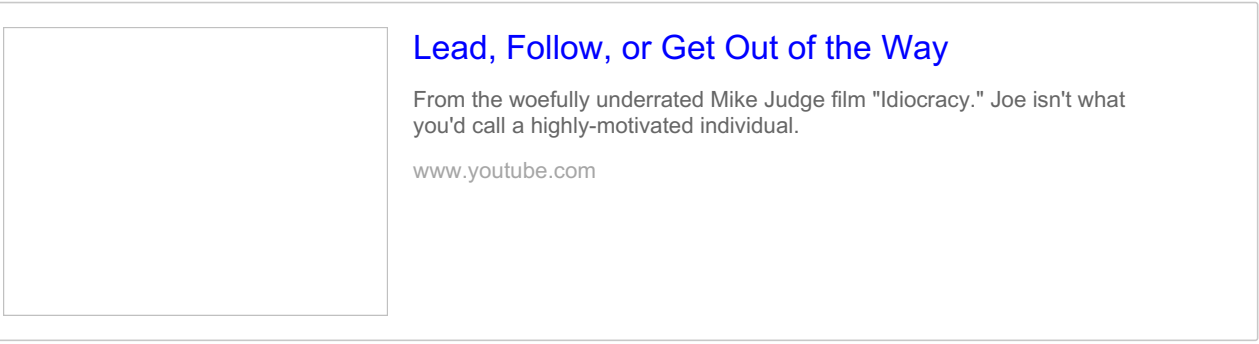
Rebekah
😂

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Cryan, Paul
Sent: Wednesday, April 15, 2020 7:11 PM
To: Kading,Rebekah >; Kingston, Tigga < >
Cc: olival ecohealthalliance.org>
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Great to know we're on the same path! I'm finding that coordinating and obsessively researching/writing/getting-up-to-speed on a issue are difficult to pull off at the same time!

https://www.youtube.com/watch?v=onoaKEEyNEI



Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Kading,Rebekah
Sent: Wednesday, April 15, 2020 8:43 AM
To: Kingston, Tigga >; Cryan, Paul
Cc: olival ecohealthalliance.org>
Subject: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Hi Paul, Kevin, Tigga,

I'll just reply to this thread. □ Yes, I'd be happy to take a look at the paper as well -- thank you very much for spearheading that effort! As Tigga mentioned we're working on something as well that we'll reach out to you guys separately about. Seems like BOHRN is mobilizing on multiple fronts, which is great to see.

Take care and talk to you soon -
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kingston, Tigga >
Sent: Wednesday, April 15, 2020 7:52 AM
To: Cryan, Paul >; Kading,Rebekah >
Cc: olival ecohealthalliance.org>
Subject: RE: SARS-CoV-2 spillback risk to North American bats

Hi Paul
Very interested to see the MS. Rebekah and I have been working on something that arose out of BOHRN that would be very complementary and might be worth trying to coordinate dissemination in some way. We are meeting today and will take stock of where we are at.

I just started an email to you and Kevin about the state of affairs as we Rodrigo and I are getting quite a bit of push-back on the IUCN BSG recommendation to suspend field studies while further data are gathered (primarily from western scientists with access to PPE). It would be good to hear what those committees are finding sooner rather than later.

Best wishes
Tigga

From: Cryan, Paul
Sent: Tuesday, April 14, 2020 2:16 PM
To: Kingston, Tigga >
Cc: ecohealthalliance.org
Subject: SARS-CoV-2 spillback risk to North American bats

Hi Tigga,

Sorry for the silence since my call for help about the risks of humans potentially infecting bats in North America with the SARS-CoV-2 virus. Thanks for your patience and willingness to get involved in what we're hoping can be another disease response where scientists coming at disparate aspects of bats and pathogens can help each other. Those of us in the bat research world that focused most of our past efforts in the U.S. on conservation and management of bat populations can certainly use your expertise and help adjusting to the new situation.

A lot happened during my silence. Another group in USGS has been working at the behest of decision makers across federal and state natural resource management agencies to pull off a formal risk assessment by querying a subset of the experts we've reached out to. You lucked out and were not chosen for that exercise (yet), but we will keep you posted on the outcomes of that rapid assessment.

The other thing keeping me silent over the past couple of weeks is a short manuscript (currently 5 pages single spaced) that Kevin Olival and I drafted to articulate the potential risks of humans infecting North American temperate-zone bats with SARS-CoV-2, potentially relevant patterns we observed in bat-CoV distributions at a global scale, and the likely benefits of disease and bat researchers working together to draw on the strengths of our various disciplines. We hope to have a draft to circulate by tomorrow and would appreciate input and feedback from any of you willing to read it and help us stress test the concepts and assertions therein. Please let me know if you are interested.

Thanks again for your help and patience.

All the best,
Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Kading,Rebekah on behalf of Kading,Rebekah >
Sent: Friday, April 17, 2020 3:57 PM EDT
To: Cryan, Paul ; Kingston, Tigga >
CC: olival ecohealthalliance.org>
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Hi Paul,

Thanks so much for sending this along - I look forward to reading it! Will return comments asap.
I hope everyone has a great weekend!

Cheers-
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Cryan, Paul >
Sent: Friday, April 17, 2020 11:14 AM
To: Kading,Rebekah ; Kingston, Tigga >
Cc: olival <
Subject: Re: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Hi Rebekah and Tigga,

Without further adieu, I'm attaching the manuscript draft that Kevin and I put together over the past week and would very much like your input on. Its much leaner and meaner than the rambling draft that went out to the decision-making group last week.

Please take a look if you have the time and consider joining us in trying to get it published somewhere fairly high profile in the coming weeks.

All the best,
Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Kading,Rebekah >
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To: Cryan, Paul ; Kingston, Tigga >
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Sent: Wednesday, April 15, 2020 7:11 PM

To: Kading,Rebekah Kingston, Tigga
Cc: olival ecohealthalliance.org>
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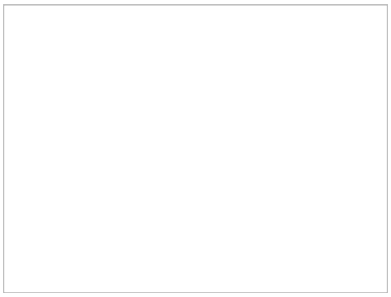
Great to know we're on the same path! I'm finding that coordinating and obsessively researching/writing/getting-up-to-speed on a issue are difficult to pull off at the same time!

https://www.youtube.com/watch?v=onoaKEEyNEI



Lead, Follow, or Get Out of the Way

From the woefully underrated Mike Judge film "Idiocracy." Joe isn't what you'd call a highly-motivated individual.

www.youtube.com

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Kading,Rebekah >
Sent: Wednesday, April 15, 2020 8:43 AM
To: Kingston, Tigga ; Cryan, Paul
Cc: olival < ecohealthalliance.org>
Subject: [EXTERNAL] Re: SARS-CoV-2 spillback risk to North American bats

Hi Paul, Kevin, Tigga,

I'll just reply to this thread. Yes, I'd be happy to take a look at the paper as well -- thank you very much for spearheading that effort! As Tigga mentioned we're working on something as well that we'll reach out to you guys separately about. Seems like BOHRN is mobilizing on multiple fronts, which is great to see.

Take care and talk to you soon -
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kingston, Tigga <>
Sent: Wednesday, April 15, 2020 7:52 AM
To: Cryan, Paul >; Kading,Rebekah <
Cc: olival ecohealthalliance.org>
Subject: RE: SARS-CoV-2 spillback risk to North American bats

Hi Paul
Very interested to see the MS. Rebekah and I have been working on something that arose out of BOHRN that would be very complementary and might be worth trying to coordinate dissemination in some way. We are meeting today and will take stock of where we are at.

I just started an email to you and Kevin about the state of affairs as we Rodrigo and I are getting quite a bit of push-back on the IUCN BSG recommendation to suspend field studies while further data are gathered (primarily from western scientists with access to PPE). It would be good to hear what those committees are finding sooner rather than later.

Best wishes
Tigga

From: Cryan, Paul
Sent: Tuesday, April 14, 2020 2:16 PM
To: Kingston, Tigga
Cc: ecohealthalliance.org
Subject: SARS-CoV-2 spillback risk to North American bats

Hi Tigga,

Sorry for the silence since my call for help about the risks of humans potentially infecting bats in North America with the SARS-CoV-2 virus. Thanks for your patience and willingness to get involved in what we're hoping can be another disease response where scientists coming at disparate aspects of bats and pathogens can help each other. Those of us in the bat research world that focused most of our past efforts in the U.S. on conservation and management of bat populations can certainly use your expertise and help adjusting to the new situation.

A lot happened during my silence. Another group in USGS has been working at the behest of decision makers across federal and state natural resource management agencies to pull off a formal risk assessment by querying a subset of the experts we've reached out to. You lucked out and were not chosen for that exercise (yet), but we will keep you posted on the outcomes of that rapid assessment.

The other thing keeping me silent over the past couple of weeks is a short manuscript (currently 5 pages single spaced) that Kevin Olival and I drafted to articulate the potential risks of humans infecting North American temperate-zone bats with SARS-CoV-2, potentially relevant patterns we observed in bat-CoV distributions at a global scale, and the likely benefits of disease and bat researchers working together to draw on the strengths of our various disciplines. We hope to have a draft to circulate by tomorrow and would appreciate input and feedback from any of you willing to read it and help us stress test the concepts and assertions therein. Please let me know if you are interested.

Thanks again for your help and patience.

All the best,
Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Kading,Rebekah on behalf of Kading,Rebekah
Sent: Wednesday, August 26, 2020 10:43 AM EDT
To: Stokes, Martha M CIV (USA) Katie Leahy < >; Kingston, Tigga
CC: Hoyle, Jamechia D CTR (USA) < >; Guzal Masharipova epstein ecohealthalliance.org>
Subject: Re: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication
Attachment(s): "Kading and Kingston 2020_bat network resubmission.docx","Kading and Kingston 2020_Supplementary Methods.docx"

Hi Marty - yes of course, here you go! This is the version that came back for us to revise. (Stefanie Campbell has also recently put this through BTRP clearance, as a heads up.)
Thanks!
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Stokes, Martha M CIV (USA)
Sent: Wednesday, August 26, 2020 8:28 AM
To: Kading,Rebekah >; Katie Leahy Kingston, Tigga
Cc: Hoyle, Jamechia D CTR (USA) Guzal Masharipova ; epstein ecohealthalliance.org>
Subject: RE: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

Hi Rebekah,

Is there any way we could get a draft of the manuscript? We would maintain confidentiality and keep it close hold.

Thanks so much.

Best,
Marty

-----Original Message-----
From: Kading,Rebekah
Sent: Tuesday, August 25, 2020 3:04 PM
To: Katie Leahy ; Kingston, Tigga ; Stokes, Martha M CIV (USA)
Cc: Hoyle, Jamechia D CTR (USA) ; Guzal Masharipova epstein ecohealthalliance.org>
Subject: [Non-DoD Source] Re: [External Sender] RE: BOHRN Status, publication

All active links contained in this email were disabled. Please verify the identity of the sender, and confirm the authenticity of all links contained within the message prior to copying and pasting the address to a Web browser.

Hi Katie, Marty, and Guzal -

Just chiming in to say hello and THANK YOU for the quick response and support for this effort! This is all great to hear, and I think we have a fantastic opportunity with this paper to provide another way to invigorate and draw attention to BOHRN. As Tigga and I were discussing the reviewer's suggestion, we basically converged on "Hey, BOHRN has already done all of this!" So it is wonderful to hear that we can move forward together to use this paper to direct people to BOHRN, which is where the rubber will hit the road. Looking forward to moving this forward, and we'll keep in touch with the revised manuscript. Thanks!

Best,
Rebekah :-)

Rebekah C. Kading, PhD

Assistant Professor

Department of Microbiology Immunology and Pathology

Colorado State University

From: Katie Leahy >
Sent: Tuesday, August 25, 2020 11:54 AM
To: Kingston, Tigga ; martha.m.stokes.civ
Cc: jamechia.d.hoyle.ctr Guzal Masharipova ; Kading,Rebekah >; epstein ecohealthalliance.org>
Subject: Re: [External Sender] RE: BOHRN Status, publication

Hi, Tigga. Guzal (copied) should be able to help. I can make sure she has all the passwords; give us a day to make sure all the links are active. I talked with her today about it and she is ready to support in any way.

V/r,

Katie Leahy

KATIE LEAHY | Director, Science Engagement

Global Systems Engineering, LLC

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< Caution-https://nam01.safelinks.protection.outlook.com/?url=http%3A%2F%2FCaution-www.globalsyseng.com%2F&data=02%7C01%7CRebekah.Kading%40colostate.edu%7C88f9eccb29b346164b8b08d849cccd65%7Cafb58802ff7a4bb1ab21367ff2ecfc8b%7C0%7C0%7C637340491251239802
>

If you are not the intended recipient, any use or distribution is prohibited; please notify the sender and delete from your system.

From: "Kingston, Tigga"
Date: Tuesday, August 25, 2020 at 1:51 PM
To: "martha.m.stokes.civ"
Cc: Katie Leahy , "jamechia.d.hoyle.ctr" Guzal Masharipova , "Kading,Rebekah" < >, Jon Epstein ecohealthalliance.org>
Subject: [External Sender] RE: BOHRN Status, publication

Dear Marty

Thanks for the speedy response and support! Great to hear of the documentation efforts and continued commitment.

The lynchpin to everything that we'd like to do is the BOHRN website - is there a webmaster, or can one be allocated, so that we can host content, build membership, post some of the materials that have been developed.

Best

Tigga

From: Stokes, Martha M CIV (USA) >
Sent: Tuesday, August 25, 2020 8:45 AM
To: Kingston, Tigga >
Cc: Katie Leahy >; Hoyle, Jamechia D CTR (USA) ; Guzal Masharipova < ; Kading,Rebekah ; Jon Epstein cohealthalliance.org>
Subject: RE: BOHRN Status, publication

Hi Tigga,

Congratulations on having your piece accepted (with revisions, as always)! I would really appreciate you adding detail about BOHRN and highlighting the network's efforts. All of the positive outcomes you mention are well noted and align with our goals and objectives, which remain steadfast.

The current situation has certainly created unexpected challenges for all our work, but we're adapting, and want to ensure that we continue moving forward and position the network to pick up where it left off last summer, once things return to a more normal environment. In the meantime, we'll do what we are able virtually.

Let us know what you need to support this. Katie and I, along with our teams, recently updated a huge amount of documentation, reports, participant lists, etc. for BOHRN and other our TRNs for the incoming BTRP Director, in order to deposit it on our internal database, so it should be very easy to provide whatever you need. Just let us know how we can help.

Thanks so much!

Best,

Marty

Martha M Stokes, PhD

Southeast Asia Regional Science Manager

Biological Threat Reduction Program (BTRP)

From: "Kingston, Tigga" <

Date: Monday, August 24, 2020 at 5:09 PM

To: "martha.m.stokes.civ"

Cc: Katie Leahy < Caution-mailto: "jamechia.d.hoyle.ctr" < < Caution-mailto >, Guzal Masharipova < Caution-mailto >, "Kading,Rebekah" < Caution-mailto Jon Epstein ecohealthalliance.org < Caution-mailto:

Subject: [External Sender] BOHRN Status, publication

Dear Marty,

Rebekah Kading and I wrote a perspectives piece that is in revision for PLOS Biology. It calls for greater integration of ecologists/virologists (hmm, sounds familiar) and builds on analysis of a publication coauthor network. We conceptualized this at BORHN meetings and consider it a true BOHRN output, supporting BOHRN's message.

One of the reviewers specified some simple, but concrete actions that they would like to see in the revision. These actions closely ally with things we've begun at BOHRN (e.g., mission statement, contact lists of researchers). We would really like to be able to respond using BOHRN's infrastructure as it would be a good fit and would draw substantial attention to BOHRN and help boost the distributed membership and get us more on the map. The reviewer called for a mission statement, a list of who is doing what, and other simple things that could easily be integrated into the BOHRN website.

Currently, we refer to BOHRN in the acknowledgements, but have been reluctant to feature the network too centrally because we are unsure of its status and stability. It would be great to move forward with BOHRN featured more prominently, but we could do with some clarity of where things are heading. At minimum we need support of the website as that is where we will be directing people. Currently people can't join, or reset passwords etc, and we would need to work with someone on updates supporting these simple collations of information.

We have a bit less than a month to turn this around and get our revision in, so it would be great to hear your thoughts. I hope we can talk soon. I am now free fairly consistently between 10 am-Noon Mo-Thursday. I have other windows here and there as well.

All the best

Tigga

Title: Suiting up for a common cause: interdisciplinarity in bat disease research

Short title: Interdisciplinarity in bat disease research networks

Authors: Rebekah C. Kading[1]*, Tigga Kingston[2]

[1]Colorado State University, Department of Microbiology, Immunology, and Pathology, Fort Collins CO, USA.

[2]Texas Tech University, Department of Biological Sciences, Lubbock TX, USA.

*Correspondence to: Rebekah.Kading@colostate.edu

Abstract: Human perturbation of natural systems is accelerating the emergence of infectious diseases, mandating integration of disease and ecological research. Bats have been associated with recent zoonoses, but bibliometric analysis of co-author relationships identified a separation of bat ecologists and infectious disease researchers with few cross-disciplinary relationships. However, research with outcomes for both bat conservation and disease mitigation promoted integration and network connectivity. We advocate for increased engagement between ecology and infectious researchers to address such common causes. We suggest that efforts focus on leveraging existing activities, building interdisciplinary projects, and networking individuals and networks to integrate domains and coordinate resources.

Introduction

Many months into the COVID-19 pandemic, the pathway to emergence has yet to be characterized. This is not unusual; understanding disease emergence requires integration of expertise from diverse domains in complex ecological and epidemiological contexts (1). Although such interdisciplinarity is central to One Health frameworks (2), Manlove et al. (3) demonstrated that too often the requisite expertise is siloed, limiting integrative understanding of complementary fields. Here, we focus specifically on the bat research and conservation communities, in which historical silos are now challenged by the emergence of SARS-CoV-2. The virus threatens both human and bat health, thus requiring interdisciplinary cooperation in a realm that has been historically fraught with emotion and mistrust.

Trouble in Gotham City

With more than 1400 species, bats are a critical, yet highly vulnerable, component of ecosystems worldwide (4). Bats have also been implicated in the emergence of notable zoonoses. Although emergence has been well-characterized for some bat-origin zoonoses (e.g., Nipah, Hendra, SARS, Marburg), it is unclear how others have emerged, as with Ebola and now SARS-CoV-2 (5). Advancing the missions of bat conservation and public health protection have seemed, to many, to conflict. This has led to entrenched positions, with accusations of alarmist risk inflation to support funding of viral discovery on the one hand, and denial or down-play of the role of bats in emerging infectious diseases on the other. Media representation has further polarized positions, with emotive headlines that refer to bats as, for example, “breeding grounds of deadly diseases” or “the number-one carrier of disease”.

It is our contention that the integrative research needed to characterize emergence is hampered by limited effective communication and collaboration between bat ecologists and disease researchers. We undertook a bibliometric analysis of co-author relationships to investigate the

extent of cross-disciplinary collaboration between ecological- and infectious disease-oriented bat researchers (See Supplementary Methods).

The View From the Bat Cave

Consistent with previous findings (3), our analysis revealed a clear boundary between authors representing disease- and ecology-focused disciplines (Fig 1), and there were distinct clusters within disciplines. Discipline-specific expertise is the bedrock of collaborative research, so disciplinary clusters of productive research groups are expected and needed (6). However, qualified disciplinarians with strong social networks are also central to interdisciplinary success (2), and need to lead and encourage cross-disciplinary collaborations.

A few influential (betweenness centrality >500), "boundary-crossing" authors have published with colleagues both inside and outside their primary discipline (Fig 1: authors "A" from disease and "B" from ecology), but other influential authors, while extraordinarily productive and connected within their own fields, did not reach outside of their discipline (Fig 1: "C" in disease and "D" in ecology).

Suiting Up For a Common Cause

So how can we join forces to advance the field in the most integrative way? One motivation that emerged from our analysis was a common goal; common goals that motivate and engage researchers can help overcome institutional, cultural and trust barriers (6). In our analysis, integrative interdisciplinary relationships were exemplified by an international cluster that focuses on the ecology, pathology and physiology of White Nose Syndrome (WNS), a disease resulting from a fungal infection that has killed millions of bats in North America since it was first detected in 2006. The WNS cluster (blue/orange in Fig 1) meanders throughout the network and crosses disciplinary lines and, because of the diverse membership, bridges both disease and ecology clusters (red, purple, dark green).

Just as WNS has provided common ground for convergent research, understanding and mitigating other emerging zoonoses with One Health implications, like SARS-CoV-2, involve common challenges that are best met through cross-disciplinary engagement. This engagement can range from robust data collection for a complementary discipline (**leveraging**), to interdisciplinary projects designed collaboratively from the ground-up (**building**), to research networks that actively aim to integrate domains and resources (**networking**):

1) **Leveraging.** Existing research programs can leverage expertise to further specific or common agendas. For example, bat taxonomists and systematists could work alongside pathogen surveillance teams to integrate biodiversity expertise and infrastructure more effectively into virus discovery and mitigation efforts (7). Many viral discovery papers do not identify bat hosts to the species level, either because the researchers lack appropriate training and/or because the taxonomy of the sampled bats is not clearly defined. Bat diversity of many regions of biosurveillance interest is poorly known, with unresolved taxonomy of species-rich groups and likely many undescribed species. Greater bat survey and taxonomic effort is both central to effective bat conservation (8), and needed to draw correct associations between pathogen and host.

2) **Building.** Building new integrative research areas that are foundational to both research domains provides strong motivation for collaboration. For example, the question " What is a sick bat?" is central to global discussion of the ability of bats to harbor infectious agents that are highly pathogenic to people, but with [usually] little apparent health impact to themselves. Understanding bat health is directly relevant to infectious disease research and may provide important biomedical insights regarding infection tolerance. Stress induced by human disturbance or environmental modifications also threatens species conservation and management (4). Even sublethal stress can erode bat health and fitness and influence pathogen shedding and infection dynamics (9,2).

3) **Networking.** Networking individuals and existing research networks accelerate transfer of knowledge and expertise, and allow for prioritization and coordination of activities and key resources (10). Many ecologists within our co-author network have access to long-term study sites, or wild study populations, with years and sometimes decades of relevant data on ecology, life history, genetic relationships, responses to disturbance regimes, etc. These established sites and populations could provide settings for virological studies across ecological and conservation contexts. Additionally, numerous scientific questions can only be rigorously addressed with the use of captive bat colonies. Such colonies are few but distributed across the co-author network in support of research that ranges from the biomechanics of flight and the evolution of sociality, to experimental challenges with infectious agents to determine susceptibility and disease dynamics relevant to human or bat health. Thoughtful discussions and exploration of non-invasive or minimally invasive contributions that can be made by colonies held for non-disease research are needed. Ideally, networking of existing colonies could facilitate access to colonies) from each bat family, and generate associated primary cell lines, genomic, and transcriptomic data. Alignment of experimental protocols would further facilitate the comparison of biological phenomena, including susceptibility and responses to pathogens, across taxa, and the parameterization of models.

Up Up and Away!

We considered connectivity and divisions in disease and bat ecology research communities. Similar divisions likely exist between ecologists and disease researchers focused on other taxa that harbor zoonotic pathogens, such as rodents (hantaviruses and arenaviruses), birds (influenza viruses), non-human primates (retroviruses), and wild ungulates (prions). We suggest that interdisciplinary research can be accelerated when disparate domains address common, foundational causes through some combination of leveraging, building and networking.

References

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2. Anholt RM, Stephen C, Copes R. Strategies for collaboration in the interdisciplinary field of emerging zoonotic diseases. Zoonoses Public Health. 2012;59: 229–240.

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Acknowledgments: This effort was facilitated by engagements through the Bat One Health Research Network (Defense Threat Reduction Agency, Biological Threat Reduction Program); Funding: R.C.K. is receiving partial salary support from HDTRA1-19-1-0030; no specific funding was received for this analysis. Author contributions: Conceptualization, T.K. and R.C.K.; methodology, T.K.; formal analysis, R.C.K.; data curation, T.K.; writing—original draft preparation, R.C.K. and T.K.; writing—review and editing, R.C.K. and T.K.; visualization, R.C.K. All authors have read and agreed to the published version of the manuscript; Competing interests: Authors declare no competing interests; and Data and materials availability: All data

and analytical procedures are available in the main text. Figure 1 was created using BioRender.com.

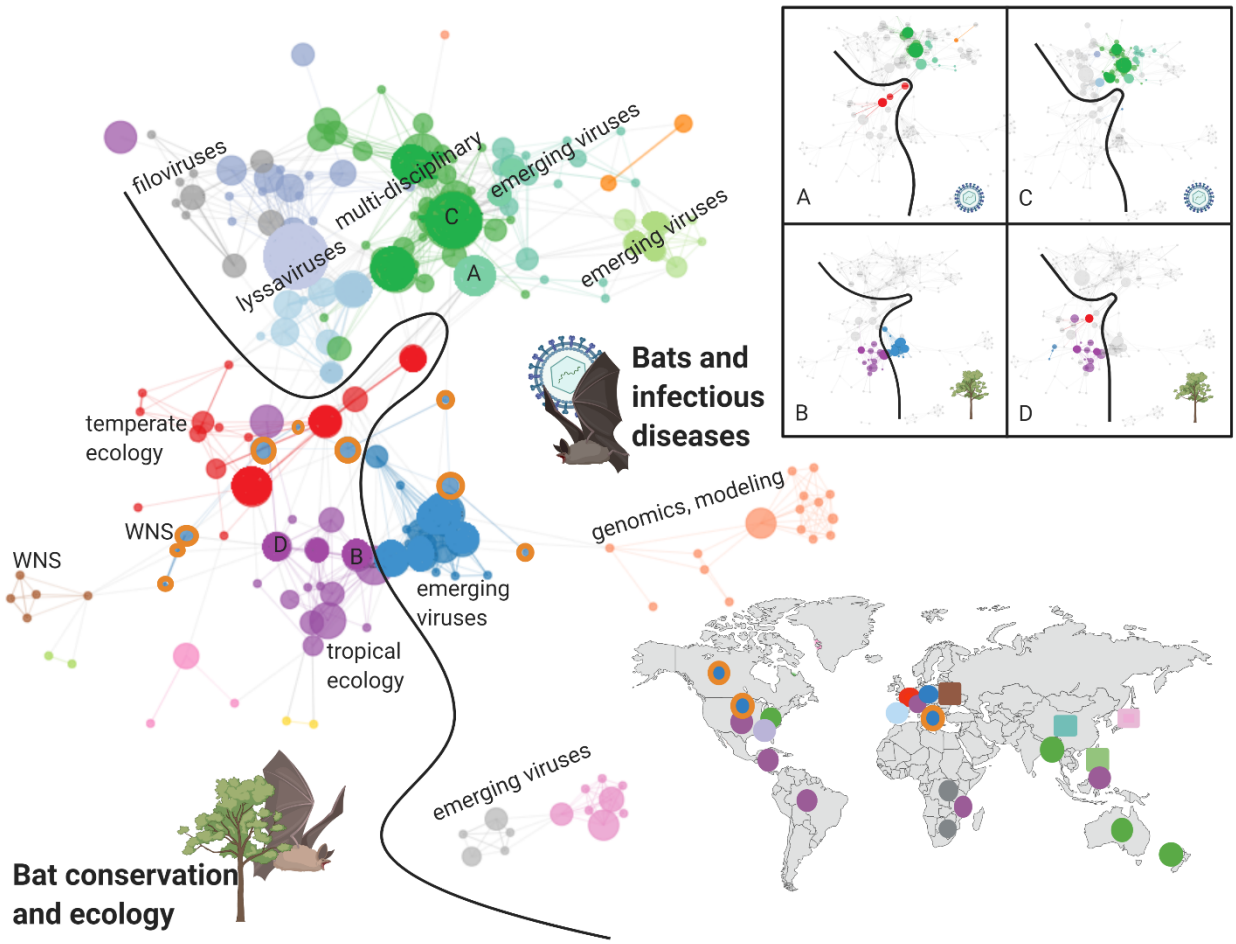

Fig. 1. Co-authorship network of the 200 most published bat researchers between 1950 and 2019. Map shows location of institutional affiliations of authors in each cluster. Colors correspond to the author network clusters; squares denote apparent segregation of research groups geographically in addition to topic area. Inset shows the publication networks of four influential authors with betweenness centrality scores >500. Authors "A" and "B" are boundary-crossing authors with collaboration networks that span clusters in both ecology and disease topic areas. Authors "C" and "D" are widely connected within either the ecology or disease communities, but do not collaborate across disciplines. Clustering was also driven by geographical and institutional boundaries associated with programmatic missions or funding (inset map) promoting homogenous perspectives within the cluster and potentially retarding dissemination of findings. WNS = White Nose Syndrome. See Supplementary Methods for additional detail on this analysis.

Supplementary Methods

From ISI Web of Science (WoS), we extracted papers under the topic “bats” or “chiroptera” from 1950 – 2019. The resulting 28,001 citations were refined to 7,425 by filtering for articles indexed by SCI and SSCI in the WoS categories “ecology”, “multidisciplinary sciences”, “biodiversity conservation”, “virology”, “infectious diseases”, and “immunology”. Unrelated papers were manually removed, reducing the final dataset to 5,645 papers. Records were imported into Bibliometrix (10). We employed co-author analysis to analyze the social structure of the field (1) and build a network map of authors (nodes) linked by co-authorships (Fig 1). Clusters, generated with the Walktrap algorithm, comprised authors who published together significantly more frequently than with others. Primary research themes of clusters were identified from professional experience and inspection of publications. Betweenness centrality scores for each author (range: 0 - 2,250) were calculated (2). Authors with high betweenness centrality connect different parts of the network, either within or across disciplinary boundaries.

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2. Pierce SJ. Boundary crossing in research literatures as a means of interdisciplinary information transfer. J Am Soc Inf Sci. 1999;50: 271–279.

From: Kading,Rebekah on behalf of Kading,Rebekah >
Sent: Thursday, June 25, 2020 6:05 PM EDT
To: Kendra Phelps ecohealthalliance.org>
Subject: Re: contact

Hi Kendra,

Great - thanks so much! I'll send Anna your way. Yes, I agree that EHA may be a great fit for her, and she is thrilled there are open positions! And the Iowa connection. We talk Iowa a lot because my husband's family farms in Iowa....right along I-80 between Omaha and DesMoines, by the yellow smiley face water tower at the Adair/Casey exit...we're headed there next week actually. Small world! I'll definitely loop you in about anything with BOHRN that you could contribute to - I appreciated all your input at the Vienna meeting and it would be great to have you involved. We had a lot of momentum after that meeting but they've been very quiet lately....DTRA seems to be going through some restructuring. But if things calm down by this fall I think they will try to have another meeting and get things going again.

Thanks!
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kendra Phelps ecohealthalliance.org>
Sent: Thursday, June 25, 2020 3:53 PM
To: Kading,Rebekah >
Subject: Re: contact

Hi Rebekah,

Great to hear from you, and I hope you are doing well too! I would be happy to chat with Anne about the available positions at EHA, please pass my email to her and we can set up a time to chat. I did a quick search of Anne, and besides being an amazing scientist that I think would be a great fit at EHA, I noticed she completed her undergrad in Iowa (which is also my home state).

In terms of BOHRN initiatives, if I can contribute in any way please feel free to contact me. I often get overlooked with both Jon and Kevin being BOHRN members.

Cheers,
Kendra

Kendra Phelps, PhD
Research Scientist

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200
New York, NY 10018

)
www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

On Jun 25, 2020, at 1:54 PM, Kading,Rebekah wrote:

Dear Kendra,

I hope this message finds you hanging in there ok during all of this! Thank you also for all your hard work on this North American bat paper! I've been interacting regularly with Tigga through the IUCN Bat Specialist Group and working on another paper; it's been nice keeping up with her outside of BOHRN. With everything going on with the bat research community and SARS-CoV-2 though, lots of BOHRN members are involved in various initiatives and and keeping pretty busy...someday when we are on the other side of this, I hope DTRA revitalizes a BOHRN meeting in person so we can all reconnect, debrief, and move some ideas forward that we had been discussing. I don't think anyone would accept another Zoom meeting at this point though!

Anyway, I'm writing to ask if I can put you in touch with a DVM/PhD student in my lab, Anna Fagre. Anna is outstanding, and interested in applying for one of the open positions at EcoHealth and just wants to do due diligence in finding out more about the position, expectations, etc. I thought of you as being a good person to provide some inside perspective, but wanted to reach out first to make sure that wouldn't put you in an awkward position, like if you're on the hiring committee or something.

Thanks so much!

Best regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kendra Phelps ecohealthalliance.org>
Sent: Tuesday, June 16, 2020 8:59 AM
To: Raina Plowright
Cc: Paul Cryan < >; Wang Linfa ; olival ecohealthalliance.org>; dreeden < >; Hume Field ecohealthalliance.org>; Charles H Calisher < ; Brian R. Amman >; Ralph S. Baric < ; Blehert, David S >; Cara Brook >; Kevin Castle >; Coleman, Jeremy T >; Peter Daszak ecohealthalliance.org>; epstein ecohealthalliance.org>; wtrick < ; Gilbert, Amy T - APHIS >; David Hayman <d >; Ip, Hon S ; William B. Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah Tigga Kingston >; Lorch, Jeffrey M >; Ian Mendenhall ; alisonpee ; Reichard, Jonathan D >; Sleeman, Jonathan M Daniel Streicker ; Jonathan S. Towner >
Subject: Re: [EXTERNAL] SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Agreed, great job Kevin and Paul for the quick turnaround.

The CNN special can be viewed on www.cnn.com/go, click on "Shows" to the left-side of the screen and the special should be an option at the top of the screen (or one scroll to the right). I think you need a cable subscription to log-in to view though.

Cheers,
Kendra

Kendra Phelps, PhD
Research Scientist

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200
New York, NY 10018

)
www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

On Jun 16, 2020, at 10:48 AM, Raina Plowright < wrote:

Thanks for doing the record turn-around! Well done everyone and great leadership Paul and Kevin!
Does anyone have a link to the full CNN documentary? I heard it was great.
Raina

On Jun 16, 2020, at 8:40 AM, Cryan, Paul < > wrote:

That was one of those unforgettable moments for me watching many of you on the CNN special...in my opinion you all came off very well! Congrats!

Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Wang Linfa
Sent: Monday, June 15, 2020 11:22 PM
To: oliva ecohealthalliance.org>; dreeder ; Hume Field ecohealthalliance.org>; Charles H Calisher ; Brian R. Amman ; Ralph S. Baric ; Blehert, David S Cara Brook >; Kevin Castle >; Coleman, Jeremy T ; Peter Daszak ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; wfrick >; Gilbert, Amy T - APHIS >; David Hayman >; Ip, Hon S ; William Karesh ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah >; Tigga Kingston < ; Lorch, Jeffrey M >; Ian Mendenhall alisonpee >; Kendra Phelps ecohealthalliance.org>; Plowright, Raina Reichard, Jonathan D < Sleeman, Jonathan M ; Daniel Streicker >; Jonathan S. Towner >
Cc: Cryan, Paul <
Subject: [EXTERNAL] RE: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Thanks Kevin and Paul for doing a great job so quickly.

I guess the CNN documentary yesterday also made this a hot (hotter) topic now and the editor may want to have “a ride on the bat wings” to get it out asap!

Fingers crossed.

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857

From: Kevin Olival ecohealthalliance.org>
Sent: Tuesday, 16 June 2020 1:19 PM
To: DeeAnn Reeder >; Hume Field ecohealthalliance.org>; Charles H Calisher < ; Brian R. Amman >; Wang Linfa Ralph S. Baric >; David S Blehert >; Cara Brook >; Kevin Castle ; Jeremy Coleman < >; Peter Daszak ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Winifred F Frick, Ph.D. < ; Gilbert, Amy T - APHIS >; David Hayman ; Hon S Ip < ; William Karesh @ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah ; Tigga Kingston < >; Lorch, Jeffrey M >; Ian Mendenhall <ian.mendenhall@ alisonpee ; Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; Jonathan D Reichard >; Jonathan M Sleeman >; Daniel Streicker Jonathan S. Towner
Cc: Paul Cryan >
Subject: Re: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

- External Email -

Hi Team,

Funny thing, bioRxiv actually rejected us! Apparently they don’t take “reviews”.

In any case we got **very positive reviews back from *PLoS Pathogens*** today, and the revised ms was just resubmitted (<24 hour turnaround). Woohooo! Finger’s crossed that the editors turn it around again quickly and we can see this published soon.

Attached is the cover letter, response to reviewers, and the resubmitted version of ms.

Cheers,
Kevin and Paul

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org
EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

On Jun 12, 2020, at 10:43 AM, Kevin Olival ecohealthalliance.org> wrote:

Dear all,

We successfully submitted to bioRxiv yesterday and it’s currently in “review” with the editorial staff and should be posted within 48 hours. Big thanks to Paul for getting the final USGS approvals and ms formatting in place.

Hume and Charlie, I understand your very valid and “traditional” concerns here, there’s a lot of riff-raff out there on pre-print servers and hence why we have the peer-review system. Nonetheless, given that there are other similar reviews being posted at the moment and the timeliness of this given the USGS/USFW Risk Assessment out last week, etc., would be best to get this out there while we’re still in review at PLOS.

Best,
Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201

New York, NY 10018

www.ecohealthalliance.org
EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

On Jun 12, 2020, at 8:24 AM, DeeAnn Reeder > wrote:

Thanks all - I am in support of bioRxrv for this paper (although I don't systematically use it - in this fast moving CoV environment, for some papers I think it is a very good option).

Cheers - DeeAnn

On Thu, Jun 11, 2020 at 7:22 PM Hume Field ecohealthalliance.org> wrote:

Thanks Kevin.. no prob, tho philosophically I'm with Charlie!

Hume

On Fri., 12 Jun. 2020, 1:23 am > wrote:

No significant objections about the manuscript but I am not crazy about pre-print servers or their purpose. I am not only old, I am a traditionalist. Lots of crap being sent out as pre-print servers that wind up not being acceptable – or withdrawn.

Charlie

From: Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) <
Sent: Thursday, June 11, 2020 8:05 AM
To: Kevin Olival

>
Subject: RE: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Thanks Kevin!

From: Kevin Olival ecohealthalliance.org>
Sent: Thursday, June 11, 2020 9:43 AM
To: Wang Linfa ; Paul Cryan >; Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) ; Ralph S. Baric < ; David S Blehert >; Cara Brook >; Charles H Calisher < >; Kevin Castle < >; Jeremy Coleman >; Peter Daszak ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Hume Field ecohealthalliance.org>; Winifred F Frick, Ph.D. >; Gilbert, Amy T - APHIS < David Hayman < >; Hon S Ip < ; William Karesh < ecohealthalliance.org>; Christine Kreuder Johnson ; Kading,Rebekah ; Tigga Kingston ; Lorch, Jeffrey M ; Ian MENDENHALL PhD >;alisonpee Kendra Phelps < ecohealthalliance.org>; Plowright, Raina ; DeeAnn Reeder < ; Jonathan D Reichard < Jonathan M Sleeman ; Daniel Streicker ; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)

Subject: Re: SARS-CoV-2 spillover risk to North American bats manuscript - FINAL version for PLOS Pathogens (new plan)

Dear all,

Update on our ms. It was submitted to PLOS Pathogens on June 2nd (you should have all received an email from the journal confirming this) and it is currently under review.

We are in the final stages of USGS approval to also submit to bioRxiv (pre-print server), and expect to finalize that and post it on bioRxiv in the next 24 hours. *Please let me know if there are any objections.*

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eight Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org
EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

On May 28, 2020, at 4:38 PM, Kevin Olival ecohealthalliance.org> wrote:

Hi Folks,

Quick update on our paper — unfortunately got news yesterday that *PNAS* was not interested in this as a Perspectives piece, and rejected our proposal. We are currently pursuing options with editors at *PLOS Pathogens* to see if they want it as a review. Will keep you all posted.

Latest version attached that has cleared CDC and USGS review. We will still aim to get this on BioRxiv, but wanted to wait until we had it cleared first and ideally in review at a journal.

Cheers,
Kevin

<Olival et al. bat CoVs 20200520_v11.3.docx>

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eight Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org
EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

On 12 May 2020, at 10:13 PM, Kevin Olival < ecohealthalliance.org> wrote:

Dear Co-authors,

Attached is the latest, submission ready version of our paper "**Possible risks of SARS-CoV-2 spillover to free-ranging wildlife: a case study of bats**". Thank you all for the last round of invaluable edits and comments. Paul and I have now gone through multiple revisions since you last saw the paper in an attempt to include everyone's feedback; so apologize for the delay in turning this around and moving towards submission.

We started a submission to *Lancet Infectious Diseases*, but after thinking more about the journal's scope and reading other recent reviews that have been published in the journal, Paul and I decided it was not the best fit after all. We instead plan to submit this as a Perspectives article to *PNAS*(https://www.pnas.org/page/authors/purpose-scope). We think *PNAS* is a better fit all around, especially given the US focus of our review. We are currently following up some leads for "sponsorship" of our paper with PNAS which would make it an invited piece. If you have any specific suggestions in this regard, please let me know.

As before, the plan is once we submit (hopefully this week) to *PNAS* we will also post as a pre-print on BioRxiv so it can be viewed and used immediately. **If there are any objections to this plan or to submit to *PNAS*, please let me know.**
Also, for those that have secured USG approval already, please let me know if these needs to be updated or if you need any more information.

This has been a fantastic exercise in group writing! Big thank you to everyone.

Cheers,
Kevin

<Olival et al. bat CoVs 20200511_V9.1.docx>

Kevin J. Olival, PhD
Vice President for Research

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460 West 34th Street, Suite 1701
New York, NY 10001

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--
DeeAnn M. Reeder, PhD
Professor
Department of Biology
Bucknell University
Lewisburg, PA 17837

http://deeannreeder.scholar.bucknell.edu

Important: This email is confidential and may be privileged. If you are not the intended recipient, please delete it and notify us immediately; you should not copy or use it for any purpose, nor disclose its contents to any other person. Thank you.

From: Kading,Rebekah on behalf of Kading,Rebekah >
Sent: Monday, August 13, 2018 11:55 PM EDT
To: Kingston, Tigga ; Megan Hudson ;
nisreen.hmoud >; joram.buza ;
cryanp ; c _demetria ;
epstein ecohealthalliance.org>; vkapur ;
kityrob >; tamar_kutateladze
ian.mendenhall >; olival
< ecohealthalliance.org>; dreeder ; ksidamonidze
; gavin.smith ; l.urushadze
spwa ; abelwade ;
raina.plowright
CC: Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) < ; Stokes, Martha M CIV
(US) ; Katie Leahy < >; Becker, Stephen M CTR DTRA J3-7
(US) >
Subject: Re: Draft Executive Summary and Website Materials

Hi Tigga and everyone,

Yes, that is challenge for me as well. I am not involved in the Georgia meeting, but have made arrangements regarding class coverage so I could travel to Vienna if we proceed with that meeting in Nov. I also would not have been able to get away for both meetings though. January, after the semester is over, is generally better timing for me too. There was a December meeting option as well, which unfortunately for me would fall during the last week of classes so I couldn't get away for that, but if that works better for the majority of the steering committee perhaps we should reconsider it?

Kind regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kingston, Tigga < >
Sent: Saturday, August 11, 2018 3:28:09 AM
To: Megan Hudson; nisreen.hmoud ; joram.buza ; cryanp ; c_demetria ;
ecohealthalliance.org; Kading,Rebekah; vkapur kityrob ; tamar_kutateladze
ian.mendenhall ecohealthalliance.org; dreeder ; ksidamonidze
gavin.smith ; l.urushadze spwa ; abelwade ; raina.plowright
Cc: Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US); Stokes, Martha M CIV (US); Katie Leahy; Becker, Stephen M CTR DTRA J3-7 (US)
Subject: RE: Draft Executive Summary and Website Materials

Hi Megan
Just trying to unpack the plans this fall, and have been reading through the Exec summary. Essentially a lot of BOHRN are going to Georgia and you propose an additional meeting in Austria a couple of months later?

I don’t want to second guess what you all decided on in Canada, but is there any chance the second meeting (currently scheduled for November) could be when the fall semester is over (i.e. early-mid December through mid January)? As I’m on the WABnet Steering Committee I have committed to the Georgia meeting, but it is challenging to get release for multiple trips during the academic semester, particularly for same entities. I am probably not the only one running into this problem or similar

Thanks for your consideration,
Tigga

From: Megan Hudson
Sent: Friday, July 13, 2018 11:02 AM
To: nisreen.hmoud ; joram.buza ; cryanp ; c_demetria
ecohealthalliance.org; rebekah.kading vkapur Kingston, Tigga
kityrob tamar_kutateladze ian.mendenhall ecohealthalliance.org;
dreeder ; ksidamonidze ; gavin.smith ; l.urushadze spwa
abelwade raina.plowright
Cc: Lancaster, Mary J CIV DTRA PARTNERSHIP AND INSP (US) >; Stokes, Martha M CIV (US)
>; Katie Leahy < >; Becker, Stephen M CTR DTRA J3-7 (US)

Subject: Draft Executive Summary and Website Materials

All,

Please find the draft report from our BOHRN meeting 20-21 June. This report includes an executive summary, action items, participant list, working group outcomes, and your research quad charts.

We ask that you provide constructive comments (e.g., content changes) no later than 18 July. It is our intent to adjudicate and incorporate any comments to then publish a final report.

In addition, you will find an updated version of the website map here (https://docs.google.com/document/d/1x5GdAKEPpKXTol9utZiYvaGoXNtOQsyTdlub1WvN0tk/edit?usp=sharing). Each page has the title of the website page and the content, make edits, as you see fit, to the language to help us better develop the website.

As a reminder, we will be adding individual bios to the website. If you have not already done so, you may submit your information here: https://www.surveymonkey.com/r/BPMTG2T

You will find the report contains softened language to add a more conservationist view point, please review the language within the report and on the website.

v/r,

Megan

Megan Hudson
Task Lead | Global Systems Engineering
6303 Little River Turnpike #208
Alexandria, VA 22312

http://globalsyseng.com

From: Kading,Rebekah on behalf of Kading,Rebekah
Sent: Wednesday, April 29, 2020 7:05 PM EDT
To: Kevin Olival ecohealthalliance.org>; Paul Cryan
Subject: Re: Final version of North American bat/SARS2 ms - PLEASE REVIEW

Hi Kevin,

Very nice job on this! Only spotted a couple small things.
1) "highlights" is misspelled on line 128.
2) looks like a ref is still needed in line 342 regarding PPE usage in the field. This ref might fit...it's more broadly on wildlife professionals though (PMID: 31993824)
3) don't forget to delete the [...] on line 421

Yes, I would be delighted to be a co-author.

Thanks so much!
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kevin Olival ecohealthalliance.org>
Sent: Sunday, April 26, 2020 10:11 PM
To: Paul Cryan ; Brian R. Amman ; Ralph S. Baric >; David S Blehert >; Cara Brook >; Charles H Calisher >; Kevin Castle ; Jeremy Coleman >; Peter Daszak ecohealthalliance.org>; epstein ecohealthalliance.org>; Hume Field ecohealthalliance.org>; Winifred F Frick, Ph.D. >; Gilbert, Amy T - APHIS >; David Hayman ; Hon S Ip William Karesh ecohealthalliance.org>; Christine Kreuder Johnson >; Kading,Rebekah >; Tigga Kingston >; Lorch, Jeffrey M ; Ian Mendenhall >; alisonpee >; Kendra Phelps ecohealthalliance.org>; Plowright, Raina ; DeeAnn Reeder Jonathan D Reichard >; Jonathan M Sleeman >; Daniel Streicker Jonathan S. Towner
Subject: Final version of North American bat/SARS2 ms - PLEASE REVIEW

Dear Esteemed Colleagues,

Please review the attached penultimate draft of our manuscript (now entitled: **"Possible risks of SARS-CoV-2 spillover to free-ranging wildlife: a case study of bats")**, together with the supplementary table and refs. Our plan is to submit to *Lancet Infectious Diseases* as a review article (correct length and they allow 150 refs) in the next week - references are currently formatted for that journal. We would also like to post it on bioRxiv as a pre-print once we get it submitted to *Lancet ID*. Please let me know if you have any concerns with that plan.

Thank you all for your excellent comments and edits on the previous draft. Paul and I have gone back and forth on several rounds of revisions since then (and multiple late night texts), aiming to take each and every suggestion into account, and we believe it's a much better manuscript now! Very excited about this one, and looking forward to getting it published!

By Thursday April 30th (or ASAP), could you each please:

1. Confirm that you agree to be a co-author.
2. Double check your name and affiliation, and send me your ORCID number if you have one.
3. Read through the ms and send any important, last minute changes or edits you feel are necessary. Please use track changes. If you're okay with the ms as is, please just confirm so.
4. For my Federal US Gov't friends (USFWS, USGS, CDC, USDA) - please let us know what we need to do for approval on your end. I know Paul is working with USGS now to hopefully get rapid clearance.

No need to cc all if you don't want, but please include both me and Paul on your response.

Looking forward to hearing from you all soon!

Cheers,
Kevin and Paul

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
460 West 34th Street, Suite 1701
New York, NY 10001

)
www.ecohealthalliance.org
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From: Kading,Rebekah on behalf of Kading,Rebekah >
Sent: Friday, August 07, 2020 3:22 PM EDT
To: Kingston, Tigga >; Dr. Melinda Rostal ecohealthalliance.org>; Rodrigo Medellin

CC: Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Isabella Mandl
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Hi everyone,

Just chiming in to say thank you for the discussion and interest in the Infographic! I'm so glad it has been a good communication tool - the suggested modifications would be very easy to make.

Kind regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kingston, Tigga >
Sent: Friday, August 7, 2020 10:04 AM
To: Dr. Melinda Rostal ecohealthalliance.org>; Rodrigo Medellin
Cc: Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Kading,Rebekah ; Isabella Mandl
Subject: RE: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Dear Melinda
That sounds appropriate to me. Our group meets early on Tuesday morning, so I'd like to run this by them then for final agreement, if that's OK, but I don't imagine any objections.

Best
Tigga

From: Dr. Melinda Rostal < ecohealthalliance.org>
Sent: Friday, August 7, 2020 10:39 AM
To: Rodrigo Medellin
Cc: Kingston, Tigga >; Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Kading,Rebekah >; Isabella Mandl >
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Dear Rodrigo and Tigga,

I spoke to my colleagues and we would propose to change "bats" to either "mammals" or "wild mammals", change the graphic in the center to include a smaller version of the bat that is there as well as an ape and a mustelid, change the example in the Minimize box from "i.e. implement acoustic surveys" to "i.e. collect environmental samples", and change the figure of the bat calling to a figure of collecting an environmental sample.

The risks and mitigation strategies are really nicely laid out as you originally made it so we wouldn't need to change that or the rest of the text/figures. We support your MAP plan.

Do you think that would be acceptable? We think it remains very consistent with your message.

If yes, what is the best way to proceed with the modification?

Kind regards,

Mindy

Melinda Rostal DVM, MPH, PhD
Principal Scientist, Vector-Borne Diseases

Rift Valley Fever Virus Project Manager

EcoHealth Alliance
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New York, NY 10018

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460 West 34th Street – 17th floor
New York, NY 10001

On Aug 4, 2020, at 5:14 PM, Rodrigo Medellin wrote:

Hi everyone

Thank you Tigga for copying me with the good email address. Mindy good talking to you again. I fully concur with Tigga about being mindful of the brains behind the infographic, and of course about any changes. If at all possible Mindy we would rather have it presented with due credits verbatim. Multiple version will be confusing, regardless of whether the different versions clash with each other. Stay safe.

--

Dr. Rodrigo A. Medellin
Instituto de Ecología, UNAM
Ap. Postal 70-275
04510 Ciudad Universitaria, D. F.
MEXICO

DIRECCION FISICA (STREET ADDRESS):

Dr. Rodrigo A. Medellín
Instituto de Ecologia, UNAM
Circuito Exterior s/n junto al Jardín Botánico Exterior
04510 Ciudad Universitaria, D. F.
MEXICO

https://www.facebook.com/rodrigo.a.medellin
https://www.instagram.com/rodrigomedellin1223/
https://twitter.com/rodrigomedellin

Check out our YouTube channel with dozens of cool, short videos on bats: https://www.youtube.com/user/RMedellinbats
http://web.ecologia.unam.mx/medellin/

On Tue, Aug 4, 2020 at 9:22 AM Kingston, Tigga > wrote:

> Dear Mindy
>
> The infographic was constructed in BioRender by Dr Rebekah Kading, so they would probably need to be manipulated in that environment. I've copied Rebekah and Dr Bella Mandl – who is also leading our graphics – on this email.
>
> They have also worked up infographics for rehabbers and cavers and the original is now in a number of languages. Rebekah is a whizz at adapting the base design, but we of course need to be mindful of her time.
>
> **Critically, we would need to review and sanction any changes because we don't want any messages to conflict with our own.** It would be confusing to have essentially the same graphic circulating saying different things. Our messaging is organized around the MAP concept so we don't want that disrupted, for example.
>
> Do you have a clearer idea of how you would use the infographic?
>
> Caveats aside, happy to work with you of course!!
>
> Best wishes
> Tigga
>
> P.S. I copied Rodrigo with his current email.

From: Melinda Rostal ecohealthalliance.org>
Sent: Monday, August 3, 2020 8:41 PM
To: Kingston, Tigga >; Rodrigo A. Medellín >
Cc: Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps @ecohealthalliance.org>
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Dear Tigga,
I just wanted to let you know that I've sent this to 2 email addresses for Rodrigo and it seems they have bounced back. I am not sure if he has seen my request.

I hope to hear from you soon about whether the Wildlife Health Specialist Group can use or modify your infographic (with the appropriate credit).

Best,
Mindy

Sent from my iPhone

On Jul 29, 2020, at 3:11 PM, Dr. Melinda Rostal ecohealthalliance.org> wrote:

> Dear Rodrigo and Tigga,
>
> Rodrigo, it's been several years since we have spoken and I hope you are well.
> I hope you are both managing to stay safe during the pandemic.
>
> I have been working with Billy Karesh, some folks from the Wildlife Health Specialist Group and the OIE to come up with some recommendations for working with free-living, wild mammals during the pandemic. We thought that the documents that the Bat Specialist Group wrote were great and we certainly refer anyone working with bats to review your guidelines as well.
>
> We really liked the figure you used (pasted below) and were wondering if we could reproduce it and/or modify it slightly in our document. We would certainly credit your group with creating it.
>
> If it is ok to modify it, would it be possible to get a powerpoint slide or photoshop document to allow for easy modification?
>
> I look forward to hearing from you and we would be happy to promote your work.
>
> Kind regards,
>
> Mindy
>
> <PastedGraphic-3.png>

Melinda Rostal DVM, MPH, PhD
Principal Scientist, Vector-Borne Diseases

Rift Valley Fever Virus Project Manager

EcoHealth Alliance
520 Eighth Ave, Ste. 1200
New York, NY 10018

www.ecohealthalliance.org

From: Kading,Rebekah on behalf of Kading,Rebekah >
Sent: Thursday, August 20, 2020 10:43 AM EDT
To: Dr. Melinda Rostal ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>
CC: Tigga Kingston >; Rodrigo Medellin ; Billy Karesh ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Isabella Mandl
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure
Attachment(s): "IUCN infographic wildlife version_cc.pdf","IUCN infographic wildlife version_cc.png"

Hi everyone -

So sorry for the delay! I'm attaching the Infographic -- a pdf version with clickable links and a png version which may be easier for social media postings. Just let me know if you have any final suggestions. We are very happy to collaborate with you on aligning the messaging coming from our working groups on this issue - thank you again very much for reaching out about this!

Kind regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Dr. Melinda Rostal ecohealthalliance.org>
Sent: Tuesday, August 18, 2020 8:29 AM
To: Dr. Kevin Olival ecohealthalliance.org>
Cc: Kading,Rebekah >; Tigga Kingston >; Rodrigo Medellin ; Billy Karesh ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Isabella Mandl
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Dear Tigga and Rodrigo,
Attached is the figure with the acknowledgment. The WHSG would prefer not to include logos on the figure if possible as it is positioned in the middle of our text. However, I want to ensure you are satisfied with it. So if you have any concerns about the acknowledgement, please let me know by Thursday Aug 20.

Thanks very much!

And thanks again to you and Rebekah for letting us modify your great figure:)

Best,

Mindy

Melinda Rostal DVM, MPH, PhD
Principal Scientist, Vector-Borne Diseases

Rift Valley Fever Virus Project Manager

EcoHealth Alliance
520 Eighth Ave, Ste. 1200
New York, NY 10018

)
www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.
EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

On Aug 12, 2020, at 2:49 PM, Kevin Olival ecohealthalliance.org> wrote:

Looks wonderful, and thanks all for adapting this for a wider distribution.

Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

On Aug 11, 2020, at 9:47 AM, Kading,Rebekah wrote:

Hi Mindy, Billy, Kevin, and Kendra -

I hope your week has gotten off to a good start!

I'm attaching a draft infographic for your review. I've modified the current BSG MAP infographic per your suggestions for a wildlife version. I can also add a logo, QR, and/or website at the bottom if you'd like. Not sure of exactly the best way to portray environmental samples...I was assuming this will comprise activities like passive fecal sample collections...so please let me know if this captures what you had in mind or if there is something else you're envisioning and I can revise accordingly! (BioRender does have an amusing variety of poo icons, but I was trying to keep it classy and professional.) ��

Take care, and I'll look forward to your feedback.

Best,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Dr. Melinda Rostal ecohealthalliance.org>
Sent: Friday, August 7, 2020 2:16 PM
To: Kading,Rebekah
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That's great Rebekah!

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<IUCN infographic wildlife version.png>

Preventing transmission of SARS-CoV-2 from humans to wild mammals

Exposure Risks

Contact exposure
Mammals coming into contact with contaminated hands or equipment

Aerosol exposure
Infectious droplets from handlers holding mammals in close proximity

Environmental exposure
Sharing enclosed, poorly-ventilated spaces with mammals, where virus may persist in the air or on surfaces

MAP your plan to prevent transmission to mammals!

Mitigation Strategies

Minimize

Delay, prioritize, or avoid handling mammals when possible, i.e. collect environmental samples

Assess

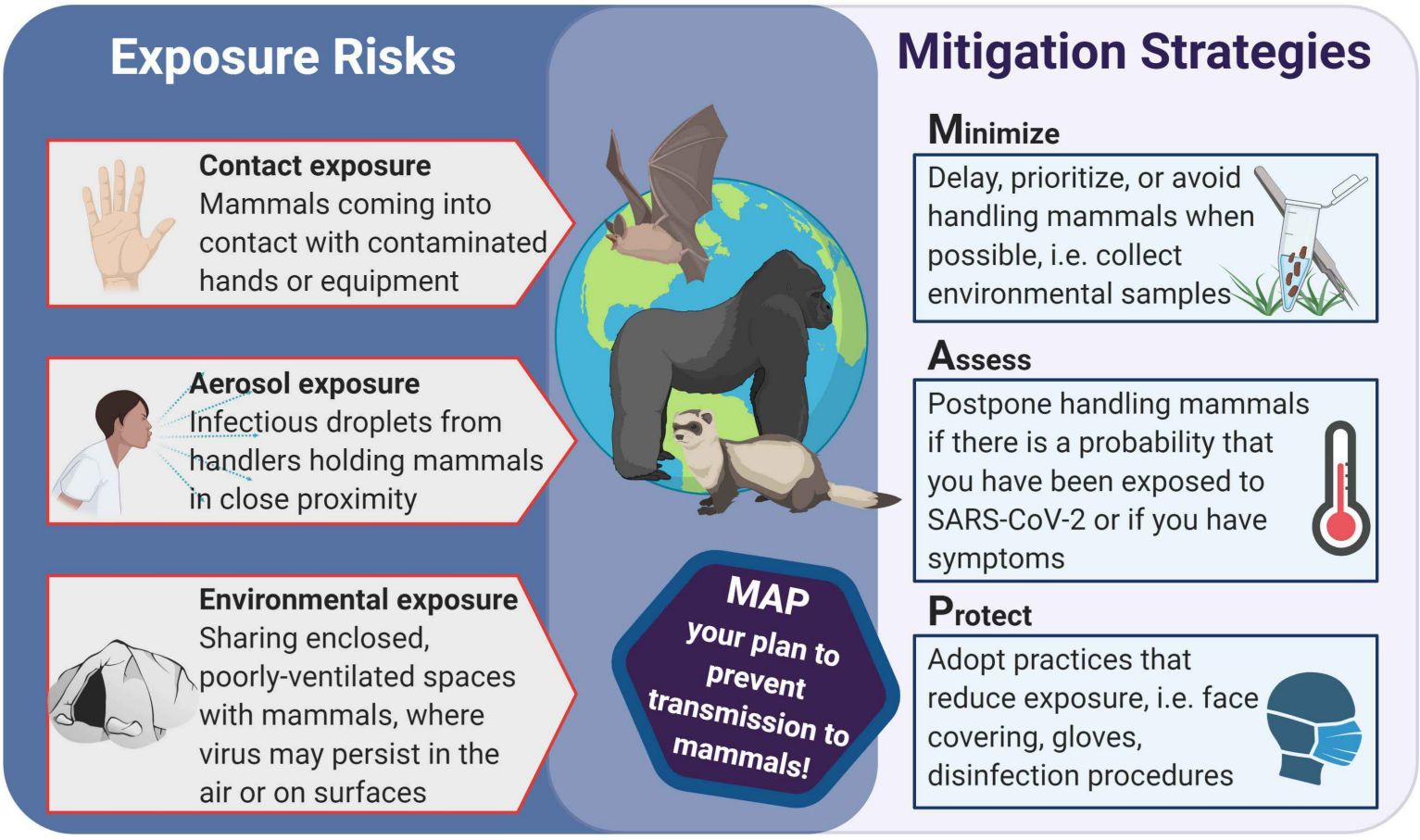
Postpone handling mammals if there is a probability that you have been exposed to SARS-CoV-2 or if you have symptoms

Protect

Adopt practices that reduce exposure, i.e. face covering, gloves, disinfection procedures

This figure was adapted in collaboration with the IUCN Bat Specialist group.

Preventing transmission of SARS-CoV-2 from humans to wild mammals



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Hi Mindy,

Thanks - I'm so glad you like it! I'll await to hear about any final edits the group might want to see. I'll also defer to Tigga and Rodrigo for how they'd like to handle the branding on this infographic. I do think the infographic alignment between the working groups is pretty cool, and will be good for consistency in messaging.

Kind regards,
Rebekah

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Dear Rebekah,

This looks awesome!! I shared it this evening with our small team that is preparing the guidelines for the rest of the specialist group to review and they like it very much (that's a great ferret:)! We are going to share the guidelines tomorrow with a larger team in the specialist group for the final review so this is perfect timing.

I will also find out about branding from the WHSG and will get back to you on that. I also want to make sure we also give credit your specialist group. Tigga and Rodrigo, as I mentioned we will include a statement that this is modified from the BSG's figure. Please advise on any other branding requirements.

Thanks very much!!

Kind regards,

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<PastedGraphic-3.png>

Melinda Rostal DVM, MPH, PhD
Principal Scientist, Vector-Borne Diseases

Rift Valley Fever Virus Project Manager

EcoHealth Alliance
520 Eighth Ave, Ste. 1200
New York, NY 10018

www.ecohealthalliance.org

Preventing transmission of SARS-CoV-2 from humans to wild mammals

Exposure Risks

Contact exposure
Mammals coming into contact with contaminated hands or equipment

Aerosol exposure
Infectious droplets from handlers holding mammals in close proximity

Environmental exposure
Sharing enclosed, poorly-ventilated spaces with mammals, where virus may persist in the air or on surfaces

MAP your plan to prevent transmission to mammals!

Mitigation Strategies

Minimize

Delay, prioritize, or avoid handling mammals when possible, i.e. collect environmental samples

Assess

Postpone handling mammals if there is a probability that you have been exposed to SARS-CoV-2 or if you have symptoms

Protect

Adopt practices that reduce exposure, i.e. face covering, gloves, disinfection procedures

From: Kading,Rebekah on behalf of Kading,Rebekah <
Sent: Tuesday, August 11, 2020 6:31 PM EDT
To: Kendra Phelps ecohealthalliance.org>
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Hi Kendra -

Thank you! I'm glad you like it! I have a subscription to BioRender for my lab...well worth the investment...so we get unlimited images, don't have the watermark on it, and can export high resolution for use in publications, grants, presentations etc. I started playing around with the free version though just to be sure I liked it, and its been a huge hit with my lab!

Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kendra Phelps ecohealthalliance.org>
Sent: Tuesday, August 11, 2020 2:49 PM
To: Kading,Rebekah
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Hi Rebekah,

Wow, that is amazing! The environmental sampling icons are perfect!

I was checking into BioRender today to make a schematic for a publication, do you use the free version?

Cheers,
Kendra

P.S. Fingers and toes crossed for Anna's interview with EHA this Friday:)

Kendra Phelps, PhD
Research Scientist

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200
New York, NY 10018

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

> On Aug 11, 2020, at 3:47 PM, Kading,Rebekah wrote:
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> Hi Mindy, Billy, Kevin, and Kendra -
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> Take care, and I'll look forward to your feedback.
>
> Best,
> Rebekah
>
> **Rebekah C. Kading, PhD**
> Assistant Professor

Department of Microbiology Immunology and Pathology
Colorado State University

From: Dr. Melinda Rostal ecohealthalliance.org>
Sent: Friday, August 7, 2020 2:16 PM
To: Kading,Rebekah >
Cc: Kingston, Tigga ; Rodrigo Medellin Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Isabella Mandl <
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

That's great Rebekah!

Thanks! I'm happy to chat more with you about it, if that's helpful:)

~ Mindy

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Kind regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kingston, Tigga >
Sent: Friday, August 7, 2020 10:04 AM
To: Dr. Melinda Rostal ecohealthalliance.org>; Rodrigo Medellin >
Cc: Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps < ecohealthalliance.org>; Kading,Rebekah >; Isabella Mandl

Subject: RE: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Dear Melinda
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Best
Tigga

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Sent: Friday, August 7, 2020 10:39 AM
To: Rodrigo Medellin >
Cc: Kingston, Tigga < >; Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Kading,Rebekah

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The risks and mitigation strategies are really nicely laid out as you originally made it so we wouldn’t need to change that or the rest of the text/figures. We support your MAP plan.

Do you think that would be acceptable? We think it remains very consistent with your message.

If yes, what is the best way to proceed with the modification?

Kind regards,

Mindy

Melinda Rostal DVM, MPH, PhD
Principal Scientist, Vector-Borne Diseases

Rift Valley Fever Virus Project Manager

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On Aug 4, 2020, at 5:14 PM, Rodrigo Medellin > wrote:

Hi everyone

Thank you Tigga for copying me with the good email address. Mindy good talking to you again. I fully concur with Tigga about being mindful of the brains behind the infographic, and of course about any changes. If at all possible Mindy we would rather have it presented with due credits verbatim. Multiple version will be confusing, regardless of whether the different versions clash with each other. Stay safe.

--

Dr. Rodrigo A. Medellin
Instituto de Ecología, UNAM
Ap. Postal 70-275
04510 Ciudad Universitaria, D. F.
MEXICO

DIRECCION FISICA (STREET ADDRESS):

Dr. Rodrigo A. Medellín
Instituto de Ecologia, UNAM
Circuito Exterior s/n junto al Jardín Botánico Exterior
04510 Ciudad Universitaria, D. F.
MEXICO

https://www.facebook.com/rodrigo.a.medellin
https://www.instagram.com/rodrigomedellin1223/
https://twitter.com/rodrigomedellin

Check out our YouTube channel with dozens of cool, short videos on bats:https://www.youtube.com/user/RMedellinbats

http://web.ecologia.unam.mx/medellin/

On Tue, Aug 4, 2020 at 9:22 AM Kingston, Tigga < > wrote:

> Dear Mindy
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> The infographic was constructed in BioRender by Dr Rebekah Kading, so they would probably need to be manipulated in that environment. I've copied Rebekah and Dr Bella Mandl – who is also leading our graphics – on this email.
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> They have also worked up infographics for rehabbers and cavers and the original is now in a number of languages. Rebekah is a whizz at adapting the base design, but we of course need to be mindful of her time.
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> **Critically, we would need to review and sanction any changes because we don't want any messages to conflict with our own.** It would be confusing to have essentially the same graphic circulating saying different things. Our messaging is organized around the MAP concept so we don't want that disrupted, for example.
>
> Do you have a clearer idea of how you would use the infographic?
>
> Caveats aside, happy to work with you of course!!
>
> Best wishes
> Tigga
>
> P.S. I copied Rodrigo with his current email.

From: Melinda Rostal ecohealthalliance.org>
Sent: Monday, August 3, 2020 8:41 PM
To: Kingston, Tigga >; Rodrigo A. Medellín

Cc: Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Dear Tigga,
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I hope to hear from you soon about whether the Wildlife Health Specialist Group can use or modify your infographic (with the appropriate credit).

Best,
Mindy

Sent from my iPhone

On Jul 29, 2020, at 3:11 PM, Dr. Melinda Rostal ecohealthalliance.org> wrote:

> Dear Rodrigo and Tigga,
>
> Rodrigo, it's been several years since we have spoken and I hope you are well.
> I hope you are both managing to stay safe during the pandemic.
>
> I have been working with Billy Karesh, some folks from the Wildlife Health Specialist Group and the OIE to come up with some recommendations for working with free-living, wild mammals during the pandemic. We thought that the documents that the Bat Specialist Group wrote were great and we certainly refer anyone working with bats to review your guidelines as well.
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> We really liked the figure you used (pasted below) and were wondering if we could

reproduce it and/or modify it slightly in our document. We would certainly credit your group with creating it.

If it is ok to modify it, would it be possible to get a powerpoint slide or photoshop document to allow for easy modification?

I look forward to hearing from you and we would be happy to promote your work.

Kind regards,

Mindy

<PastedGraphic-3.png>

Melinda Rostal DVM, MPH, PhD
Principal Scientist, Vector-Borne Diseases

Rift Valley Fever Virus Project Manager

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New York, NY 10001

<IUCN infographic wildlife version.png>

From: Kading,Rebekah on behalf of Kading,Rebekah < >
Sent: Tuesday, August 25, 2020 12:35 PM EDT
To: William B. Karesh ecohealthalliance.org>
CC: Dr. Melinda Rostal ecohealthalliance.org>; Kevin Olival ecohealthalliance.org>; Tigga.Kingston_
; Rodrigo Medellin >; Kendra Phelps ecohealthalliance.org.test-google-a.com>; Isabella Mandl
-to-bat transmission of SARS-CoV-2 Figure
Attachment(s): "IUCN BSG MAP TRANSLATION SHEET.docx","IUCN infographic wildlife version_cc.pdf"

Hi Billy,

The pdf version should be editable, so they should be able to work directly on that and then re-save as an image file. As an alternative, if anyone in your working group or OIE has a BioRender license, I can share the infographic file directly with that person through BioRender to edit. Third option - I'm attaching a translation sheet that could be used as a template. It still has the bat infographic language on it, but if this is updated with the French and Spanish translations for the wildlife infographic, feel free to send those translations back to me and I'd be happy to update the infographic.

Hope that helps, and just let me know how you'd like to proceed.

Best regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: William B. Karesh ecohealthalliance.org>
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>; Rodrigo Medellin ; Kendra Phelps ecohealthalliance.org.test-google-a.com>; Isabella Mandl

Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Hi Rebekah and all.

Thanks again for the graphic.

OIE is distributing our joint WHSG/OIE guidelines and also translating it to French and Spanish as they normally do. They would like to change the language in the graphic also but need either the editable file or at least the background images on which they can overlay the French and Spanish. Are either of those something you could provide?

Thanks,

Billy

William B. Karesh, D.V.M
Executive Vice President for Health and Policy

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018 USA

www.ecohealthalliance.org

President, OIE Working Group on Wildlife

Co-chair, IUCN Species Survival Commission - Wildlife Health Specialist Group

EPT Partners Liaison, USAID Emerging Pandemic Threats - PREDICT-2 Program

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

On Aug 20, 2020, at 10:43 AM, Kading,Rebekah > wrote:

Hi everyone -

So sorry for the delay! I'm attaching the Infographic -- a pdf version with clickable links and a png version which may be easier for social media postings. Just let me know if you have any final suggestions. We are very happy to collaborate with you on aligning the messaging coming from our working groups on this issue - thank you again very much for reaching out about this!

Kind regards,
Rebekah

Rebekah C. Kading, PhD

Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Dr. Melinda Rostal ecohealthalliance.org>
Sent: Tuesday, August 18, 2020 8:29 AM
To: Dr. Kevin Olival ecohealthalliance.org>
Cc: Kading,Rebekah >; Tigga Kingston >; Rodrigo Medellin >; Billy Karesh ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Isabella Mandl
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Dear Tigga and Rodrigo,
Attached is the figure with the acknowledgment. The WHSG would prefer not to include logos on the figure if possible as it is positioned in the middle of our text. However, I want to ensure you are satisfied with it. So if you have any concerns about the acknowledgement, please let me know by Thursday Aug 20.

Thanks very much!

And thanks again to you and Rebekah for letting us modify your great figure:)

Best,

Mindy

Melinda Rostal DVM, MPH, PhD
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On Aug 12, 2020, at 2:49 PM, Kevin Olival <

a wider distribution.

Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
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MEXICO

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Circuito Exterior s/n junto al Jardín Botánico Exterior
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MEXICO

https://www.facebook.com/rodrigo.a.medellin
https://www.instagram.com/rodrigomedellin1223/
https://twitter.com/rodrigomedellin

Check out our YouTube channel with dozens of cool, short videos on bats:https://www.youtube.com/user/RMedellinbats
http://web.ecologia.unam.mx/medellin/

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Principal Scientist, Vector-Borne Diseases

Rift Valley Fever Virus Project Manager

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<IUCN infographic wildlife version.png>

<IUCN infographic wildlife version_cc.pdf><IUCN infographic wildlife version_cc.png>

Translation Sheet. Please translate the English to your language as closely as possibly and use the same format for the section. If you can retain the “MAP” – Minimize, Assess, Protect that is ideal, but it of course depends on the translation.
Example

Section	**English**	
Title	**Preventing human-to-bat transmission of SARS-CoV-2**	
Tagline	MAP your plan to prevent transmission to bats	
Heading 1	**Exposure Risk**	
Heading 2	*Contact exposure*	
	Bats coming into contact with contaminated hands or equipments	
Heading 2	*Aerosol exposure*	
	Infectious droplets from handler holding bats in close proximity	
Heading 2	*Environmental exposure*	
	Sharing enclosed, poorly ventilated spaces with bats, where virus may persist in the air or on surface	
Heading 1	**Mitigation strategies**	
Heading 2	*Minimize*	
	Delay, prioritize, or avoid handling bats when possible, i.e. implement acoustic surveys	
Heading 2	*Assess*	
	Postpone handling bats if there is probability that you have been exposed to SARS-CoV-2 or if you have to symptoms	
Heading 2	*Protect*	
	Adopt practices that reduce exposure, i.e. face covering, gloves, disinfection procedures	

EXAMPLE

Section	English	LANGUAGE
Title	**Preventing human-to-bat transmission of SARS-CoV-2**	**Cegah Penularan SARS-CoV-2 dari manusia-ke-kelelawar**
Tagline	MAP your plan to prevent transmission to bats	**KENAL**[1] dan rencanakan pencegahan penularan ke kelelawar [1]KENAL: Kurangi, Nilai dan Lindungi Note: Kenal in Indonesia means know, be familiar
Heading 1	**Exposure Risk**	**Risiko Paparan**
Heading 2	*Contact exposure*	*Paparan kontak*
	Bats coming into contact with contaminated hands or equipments	Kelelawar kontak langsung dengan tangan atau peralatan yang terkontaminasi
Heading 2	*Aerosol exposure*	*Paparan aerosol*
	Infectious droplets from handler holding bats in close proximity	Droplet infeksius dari pemegang kelelawar dalam jarak dekat
Heading 2	*Environmental exposure*	*Paparan lingkungan*
	Sharing enclosed, poorly ventilated spaces with bats, where virus may persist in the air or on surface	Berada satu tempat dengan kelelawar di ruang tertutup, dan minim ventilasi dimana virus dapat bertahan di udara atau di permukaan benda
Heading 1	**Mitigation strategies**	**Strategi mitigasi**
Heading 2	*Minimize*	*Kurangi*
	Delay, prioritize, or avoid handling bats when possible, i.e. implement acoustic surveys	Menunda, memprioritaskan, atau sebisa mungkin hindari memegang kelelawar, misalnya menerapkan survei akustik

Heading 2	*Assess*	*Nilai*
	Postpone handling bats if there is probability that you have been exposed to SARS-CoV-2 or if you have to symptoms	Tidak memegang kelelawar jika anda merasa ada kemungkinan terinfeksi SARS-CoV-2 atau memiliki gejala
Heading 2	*Protect*	*Lindungi*
	Adopt practices that reduce exposure, i.e. face covering, gloves, disinfection procedures	Lakukan tindakan yang dapat mengurangi paparan, seperti menggunakan pelindung wajah, masker, sarung tangan, dan langkah desinfeksi

Preventing transmission of SARS-CoV-2 from humans to wild mammals

Exposure Risks

Contact exposure
Mammals coming into contact with contaminated hands or equipment

Aerosol exposure
Infectious droplets from handlers holding mammals in close proximity

Environmental exposure
Sharing enclosed, poorly-ventilated spaces with mammals, where virus may persist in the air or on surfaces

MAP your plan to prevent transmission to mammals!

Mitigation Strategies

Minimize

Delay, prioritize, or avoid handling mammals when possible, i.e. collect environmental samples

Assess

Postpone handling mammals if there is a probability that you have been exposed to SARS-CoV-2 or if you have symptoms

Protect

Adopt practices that reduce exposure, i.e. face covering, gloves, disinfection procedures

This figure was adapted in collaboration with the IUCN Bat Specialist group.

From: Kading,Rebekah on behalf of Kading,Rebekah
Sent: Monday, August 31, 2020 12:15 AM EDT
To: Aleksei Chmura ecohealthalliance.org>
CC: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Re: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

Hi Aleksei,

This is wonderful news!! I'm thrilled for Anna. She really is a shining star and I will be sad to see her go when that time comes, but I know she has an amazing future ahead of her and its been exciting to see her career blossom already. I'd be happy to put my thoughts into a letter of recommendation this week if that's what you prefer? Otherwise Tuesday and Friday are my most open days this week for a phone call; I could talk Tuesday anytime between 1-5 Eastern time or Friday is wide open.

Best regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Aleksei Chmura ecohealthalliance.org>
Sent: Sunday, August 30, 2020 4:26 PM
To: Kading,Rebekah >
Cc: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

Dear Dr. Kading,

We just interviewed Anna Fagre for a position here at EcoHealth Alliance as a Research Scientist and Project Manager. Our hiring committee thought she was terrific with the right background and attitude for our team. Anna listed you as a reference. If you would be willing to send some comments about Anna, that would be terrific!

I have attached our position advertisement, so you may know more about the position - though based on her skillset, the specifics would evolve a bit. This position would focus primarily on our emerging infectious disease projects based in Southeast Asia including our recently awarded, NIAID funded EID-SEARCH program:

- https://www.ecohealthalliance.org/program/south-east-asia-research-collaboration-hub

I look forward to your reply and should a phone call be more convenient, we could do that as well.

On behalf of our whole committee, I sincerely appreciate your time.

-Aleksei

Aleksei Chmura, PhD
Chief of Staff

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-4182

www.ecohealthalliance.org

From: Kading,Rebekah on behalf of Kading,Rebekah
Sent: Tuesday, September 01, 2020 3:57 PM EDT
To: Aleksei Chmura ecohealthalliance.org>
CC: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Re: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

Dear Aleksei, Peter, and Hongying,

I enthusiastically recommend Dr. Anna Fagre for the Research Scientist and Project Manager position at EcoHealth Alliance.

To speak to Anna's **research experience and capability**: I've known Anna since I joined the CSU faculty in 2016, when she arranged to a rotation as part of her microbiology residency. Anna formally joined my laboratory as a PhD student in July 2017. Her dissertation is focused on the role of bats as reservoirs of emerging arboviruses, and she has made significant progress on both *in vitro* and *in vivo* studies involving bat-associated orbiviruses. The primary emphasis of these studies is on characterization of Bukakata orbivirus, a novel virus that I isolated from a fruit bat in Uganda in 2013. Bukakata orbivirus is putatively tick-borne, based on the phylogenetic analyses we have conducted. To study this virus in the broader context of other orbiviruses that have been isolated from naturally-infected bats, we acquired all three of the remaining bat-associated orbiviruses from the CDC reference collection as well as Chobar Gorge virus, a tick-borne orbivirus to which Bukakata appears to be closely related. Anna's molecular and phylogenetic characterization of Bukakata and other bat-associated orbiviruses was published in a special collection on bat viruses, in the journal Viruses (PMID: 30832334) along with a comprehensive review of the potential for bats to serve as reservoirs for arboviruses (PMID: 30832426). Since the time these papers were completed, Anna has also put significant effort into investigating the use of subgenomic RNA derived from the 3'UTR of flaviviruses to look for evidence of past infection in archived tissue samples. Because of the complex hairpin structure of the viral RNA in the 3'UTR, it is protected from RNA degradation by the exonuclease XRN1, so we hypothesized that we would find residual viral RNA that could be amplified and sequenced. After optimizing this methodology, Anna screened all of our remaining bat tissue samples from Uganda, going back 10 years, and discovered that 4 bats between 2009 – 2013 had been infected with Zika virus. Moreover, this Zika virus sequence was most similar to the Asian lineage, suggesting either diversification of Zika virus strains prior to the virus expanding into Asian in the ~1960s or spillback into Africa of the epidemic strain much earlier than we have appreciated. This manuscript is currently in review. All in all, Anna's work in my lab has been top-notch. She is meticulous and hard-working and has an excellent grasp of the molecular methodologies and big picture of how they can be applied innovatively in an ecological context. In each of these projects, she has done an excellent job leading, and taken initiatives beyond the original study scope that have made the work much stronger in the end. Her **background in veterinary medicine** has also added valuable perspective, and been very much in-demand as she has helped other laboratories on campus during this pandemic with *in vivo* studies involving SARS-CoV-2.

Other key attributes relevant to the current opportunity:

Anna is highly **collaborative,** personable, and very proactive in seeking these collaborations. This year she has re-connected with a former CSU graduate school colleague who is now in Bangladesh, and has been actively developing some research ideas and using her own funding to generate preliminary data. She also joined the VERENA consortium and has been working on a review paper with collaborators in that group. She works very well with others, as a leader of diverse teams as well as a contributing member. She has had the opportunity to contribute to a number of **international projects** both as part of my lab and during her previous experience, and is very adaptable, capable, and enthusiastic about working internationally. Over the past year she has been an invaluable member of an global initiative led by the CSU Office of the Vice President for Research, and has earned the respect of the highest CSU leadership for her contributions to this team.

Anna has been successful at **securing extramural funding**, of her own initiative. Since joining my lab, she has been awarded three highly-competitive fellowships and grants: An NIH TL1 fellowship through the Colorado Clinical and Translational Science Institute, a spot on the NIH T32 award to CSU, and the 2019 Robert E. Shope International Fellowship in Infectious Diseases through ASTMH/ACAV.

Anna is an excellent writer and **science communicator**, and also publishes frequently on blogs and other social media platforms in addition to her prolific peer-reviewed publications. She is the literature watchdog of the lab, and somehow seems to know about every relevant paper or report that is published within a half hour of it hitting the press. Anna has excellent soft skills when interacting with other professionals. She was featured in a documentary video made by CSU, and had a very natural presence and ability to clearly explain her research and general principles of disease ecology in lay terms.

In conclusion, I give Anna my highest recommendation and think she would be a fantastic addition to your team. Anna is extremely proactive, self-motivated, skilled, and has brought a wonderful energy and work ethic to my laboratory. She is an up-and-coming leader in the field, and I am thrilled to have her as part of my team. This turned out to be not-so-brief a recommendation, but I hope was a useful assessment! If you have any questions or if I can be of any additional assistance, please do not hesitate to contact me.

Best regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Aleksei Chmura ecohealthalliance.org>
Sent: Sunday, August 30, 2020 10:25 PM
To: Kading,Rebekah >
Cc: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Re: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

Dear Rebekah,

Thanks for your quick reply and it is good to read your enthusiasm about Anna! An informal, brief, and detailed email reply-to-all will be splendid - any time this week.

Much appreciated!

-Aleksei

On Aug 31, 2020, at 00:15, Kading,Rebekah > wrote:

Hi Aleksei,

This is wonderful news!! I'm thrilled for Anna. She really is a shining star and I will be sad to see her go when that time comes, but I know she has an amazing future ahead of her and its been exciting to see her career blossom already. I'd be happy to put my thoughts into a letter of recommendation this week if that's what you prefer? Otherwise Tuesday and Friday are my most open days this week for a phone call; I could talk Tuesday anytime between 1-5 Eastern time or Friday is wide open.

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Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
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Cc: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
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I look forward to your reply and should a phone call be more convenient, we could do that as well.

On behalf of our whole committee, I sincerely appreciate your time.

-Aleksei

Aleksei Chmura, PhD
Chief of Staff

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-4182

)

From: Kading,Rebekah on behalf of Kading,Rebekah >
Sent: Monday, August 31, 2020 12:36 AM EDT
To: Aleksei Chmura ecohealthalliance.org>
CC: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Re: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

Ok sounds good - I'll follow up this week.
Thanks!
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Aleksei Chmura ecohealthalliance.org>
Sent: Sunday, August 30, 2020 10:25 PM
To: Kading,Rebekah >
Cc: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Re: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

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> Department of Microbiology Immunology and Pathology
> Colorado State University
>
> ---
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> **From:** Aleksei Chmura ecohealthalliance.org>
> **Sent:** Sunday, August 30, 2020 4:26 PM
> **To:** Kading,Rebekah >
> **Cc:** Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
> **Subject:** Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance
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I look forward to your reply and should a phone call be more convenient, we could do that as well.

On behalf of our whole committee, I sincerely appreciate your time.

-Aleksei

Aleksei Chmura, PhD
Chief of Staff

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-4182

www.ecohealthalliance.org

From: Kading,Rebekah on behalf of Kading,Rebekah
Sent: Tuesday, June 02, 2020 5:25 PM EDT
To: Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) >; Grant, Evan H >; Gilbert, Amy T - APHIS >; Kevin Castle ; Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) >; epstein ecohealthalliance.org>; dreeder >; Daniel Streicker kate.e.jones Plowright, Raina wfrick ; a.peel >; Christine Kreuder Johnson
Subject: Re: SARS expert judgement - final report on the risk assessment

Thank you very much, Evan and Mike, and congratulations on completing such a tremendous amount of work! It was a pleasure to be involved in this process, and have such thorough and insightful discussions with all of you. I learned a lot, and look forward to future interactions.
Kind regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)
Sent: Tuesday, June 2, 2020 1:26 PM
To: Grant, Evan H >; Gilbert, Amy T - APHIS >; Kevin Castle ; Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) ; epstein ecohealthalliance.org>; dreeder >; Daniel Streicker >; kate.e.jones ; Kading,Rebekah ; Plowright, Raina >; wfrick >; a.peel Christine Kreuder Johnson >
Subject: RE: SARS expert judgement - final report on the risk assessment

Nice report! It was a really interesting and informative process. Many thanks for including me.
Best wishes,
Jon

Jonathan S. Towner, PhD
Lead, Virus Host Ecology Team
Viral Special Pathogens Branch
Centers for Disease Control and Prevention

From: Grant, Evan H >
Sent: Tuesday, June 2, 2020 1:39 PM
To: Gilbert, Amy T - APHIS ; Kevin Castle Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) Jon Epstein ecohealthalliance.org>; dreeder Daniel Streicker ; kate.e.jones ; Kading,Rebekah >; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) ; Plowright, Raina wfrick ; a.peel Christine Kreuder Johnson >
Subject: SARS expert judgement - final report on the risk assessment

SARS-bat Experts,
Thanks again for lending your expertise to this risk assessment. I attach here the report from this work.
Kindest regards,
Evan and Mike

From: Kading,Rebekah on behalf of Kading,Rebekah
Sent: Wednesday, April 15, 2020 10:43 AM EDT
To: Kingston, Tigga ; Cryan, Paul
CC: olival ecohealthalliance.org>
Subject: Re: SARS-CoV-2 spillback risk to North American bats

Hi Paul, Kevin, Tigga,

I'll just reply to this thread. Yes, I'd be happy to take a look at the paper as well -- thank you very much for spearheading that effort! As Tigga mentioned we're working on something as well that we'll reach out to you guys separately about. Seems like BOHRN is mobilizing on multiple fronts, which is great to see.

Take care and talk to you soon -
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kingston, Tigga
Sent: Wednesday, April 15, 2020 7:52 AM
To: Cryan, Paul ; Kading,Rebekah >
Cc: olival ecohealthalliance.org>
Subject: RE: SARS-CoV-2 spillback risk to North American bats

Hi Paul
Very interested to see the MS. Rebekah and I have been working on something that arose out of BOHRN that would be very complementary and might be worth trying to coordinate dissemination in some way. We are meeting today and will take stock of where we are at.

I just started an email to you and Kevin about the state of affairs as we Rodrigo and I are getting quite a bit of push-back on the IUCN BSG recommendation to suspend field studies while further data are gathered (primarily from western scientists with access to PPE). It would be good to hear what those committees are finding sooner rather than later.

Best wishes
Tigga

From: Cryan, Paul >
Sent: Tuesday, April 14, 2020 2:16 PM
To: Kingston, Tigga >
Cc: ecohealthalliance.org
Subject: SARS-CoV-2 spillback risk to North American bats

Hi Tigga,

Sorry for the silence since my call for help about the risks of humans potentially infecting bats in North America with the SARS-CoV-2 virus. Thanks for your patience and willingness to get involved in what we're hoping can be another disease response where scientists coming at disparate aspects of bats and pathogens can help each other. Those of us in the bat research world that focused most of our past efforts in the U.S. on conservation and management of bat populations can certainly use your expertise and help adjusting to the new situation.

A lot happened during my silence. Another group in USGS has been working at the behest of decision makers across federal and state natural resource management agencies to pull off a formal risk assessment by querying a subset of the experts we've reached out to. You lucked out and were not chosen for that exercise (yet), but we will keep you posted on the outcomes of that rapid assessment.

The other thing keeping me silent over the past couple of weeks is a short manuscript (currently 5 pages single spaced) that Kevin Olival and I drafted to articulate the potential risks of humans infecting North American temperate-zone bats with SARS-CoV-2, potentially relevant patterns we observed in bat-CoV distributions at a global scale, and the likely benefits of

disease and bat researchers working together to draw on the strengths of our various disciplines. We hope to have a draft to circulate by tomorrow and would appreciate input and feedback from any of you willing to read it and help us stress test the concepts and assertions therein. Please let me know if you are interested.

Thanks again for your help and patience.

All the best,
Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Kading,Rebekah on behalf of Kading,Rebekah >
Sent: Friday, May 22, 2020 1:32 PM EDT
To: GSE Events < ; kityrob < ; abelwade >; epstein ecohealthalliance.org>; Tigga.Kingston < >; spwa >; ian.mendenhall
CC: Stokes, Martha M CIV (USA) Jamechia Hoyle >; Katie Leahy >; Aleman, Nicki D CTR DTRA COOP THRT REDUCT (USA) >
Subject: Re: World One Health Congress and BTRP TRN Side Meeting - BOHRN

Greetings everyone! Thank you for the update - I will stay tuned to see how the situation unfolds. I am available on those dates should that work out. We could try a Zoom meeting sometime in the interim, if that would be helpful to get everyone "together"? I know many BOHRN members have been collaborating and contributing to the pandemic response in a variety of ways, which I think represents some successful grassroots mobilization of the network. Might be encouraging to have something of a group call to hear about what folks have been up to and if there's anything we can band together more formally to accomplish despite being scattered. Just an idea to throw out there!
Kind regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: GSE Events
Sent: Friday, May 22, 2020 10:51 AM
To: kityrob >; abelwade >; epstein ecohealthalliance.org>; Tigga.Kingston < ; Kading,Rebekah >; spwa >; ian.mendenhall

Cc: Stokes, Martha M CIV (USA) ; Jamechia Hoyle ; Katie Leahy ; Aleman, Nicki D CTR DTRA COOP THRT REDUCT (USA)
Subject: Re: World One Health Congress and BTRP TRN Side Meeting - BOHRN

Dear BOHRN TRN Steering Committee Members,

We hope you have been able to remain safe during these times and that this email finds you well. As you may already know, the World One Health Congress has been rescheduled to take place on October 30 - November 3 in response to worldwide travel restrictions and to coincide with International One Health Day on November 3rd. We wanted to inform you that the BTRP TRN side meetings have been rescheduled in tandem with the Congress, now aiming to take place on November 3 - 4. This is a change we are trying to implement, however, we understand the current scope of world events and anticipate further changes as we go forward. Our utmost priority is everyone's safety and we will continue to monitor the situation to act accordingly. We will be sure to keep you informed of all updates.

Please let us know if you have any questions and stay safe.

Kind Regards,

GSE Logistics Team

Global Systems Engineering, LLC
A Certified HUBZone Company
www.globalsyseng.com
signature_1234061396

From: Caitlin Devaney >
Date: Tuesday, March 10, 2020 at 2:30 PM
To: "kityrob "abelwade < >, "epstein " ecohealthalliance.org>, "Tigga.Kingston >, "Rebekah.Kading < , "spwa >, "ian.mendenhall "
Cc: "Stokes, Martha M CIV (USA)" Hoyle Katie Leahy >, Megan Hudson >, "Aleman, Nicki D CTR DTRA COOP THRT REDUCT (USA)" >

Subject: World One Health Congress and BTRP TRN Side Meeting - BOHRN

Dear BOHRN TRN Steering Committee Members,

On behalf of Dr. Martha Stokes, please accept this Save the Date to attend the World One Health Congress in Edinburgh, Scotland 15-17 June 2020 and participate in side meetings on BTRP's Threat Reduction Networks and planning for BOHRN.

Tentatively, we plan to hold two sessions at the end of the week: Thursday, 18 June - an afternoon TRN session that will include a wide group of BTRP-funded participants from its other research networks to discuss network metrics for sustainability; Friday, 19 June - a side meeting for BOHRN to map out its schedule and strategy, aligning with funding opportunities from BTRP and other entities. Attached is a tentative schedule for the week, for your reference. Due to travel and budgetary constraints we are unable to invite the entire steering committee, but intend to have productive discussions and meet objectives with the smaller group on this Save the Date email.

Please let us know if you will be able to attend the WOHC and side meetings on 18-19 June. Official invitation with travel instructions, details on arrangements, and more formal agenda will be forthcoming. Please note that there is a potential for the WOHC and BTRP side meetings to be postponed, given the current travel uncertainties related to COVID-19. We will be monitoring the status of the conference, and will keep you apprised of any cancellations should they occur. As always, let us know if you have any questions!

We hope to see you in Edinburgh!!

V/r,
Caitlin Devaney

CAITLIN DEVANEY | ***Program Manager***
Global Systems Engineering, LLC
A Certified HUBZone Company
www.globalsyseng.com

From: Kading,Rebekah on behalf of Kading,Rebekah >
Sent: Wednesday, March 11, 2020 4:25 PM EDT
To: Caitlin Devaney < >; kityrob >;
abelwade >; epstein ecohealthalliance.org>;
Tigga.Kingston >; spwa >; ian.mendenhall

CC: Stokes, Martha M CIV (USA) ; Jamechia Hoyle >; Katie Leahy
>; Megan Hudson >; Aleman, Nicki D CTR DTRA
COOP THRT REDUCT (USA) >
Subject: Re: World One Health Congress and BTRP TRN Side Meeting - BOHRN

Dear Caitlin, and hello everyone,

Thank you very much for the invitation! I would very much like to attend and participate in these discussions regarding BOHRN, but I have a couple of complications. Colorado State University currently has a restriction on international travel until further notice, but it's hard to know what things will be like in June. Hopefully that would be lifted by then. These dates also overlap with the Infectious Diseases of Bats Symposium being held at CSU June 17-19 after the American Society for Virology meeting, and I confirmed awhile ago I would participate in the bat meeting here. I think I should honor that existing commitment, which means I will not be able to attend the BOHRN steering committee meeting in Edinburgh. If this affects more steering committee members than just me, would having the BOHRN meeting in conjuction with the bat ID be a possibility? I understand if not, and I will look forward to catching up with everyone at the next opportunity!

Best regards,
Rebekah

http://www.batid.org/

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Caitlin Devaney < >
Sent: Tuesday, March 10, 2020 12:30 PM
To: kityrob ; abelwade ; epstein
ecohealthalliance.org>; Tigga.Kingston ; Kading,Rebekah
; spwa >; ian.mendenhall
>
Cc: Stokes, Martha M CIV (USA) ; Jamechia Hoyle ; Katie Leahy
; Megan Hudson < >; Aleman, Nicki D CTR DTRA COOP THRT
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We hope to see you in Edinburgh!!

V/r,
Caitlin Devaney

CAITLIN DEVANEY | ***Program Manager***
Global Systems Engineering, LLC

From: Kading,Rebekah
Sent: Tuesday, November 13, 2018 10:35 AM EST
To: Stokes, Martha M CIV (US) katie.leahy ; Megan Hudson ; Jon Epstein ecohealthalliance.org>; Kingston, Tigga >
Subject: thank you!

Dear Marty, Katie, Megan, Jon, and Tigga -

I just wanted to send a quick message to thank you for all your hard work on our BOHRN meeting last week! I know that took an amazing amount of coordination to get so many more people there, and I thought it was a very productive time! It was nice to have formal talks from some folks, and the white paper exercise was a great way to get people working together. I appreciate all the time and energy you each put into BOHRN -- it is a unique group with an important purpose and I am excited about the trajectory we are on so far! I'll look forward to touching base again soon about planning the Uganda meeting in the spring.

Take care and have a great week -

Best regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Katie Leahy
Sent: Tuesday, December 12, 2017 10:41 AM EST
To: Keti Sidamonidze < >; Robert Kityo ; Ian Mendenhall ; Joram Buza >; Vivek Kapur < ; Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Kading,Rebekah >; Lela Urushadaze Lela Urushadaze >; Tamar Kutateladze ; Supaporn Wacharapluesadee < >; Abel Wade ; Catalino Demetria ; Tigga Kingston >; Paul Cryan >; DeeAnn Reeder >; Gavin Smith >; Nisreen Alhmoud
CC: Stokes, Martha M CIV (US) >; Megan Hudson >; Lancaster, Mary J CIV (US) >; Aleman, Nicki D CTR DTRA J3-7 (US) >
Subject: BPERNet Side Meeting / PMAC

All,

By now you should have received a letter of invitation from the PMAC Organizing Committee. Please log-on and sign up to the sessions that you can attend. Our side meeting will be on the 30th at Chula Hospital. If you have confirmed attendance with us, then you should have already contacted Nicki Aleman (copied). If not, and you require travel assistance, please email me and her.

CBEP is still covering your air travel, transport to and from the airport, and hotel arrangements, so please ignore those instructions in your PMAC invitation.

Please let me know if you have any questions.

V/r,

Katie Leahy

Katie Leahy
Program Manager | Global Systems Engineering
6303 Little River Turnpike, Suite 208
Alexandria, VA 22305

http://globalsyseng.com

From: Kading,Rebekah on behalf of Kading,Rebekah >
Sent: Wednesday, January 10, 2018 10:38 AM EST
To: Katie Leahy >; lance.r.brooks >; Newman, Carl I CIV DTRA J3-7 (US) >; christopher.r.lewis ; mary.j.lancaster BounheuangK >; cryanp >; vkapur >; olival ecohealthalliance.org>; epstein ecohealthalliance.org>; ian.mendenhall ; l.urushadze >; gavin.smith abelwade >; c_demetria ; spwa >; kityrob ; tamar_kutateladze ; nisreen.hmoud >; joram.buza ; Tigga Kingston >; DeeAnn Reeder < >; Keti Sidamonidze >
CC: martha.m.stokes.civ ; Megan Hudson <
Subject: Re: Reception at U.S. Embassy (Context)

Thank you very much, Katie, for providing this context to the event. It is an honor to be invited, and I'm very much looking forward to it! A sincere thank you to CBEP as well, for all your excellent work in promoting cooperation on health issues in this region and globally. I'm looking forward to seeing all of you very soon and continuing development of the BPERNet.

Kind regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Katie Leahy
Sent: Wednesday, January 10, 2018 4:07:37 AM
To: lance.r.brooks . Newman, Carl I CIV DTRA J3-7 (US); christopher.r.lewis ; mary.j.lancaster BounheuangK ; cryanp ; Kading,Rebekah; vkapur ; ecohealthalliance.org; ecohealthalliance.org; ian.mendenhall l.urushadze gavin.smith abelwade ; c_demetria ; spwa kityrob tamar_kutateladze ; nisreen.hmoud ; joram.buza Tigga Kingston; DeeAnn Reeder; Keti Sidamonidze
Cc: martha.m.stokes. ; Megan Hudson
Subject: Reception at U.S. Embassy (Context)

All,

You likely received an invitation from “Protocol Bangkok” inviting you to a Prince Mahidol Award Reception at the U.S. Ambassador’s residence on Thursday, February 1 from 1800 – 2000.

Here is a bit of context about the event: this year, the United States became the first country to receive awards in all categories of the Prince Mahidol Awards, which are awarded annually under patronage of the Thai Royal Family to individuals and organizations that have made outstanding contributions to medicine and public health. Historically, winners have been forerunners to Nobel prizes. This year’s American awardees include the Human Genome Project and a team of researchers who developed a vaccine against Haemophilus influenza.

The U.S. Ambassador is not only proud of this historic American accomplishment, but would also like to use the opportunity to highlight the U.S. Government’s long history of military and civilian cooperation on health issues in Thailand and the greater region. The 60-year history of U.S. – Thai health cooperation is one of the lesser told success stories of the long-standing relationship with a close regional ally; and further, an alignment with the 200-year anniversary of U.S. – Thai friendship, which also occurs in 2018.

CBEP is very much a contributor to U.S.-Thai military and civilian cooperation and accomplishment on health issues; therefore, Dr. Stokes and her colleagues are co-sponsoring the celebration at the Ambassador’s residence and provided your names as their guests to the event. On behalf of her and the CBEP delegation, we very much hope you will attend.

Please let me know **if you did not receive an invitation**. Please also let me know if you have any questions. Otherwise, please follow the instructions in your invitation for favorable response.

Thank you!

V/r,

Katie Leahy

Katie Leahy
Program Manager | Global Systems Engineering
6303 Little River Turnpike, Suite 208
Alexandria, VA 22305

http://globalsyseng.com

Subject: Bat Facility meeting
Location: Microsoft Teams Meeting

Start: Tuesday, March 31, 2020 12:00 PM EDT
End: Tuesday, March 31, 2020 1:00 PM EDT
Show Time As: Tentative

Recurrence: None

Meeting Status: Not yet responded

Organizer: Kendall,Lon
Required Attendees: Kendall,Lon ; Angela Bosco-Lauth >; Bowen,Richard ; Dean,Gregg ; epstein ecohealthalliance.org>; Schountz,Tony >; Szalai,Edit >; bpope jean.patterson >; mchallberg < ; Ebel,Greg >; Cassetti, Cristina (NIH/NIAID) [E]

Here is tomorrow's agenda. Talk to you all tomorrow. You should be able to join by clicking the link below.
Introduction
Lon- why meeting was initially organized, then turf to Jon (I won't be long)
Jon- provide background about program discussions with CSU and NIAID and why we are here (Jon really sparked this discussion, and is probably best to lead)
Jean- Discuss NIAID possibilities and expectations and what's needed from CSU (Thought Jean should go sooner to help frame discussion below. I will send her agenda once we get it finalized)
Ebel- Discuss CVID abilities, and possibilities related to emerging disease, prior C06
Tony- Discuss current research and potential needs
Bowen/Angela- Discuss current research and potential needs
Determine next steps

_____
Join Microsoft Teams Meeting<https://nam01.safelinks.protection.outlook.com/ap/t-59584e83/?url=https%3A%2F%2Fteams.microsoft.com%2Fl%2Fmeetup-join%2F19%253ameeting_NzEwNWQwYWEtZDA3Yi00OTczLTgzNGMtY2Y4MGU4MWRiNDYw%2540thread.v2%2F0%3Fcontext%3D%257b%2522Tid%2522%253a%2522afb58802-ff7a-4bb1-ab21-367ff2ecfc8b%2522%252c%2522Oid%2522%253a%2522c577d4c0-7b31-47d8-891c-90b281bca62b%2522%257d&data=02%7C01%7CRichard.Bowen%40ColoState.EDU%7Ca716e5dffcb2409d015008d7d5195d2e%7Cafb58802ff7a4bb1ab21367ff2ecfc8b%7C0%7C0%7C637212177216827495
Learn more about Teams<https://nam01.safelinks.protection.outlook.com/?url=https%3A%2F%2Faka.ms%2FJoinTeamsMeeting&data=02%7C01%7CRichard.Bowen%40ColoState.EDU%7Ca716e5dffcb2409d015008d7d5195d2e%7Cafb58802ff7a4bb1ab21367ff2ecfc8b%7C0%7C0 | Meeting options<https://nam01.safelinks.protection.outlook.com/?url=https%3A%2F%2Fteams.microsoft.com%2FmeetingOptions%2F%3ForganizerId%3Dc577d4c0-7b31-47d8-891c-90b281bca62b%26tenantId%3Dafb58802-ff7a-4bb1-ab21-367ff2ecfc8b%26threadId%3D19_meeting_NzEwNWQwYWEtZDA3Yi00OTczLTgzNGMtY2Y4MGU4MWRiNDYw%40thread.v2%26messageId%3D0%26language%3Den-US&data=02%7C01%7CRichard.Bowen%40ColoState.EDU%7Ca716e5dffcb2409d015008d7d5195d2e%7Cafb58802ff7a4bb1ab21367ff2ecfc8b%7C0%7C0%7C637212177216827495&sdata=2GJzTgA9u
_____

From: Tony Schountz > on behalf of Schountz,Tony >
Sent: Wednesday, October 21, 2020 3:33 PM EDT
To: epstein ecohealthalliance.org>
Subject: Genome paper

Jon, I suspect you've seen this?

https://www.frontiersin.org/articles/10.3389/fmicb.2020.01807/full

Should be quite helpful for the grant.

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Tony Schountz > on behalf of Schountz,Tony <
Sent: Monday, October 19, 2020 4:27 PM EDT
To: epstein ecohealthalliance.org>
Subject: Monoclonal antibodies

Jon, I think a really important part of the grant will be to make monoclonal antibodies to various proteins (e.g., CD antigens, cytokines) and cytokines as reagents. If you agree, I'd like to approach a colleague of my, Brian Geiss, to see if he is willing to be on the grant. Recombinant protein expression is his "thing" and he would be a great asset for the grant.

I also think we should get as many letters of support that we can get. I can probably get at least 10 from people we've helped over the years (provided tissues and cells, conducted experimental infections, etc.).

Let me know what you think.

Just moved into our new building. It is really sweet. :)

Thanks,

T.

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Tony Schountz on behalf of Schountz,Tony <
Sent: Wednesday, October 21, 2020 4:28 PM EDT
To: epstein ecohealthalliance.org>
Subject: Re: Genome paper

Yes, I'd like to start on it next week. I have some grading to do this week plus interviews for DVM/PhD candidates for our program, so calendar is quite full. Next week is pretty good for me except (MST) Monday 2-3, Tues 12-2, Wed 3-5. Any of those work for you?

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Oct 21, 2020, at 2:05 PM, Jon Epstein ecohealthalliance.org> wrote:

Yes! I agree.

Should we schedule a time to talk? So we can start to organize for writing this thing?

On Wed, Oct 21, 2020 at 3:33 PM Schountz,Tony > wrote:

> Jon, I suspect you've seen this?
>
> https://www.frontiersin.org/articles/10.3389/fmicb.2020.01807/full
>
> Should be quite helpful for the grant.
>
> T.
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

)

web: ecohealthalliance.org

From: Tony Schountz on behalf of Schountz,Tony >
Sent: Monday, October 19, 2020 4:40 PM EDT
To: epstein ecohealthalliance.org>
Subject: Re: Monoclonal antibodies

It would be a great idea to have another building in-country for housing and staging bats for quarantine before shipping to USA.

Getting on a call with DARPA in a few minutes, so won't be responsive for an hour or so.

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Oct 19, 2020, at 2:38 PM, Jon Epstein ecohealthalliance.org> wrote:

Awesome - and agree.
I would like to brainstorm together for the letters before we approach anyone. I'll start a google doc and we can live edit it.
Let's think about who the 'dream team' will be for this.
It also occurred to me - what do you think about building in a facility in Bangladesh where we keep a captive breeding colony, that would serve as a feeder if we need more bats along the way? We could develop and fund a closed colony there, like what Cambridge did in Ghana, and we'd know the status of each bat. Brian Pope would be great at helping set this up. And it would allow the colony at CSU to fluctuate a bit in size, and we could pull in new bats as needed. I think it's a nice insurance policy to support the colony in CO as we develop it. This could be something I would manage - but I think we could convince the govt and if we provide all the funding for construction and upkeep, it could really happen.

Thoughts?

On Mon, Oct 19, 2020 at 4:27 PM Schountz,Tony wrote:

> Jon, I think a really important part of the grant will be to make monoclonal antibodies to various proteins (e.g., CD antigens, cytokines) and cytokines as reagents. If you agree, I'd like to approach a colleague of my, Brian Geiss, to see if he is willing to be on the grant. Recombinant protein expression is his "thing" and he would be a great asset for the grant.
>
> I also think we should get as many letters of support that we can get. I can probably get at least 10 from people we've helped over the years (provided tissues and cells, conducted experimental infections, etc.).
>
> Let me know what you think.
>
> Just moved into our new building. It is really sweet. :)
>
> Thanks,
>
> T.
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

web: ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

From: Tony Schountz > on behalf of Schountz,Tony < >
Sent: Wednesday, October 07, 2020 3:58 PM EDT
To: Woodson, Sara (NIH/NIAID) [E] >
CC: epstein ecohealthalliance.org>; Schountz,Tony ; Ebel,Greg >; jean.patterson ; Challberg, Mark (NIH/NIAID) [E]

Subject: Re: R24 Discussion

Yes, thanks much, Sara. I appreciate that you, Jean and Mark chatted with us today.

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Oct 7, 2020, at 1:51 PM, Woodson, Sara (NIH/NIAID) [E] wrote:

Hi Tony, Jon, and Greg;
Here are the example R24's you may want to look up in NIH Reporter:

R24AI059830 PI: Jacques Robert (University of Rochester, animal model containing)
R24AI120942 PI: Scott Weaver (University of Texas Medical Branch, WRCEVA—no model development but may be relevant if thinking about including training; may also be good to link in with them for potential distribution of critical reagents along with BEI Resources)

As Mark mentioned on the phone, NIAID doesn't allow a lot of R24 grants and thus not many are funded, so there aren't many relevant examples to what you would be putting forth in your R24. Please let me know if you have other questions or concerns!
Happy writing 😊
Sincerely, Sara

-----Original Appointment-----
From: Woodson, Sara (NIH/NIAID) [E]
Sent: Wednesday, September 30, 2020 1:22 PM
To: Woodson, Sara (NIH/NIAID) [E]; ecohealthalliance.org; Schountz, Tony; Ebel,Greg; Patterson, Jean (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Beaubien, Candice (NIH/NIAID) [E]
Subject: R24 Discussion
When: Wednesday, October 7, 2020 3:00 PM-3:30 PM (UTC-05:00) Eastern Time (US & Canada).
Where: Skype Meeting

Please use this Zoom link for our meeting this afternoon instead…..

https://www.zoomgov.com/j/1614258516?pwd=bGVHUDFrbHVxWm91M2ZGUEdWcXF4QT09

Sincerely, Sara

From: Tony Schountz
Sent: Tuesday, March 07, 2017 7:05 AM EST
To: peng.zhou
CC: Schountz,Tony >
Subject: Bat ID Abstract Submission

Thank you for submitting an abstract to the Bat ID Symposium. A decision on its disposition will be made in May.

Bat ID Abstract Submission

Presenting author email address *	
Presentation Type *	Oral Presentation
Please choose ONE or TWO categories for your abstract *	• Immunology
Title *	Dampening of STING-dependent IFN production: an implication of virus tolerance in bats?
Authors *	Xie J, Ma C, Li Y, Cui J, Wang L-F, Shi Z, Zhou P*
Institutions *	Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan 430071, China; Emerging Infectious programme, Singapore Duke-NUD Medical School, Singapore 169857, Singapore
Upload your abstract *	us_bat_conference_peng_zhou_oral1.docx 14.40 KB · DOCX

From: Tony Schountz
Sent: Wednesday, March 29, 2017 9:37 AM EDT
To: zlshi <
CC: Schountz,Tony
Subject: Bat ID Abstract Submission

Thank you for submitting an abstract to the Bat ID Symposium. A decision on its disposition will be made in May.

Bat ID Abstract Submission

Presenting author email address *	
Presentation Type *	Oral Presentation
Please choose ONE or TWO categories for your abstract *	• Coronaviruses
Title *	SARS coronavirus may have originated from frequent recombination events between SARS-like coronaviruses in a single horseshoe bat habitat
Authors *	Hu B, Zeng L-P, Yang X-L, Ge X-Y, Zhang W, Li B, Luo D-S, Zhang Y-Z, Wang M-N, Daszak P, Wang L-F, Cui J, Shi Z-L.
Institutions *	CAS Key Laboratory of Special Pathogens and Biosafety, Center for Emerging Infectious Diseases of Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China; Yunnan Institute of Endemic Diseases Control and Prevention, Dali, China; EcoHealth Alliance, New York, New York, USA; Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore
Upload your abstract *	us_bat_conference_zhengli_shi_oral.docx 16.38 KB · DOCX

From: Tony Schountz >
Sent: Saturday, April 01, 2017 9:20 PM EDT
To: huben >
CC: Schountz,Tony
Subject: Bat ID Abstract Submission

Thank you for submitting an abstract to the Bat ID Symposium. A decision on its disposition will be made in May.

Bat ID Abstract Submission

Presenting author email address *	
Presentation Type *	Poster Presentation
Please choose ONE or TWO categories for your abstract *	• Coronaviruses
Title *	Genomic characterization of diverse BatCoV HKU10 and three novel alphacoronaviruses
Authors *	Wang N, Luo CM, Yang XL, Liu HZ, Zhang W, Li B, Ge XY, Hu B, Zhu Y, Peng C, Shi ZL
Institutions *	Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan 430071, China.
Upload your abstract *	us_bat_conference_ben_hu_poster.docx 17.15 KB · DOCX

From: Tony Schountz >
Sent: Saturday, April 01, 2017 3:51 AM EDT
To: yangx
CC: Schountz,Tony
Subject: Bat ID Abstract Submission

Thank you for submitting an abstract to the Bat ID Symposium. A decision on its disposition will be made in May.

Bat ID Abstract Submission

Presenting author email address *	
Presentation Type *	Poster Presentation
Please choose ONE or TWO categories for your abstract *	• Filoviruses
Title *	Genetically Diverse Filoviruses in Rousettus and Eonycteris spp. Bats, China, 2009 and 2015
Authors *	Xing-Lou Yang, Yun-Zhi Zhang, Ren-Di Jiang, Hua Guo, Wei Zhang, Bei-Li, Ning Wang, Li-Wang, Cecilia Waruhiu, Ji-Hua Zhou, Shi-Yue Li, Peter Daszak, Lin-Fa Wang, Zheng-Li Shi
Institutions *	Wuhan Institute of Virology, Chinese Academy of Sciences
Upload your abstract *	abstract_for_bat_virus_meeting.docx 19.29 KB · DOCX

From: Schountz,Tony
Sent: Thursday, April 27, 2017 12:58 PM EDT
To: Schountz,Tony
CC: huben >
Subject: Re: Bat ID Abstract Submission

Dear Ben,

Your abstract submission has been accepted for a **POSTER** presentation. The session is **Friday, April 30 from 12:00 to 2:00 PM** in the University Center for the Arts. The maximum size of your poster **should not exceed 122 cm/48 inches height and width**. We will provide push pins for mounting your poster on the easel. If you have questions, please feel free to contact me.

Thank you and we look forward to your presentation.

Tony Schountz

On Apr 1, 2017, at 7:20 PM, Tony Schountz > wrote:

Thank you for submitting an abstract to the Bat ID Symposium. A decision on its disposition will be made in May.

Bat ID Abstract Submission

Presenting author email address *	
Presentation Type *	Poster Presentation
Please choose ONE or TWO categories for your abstract *	• Coronaviruses
Title *	Genomic characterization of diverse BatCoV HKU10 and three novel alphacoronaviruses
Authors *	Wang N, Luo CM, Yang XL, Liu HZ, Zhang W, Li B, Ge XY, Hu B, Zhu Y, Peng C, Shi ZL
Institutions *	Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan 430071, China.
Upload your abstract *	us_bat_conference_ben_hu_poster.docx 17.15 KB · DOCX

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony >
Sent: Thursday, April 27, 2017 12:47 PM EDT
To: Schountz,Tony
CC: yangxl >
Subject: Re: Bat ID Abstract Submission

Dear Xing-Lou,

Your abstract submission has been accepted for a **POSTER** presentation. The session is **Friday, April 30 from 12:00 to 2:00 PM** in the University Center for the Arts. The maximum size of your poster **should not exceed 122 cm/48 inches height and width**. We will provide push pins for mounting your poster on the easel. If you have questions, please feel free to contact me.

Thank you and we look forward to your presentation.

Tony Schountz

> On Apr 1, 2017, at 1:51 AM, Tony Schountz > wrote:
>
> Thank you for submitting an abstract to the Bat ID Symposium. A decision on its disposition will be made in May.
>
> ## Bat ID Abstract Submission
>
> | | |
> |---|---|
> | **Presenting author email address** * | |
> | **Presentation Type** * | Poster Presentation |
> | **Please choose ONE or TWO categories for your abstract** * | • Filoviruses |
> | **Title** * | Genetically Diverse Filoviruses in Rousettus and Eonycteris spp. Bats, China, 2009 and 2015 |
> | **Authors** * | Xing-Lou Yang, Yun-Zhi Zhang, Ren-Di Jiang, Hua Guo, Wei Zhang, Bei-Li, Ning Wang, Li-Wang, Cecilia Waruhiu, Ji-Hua Zhou, Shi-Yue Li, Peter Daszak, Lin-Fa Wang, Zheng-Li Shi |
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> | **Upload your abstract** * | abstract_for_bat_virus_meeting.docx
19.29 KB · DOCX |

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: 石正丽 <zlshi >
Sent: Wednesday, April 26, 2017 8:32 PM EDT
To: Schountz,Tony
Subject: Re: Re: Bat ID Abstract Submission

Dear Tony,

Thank you very much for your information and organising the meeting!

Looking forward to meeting you!

Best regards,

Zhengli,

-----原始邮件-----
发件人: "Schountz,Tony"
发送时间: 2017年4月27日 星期四
收件人: "Schountz,Tony"
抄送: "zlshi
主题: Re: Bat ID Abstract Submission

Dear Dr. Shi,

We have you scheduled to give a 15 min talk (12 minutes plus 3 minutes for questions) at the bat infectious diseases symposium, probably Friday morning, June 30. I should have the program draft up next week.

Thanks,

Tony

On Mar 29, 2017, at 7:37 AM, Tony Schountz > wrote:

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Bat ID Abstract Submission

Presenting author email address *	
Presentation Type *	Oral Presentation
Please choose ONE or TWO categories for your abstract *	• Coronaviruses
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Institutions *	CAS Key Laboratory of Special Pathogens and Biosafety, Center for Emerging Infectious Diseases of Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China; Yunnan Institute of Endemic Diseases Control and Prevention, Dali, China; EcoHealth Alliance, New York, New York, USA; Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore
Upload your abstract *	us_bat_conference_zhengli_shi_oral.docx 16.38 KB · DOCX

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: zlshi >
Sent: Wednesday, July 12, 2017 9:39 PM EDT
To: Schountz,Tony >
CC: 周鹏 <peng.zhou linfa.wang
Subject: 回复: Re: Bat ID Abstract Submission

Dear Tony,

Thank you for your organizing the nice bat ID symposium. We enjoy very much th discussion with the scientists of different speciality.

Thank you for your considering to participate in the meeting "8th International symposium on emerging viral dieases" to be held in Wuhan in Ocotber, 2018. We will add you at the email distribution list and let you know as soon as we have a fixed date. Usually, the meeting will be held at the 4th week with the duration of 3 days (with 2 days of scientifc activity).

Looking forward to meeting you again,

Best regards,
Zhengli,

发件人： Schountz,Tony
发送时间： 2017-07-13 08:16
收件人： 石正丽
主题： Re: Re: Bat ID Abstract Submission

Hi Zhengli,

I hope your travel home was peaceful. I wanted to thank you for your attendance and presentation at the bat ID symposium. I think it was a very good meeting and I hope others benefited from it. We are already planning to host it again in 2020.

If you have an email distribution list for the conference you're hosting next year, could you please add me to it? It looks like a great meeting and if I can get travel arranged I would like to come.

Thank you,

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: 石正丽 <zlshi >
Sent: Wednesday, April 26, 2017 6:32 PM
To: Schountz,Tony
Subject: Re: Re: Bat ID Abstract Submission

Dear Tony,
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Best regards,

Zhengli,

-----原始邮件-----
发件人: "Schountz,Tony"
发送时间: 2017年4月27日 星期四
收件人: "Schountz,Tony"
抄送: "zlshi "
主题: Re: Bat ID Abstract Submission

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Institutions *	CAS Key Laboratory of Special Pathogens and Biosafety, Center for Emerging Infectious Diseases of Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China; Yunnan Institute of Endemic Diseases Control and Prevention, Dali, China; EcoHealth Alliance, New York, New York, USA; Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore
Upload your abstract *	us_bat_conference_zhengli_shi_oral.docx 16.38 KB · DOCX

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

Subject: Bat Facility meeting
Location: Microsoft Teams Meeting

Start: Tuesday, March 31, 2020 12:00 PM EDT
End: Tuesday, March 31, 2020 1:00 PM EDT
Show Time As: Busy

Recurrence: None

Meeting Status: Not yet responded

Organizer: Kendall,Lon
Required Attendees: Kendall,Lon >; Angela Bosco-Lauth < >; Bowen,Richard < ; Dean,Gregg ; epstein ecohealthalliance.org>; Schountz,Tony >; Szalai,Edit bpope < >; jean.patterson ; mchallberg >; Ebel,Greg >; Cassetti, Cristina (NIH/NIAID) [E]

Here is tomorrow's agenda. Talk to you all tomorrow. You should be able to join by clicking the link below.
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Ebel- Discuss CVID abilities, and possibilities related to emerging disease, prior C06
Tony- Discuss current research and potential needs
Bowen/Angela- Discuss current research and potential needs
Determine next steps

Join Microsoft Teams Meeting<https://nam01.safelinks.protection.outlook.com/ap/t-59584e83/?url=https%3A%2F%2Fteams.microsoft.com%2Fl%2Fmeetup-join%2F19%253ameeting_NzEwNWQwYWEtZDA3Yi00OTczLTgzNGMtY2Y4MGU4MWRiNDYw%2540thread.v2%2F0%3Fcontext%3D%257b%2522Tid%2522%253a%2522afb58802-ff7a-4bb1-ab21-367ff2ecfc8b%2522%252c%2522Oid%2522%253a%2522c577d4c0-7b31-47d8-891c-90b281bca62b%2522%257d&data=02%7C01%7CTony.Schountz%40colostate.edu%7Ca716e5dffcb2409d015008d7d5195d2e%7Cafb58802ff7a4bb1ab21367ff2ecfc8b%7C0%7C0%7C637212177217988770
Learn more about Teams<https://nam01.safelinks.protection.outlook.com/?url=https%3A%2F%2Faka.ms%2FJoinTeamsMeeting&data=02%7C01%7CTony.Schountz%40colostate.edu%7Ca716e5dffcb2409d015008d7d5195d2e%7Cafb58802ff7a4bb1ab21367ff2ecfc8b%7C0%7C0 | Meeting options<https://nam01.safelinks.protection.outlook.com/?url=https%3A%2F%2Fteams.microsoft.com%2FmeetingOptions%2F%3ForganizerId%3Dc577d4c0-7b31-47d8-891c-90b281bca62b%26tenantId%3Dafb58802-ff7a-4bb1-ab21-367ff2ecfc8b%26threadId%3D19_meeting_NzEwNWQwYWEtZDA3Yi00OTczLTgzNGMtY2Y4MGU4MWRiNDYw%40thread.v2%26messageId%3D0%26language%3Den-US&data=02%7C01%7CTony.Schountz%40colostate.edu%7Ca716e5dffcb2409d015008d7d5195d2e%7Cafb58802ff7a4bb1ab21367ff2ecfc8b%7C0%7C0%7C637212177217988770&sdata=wiFrH%2Fv

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From: jid_oup o>
Sent: Monday, January 13, 2020 1:01 AM EST
To: vincent.munster >; jnls.author.support ;
jonathan.schulz >; stephanie.seifert < ;
jthompson >; victoria.avanzato
lianying.yan. >; spencer.sterling.ctr
; michael.letko ; matthew.matson
; fischerro < >; atremeau
; jseetahal ; vernie.ramkisson
>; jerome.foster >; tgoldstein
; sja ; epstein
ecohealthalliance.org>; eric.laing ; christopher.broder
; christine.carrington >; Schountz,Tony

Subject: Action needed: check your proof 10.1093/infdis/jiz648

Dear Dr. Vincent Munster,

You must check your proof now to avoid delaying publication.

What you need to do now:

1. Access your proof https://pubkit.newgen.co/auth_token_login/af89fcf9-b35f-40b5-a782-420952f1a4a4

2. Respond on the proof to any copyeditor queries.

3. Approve your proof for publication or submit minor formatting corrections within one working day.

Please note that this is causing a delay to the publication of your manuscript. Please contact us if you need any help.

Best wishes,

The Journal of Infectious Diseases production team

Oxford University Press

From: 胡犇 <huben >
Sent: Friday, September 28, 2018 11:17 PM EDT
To: Schountz,Tony >
Subject: Agenda of the 8th International Symposium of Emerging Viral Diseases
Attachment(s): "Program of the 8th ISEVD.pdf"

Dear speaker:

We have made the program for our emerging virus symposium. Your presentation is scheduled in the afternoon of 21st October, in the session "emerging viral pathogens".

I have attached the program for your information.

We have reserved accommodation for you at the conference venue, Optic Valley Plaza hotel. Please provide me your flight information once it is available, and we will arrange pick-up service at the airport.

Also, please send me your update CV by 7th October, as we would like to include the CV of our speakers together with the abstracts in the conference proceedings.

Thank you!

Best wishes

Ben Hu Ph.D

Wuhan Institute of Virology, CAS
Secretary of the 8th ISEVD

Program of
The 8th International Symposium on Emerging Viral Diseases

Date 日期	Time 时间	Content 议程
Saturday 星期六 Oct. 20, 2018 10 月 20 日	**Venue 地点** 09:00-21:00	**Registration**/报到注册 Ground Floor, Optics Valley Kingdom Plaza Hotel/光谷金盾大酒店一楼大厅
Sunday 星期日 Oct. 21, 2018 10 月 21 日	**Day 1, Morning Session /第一天上午**	
	Venue 地点	Banquet Hall of Optics Valley Kingdom Plaza 3nd floor of the hotel 光谷金盾大酒店三楼宴会厅
	08:30-08:40	**Opening Address/开幕式致词**
	08:40-11:50	**Session 1: Antiviral Immunity** **Session Chairs: Peng ZHOU, Linfa WANG**
	08:40-09:10 Keynote Speech S-01	**Title:** Holy immune balance, batman! **Speaker: Linfa Wang** Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore
	09:10-09:30 S-02	**Title: To be determined** **Speaker: Yanyi Wang** Wuhan Institute of Virology, Chinese Academy of Sciences
	09:30-09:50	Group Photo of Symposium Participants/与会代表合影 Coffee Break /茶歇
	09:50-10:10 S-03	**Title:** Recent advances in developing therapeutics monoclonal antibodies Against Ebola Virus Infection **Speaker: Xiangguo Qiu** Special Pathogens Program, National Microbiology laboratory, Public Health Agency of Canada
	10:10-10:30 S-04	**Title:** Nipah virus and Hendra Virus: Basic Science to Global Countermeasures **Speaker: Christopher Broder** Department of Microbiology, Uniformed Services University, Bethesda, MD, USA
	10:30-10:50 S-05	**Title:** Immunopathogenesis of Nipah virus infection **Speaker: Branka Horvat** International Center for Infectiology Research - CIRI, INSERM U1111, University Lyon 1, France
	10:50-11:10 S-06	**Title:** Incorporation of NS1 and PrM/M confer more effective protection for ZIKA virus vaccine **Speaker: Ling Chen** Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences, Guangzhou, China

11:10-11:30 S-07	**Title:** Antiviral RNAi immunity – from basic to translation **Speaker: Xi Zhou** Wuhan Institute of Virology, Chinese Academy of Sciences
11:30-11:50 S-08	**Title:** To be determined **Speaker: Shi Liu** Wuhan University, China
11:50-12:05 Sponsor Presentation	Newly Technology development of Cryo TEM by JEOL **By Jianzhong Yuan** TEM product manager of JEOL in China
12:05-14:00	Lunch/午餐
Day 1, Afternoon Session /第一天下午	
14:00-17:30	**Session 2: Emerging viral pathogens** **Session Chairs: Zhengli SHI, Peter DASZAK**
14:00-:14:30 Keynote Speech S-09	**Title:** To be determined **Speaker: Hualan Chen** Harbin Veterinary Research Institute, Chinese Academy of Agricultural Sciences, Harbin, China
14:30-14:50 S-10	**Title:** Forecasting future viral pandemics and the Global Virome Project **Speaker: Peter Daszak** EcoHealth Alliance, New York, USA
14:50-15:10 S-11	**Title:** Infection and Immune Responses of Jamaican Fruit Bats (*Artibeus jamaicensis)* Experimentally Challenged with a Bat HL18NL11 Influenza A Virus **Speaker: Tony Schountz** Department of Microbiology, Immunology and Pathology, College of Veterinary Medicine and Biomedical Sciences, Colorado State University
15:10-15:30 S-12	**Title:** To be determined **Speaker: Di Liu** Wuhan Institute of Virology, Chinese Academy of Sciences
15:30-15:50	Coffee Break and Poster Presentation/茶歇和展板
15:50-16:10 S-13	**Title:** Risks of MERS-cluster coronaviruses in China **Speaker: Peng Zhou** Wuhan Institute of Virology, Chinese Academy of Sciences
16:10-16:30 S-14	**Title:** Molecular mechanisms for cross-species transmissions of SARS and MERS coronaviruses **Speaker: Fang Li** Department of Veterinary and Biomedical Sciences, University of Minnesota
16:30-16:50 S-15	**Title:** Human coronavirus OC43 (HCoV-OC43) and bovine coronavirus (BCoV) **Speaker: Astrid Vabret** Laboratory of Virology, University Hospital of Caen, France

	16:50-17:10 S-16	**Title:** Origin and cross-species transmission of bat coronaviruses in China **Speaker: Alice Latine** EcoHealth Alliance, New York, USA
	17:10-17:30 S-17	**Title:** Coronaviruses phylogenetics and intra-colony evolution of the SARS-CoV sister-clade Betacoronavirus in bats in western Palearctics **Speaker: Meriadeg Ar Gouilh** Groupe de Recherche sur l'Adaptation Microbienne, Normandy University, France
	18:00-20:00	Banquet 会议晚宴

Program of
The 8th International Symposium on Emerging Viral Diseases

Date 日期	Time 时间	Content 议程
Monday 星期一 Oct. 22, 2018 10 月 22 日		**Day 2, Morning Session /第二天上午**
	08:30-12:10	**Session 3: Virus-Host Interaction** **Session Chair: Xi ZHOU, Ralph BARIC**
	08:30-09:00 Keynote Speech S-18	**Title:** To be determined **Speaker: Ralph Baric** Department of Epidemiology, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA
	09:00-09:30 Keynote Speech S-19	**Title:** Peptide-based Virus Entry Inhibitors against Class I and II Enveloped Viruses **Speaker: Shibo Jiang** Basic Medical College, Fudan University, Shanghai, China
	09:30-09:50 S-20	**Title:** Small molecules as filoviral entry inhibitors and chemical probes **Speaker: Lijun Rong** Department of Microbiology and Immunology, College of Medicine, University of Illinois at Chicago, Chicago, IL, USA
	09:50-10:10 S-21	**Title:** Entry mechanisms of highly pathogenic coronaviruses: MERS-CoV and SARS-CoV **Speaker: Yi Shi** CAS Key Laboratory of Pathogenic Microbiology and Immunology, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China
	10:10-10:30	Coffee Break and Poster Presentation/茶歇和展板
	10:30-10:50 S-22	**Title:** Pathology of and development of antiviral therapy with favipiravir for severe fever with thrombocytopenia syndrome **Speaker: Masayuki Saijo** Department of Virology, National Institute of Infectious Diseases, Tokyo, Japan
	10:50-11:10 S-23	**Title:** Epistasis and complementation contribute to the evolution of the Rabies virus phosphoprotein in the face of severe functional constraints within the replication complex **Speaker: Hervé Bourhy** Institut Pasteur, Unit of Lyssavirus Dynamics and Host Adaptation, Paris, France
	11:10-11:30 S-24	**Title:** Influenza A virus-derived siRNAs increase in the absence of NS1 yet fail to inhibit virus replication **Speaker: Kevin Tsai** Department of Molecular Genetics and Microbiology, Duke University Medical Center, Durham, North Carolina, USA

	11:30-11:50 S-25	**Title:** Mechanisms of Herpesvirus capsid assembly and maturation **Speaker: Xiangxi Wang** Institute of Biophysics, Chines Academy of Sciences, Beijing, China
	11:50-12:10 S-26	**Title:** To be determined **Speaker: Yu Chen** Wuhan University, China
	12:10-13:40	Lunch/午餐
	Day 2, Afternoon Session /第二天下午	
	13:40-17:30	**Session 4: Arbovirus** **Session Chairs: Zhihong HU, Pei-Yong SHI**
	13:40-14:10 Keynote Speech S-27	**Title:** Zika Virus: Emergence and Vaccine Development **Speaker: Pei-Yong Shi** University of Texas Medical Branch, Galveston, Texas, USA
	14:10-14:30 S-28	**Title:** Replicase Proteins of Alphaviruses as Determinants of Viral Pathogenesis and Vector Transmission **Speaker: Andres Merits** Institute of Technology, University of Tartu, Estonia
	14:30-14:50 S-29	**Title:** Identification of prognostic biomarkers for Dengue disease severity through an integrated 'omics analysis of patient serum **Speaker: Andrew Davidson** University of Bristol, Bristol, United Kingdom
	14:50-15:10 S-30	**Title:** Zika virus tropism for neural stem cells: the bad and the good **Speaker: Cheng-Feng Qin** Beijing Institute of Microbiology and Epidemiology, Academy of Military Medical Sciences, Beijing, China
	15:10-15:30 S-31	**Title:** A gut commensal bacterium promotes mosquito permissiveness to arboviruses **Speaker: Gong Cheng** Tsinghua-Peking Center for Life Sciences, School of Medicine, Tsinghua University, Beijing, China
	15:30-15:50	Coffee Break 茶歇
	15:50-16:10 S-32	**Title:** The fabulous NSs protein of Rift Valley fever virus **Speaker: Pierre-Yves Lozach** Cluster of Excellence and Center for Integrative Infectious Disease Research, University Hospital Heidelberg, Germany
	16:10-16:30 S-33	**Title:** Novel delivery of a live-attenuated chikungunya virus vaccine candidate **Speaker: Adam Taylor** Griffith University, Southport, Queensland, Australia

	16:30-16:50 S-34	**Title:** To be determined **Speaker: Fei Deng** Wuhan Institute of Virology, Chinese Academy of Sciences
	16:50-17:10 S-35	**Title:** Species-specific disruption of STING-dependent antiviral cellular defenses by the Zika virus NS2B3 protease **Speaker: Qiang Ding** School of Medicine, Tsinghua University, Beijing, China
	17:10-17:30 S-36	**Title:** ISG15 regulates Zika Virus Replication through Jak/STAT Signaling pathway and its ISGylation **Speaker: Yancui Wang** Institute of Blood Transfusion, Chinese Academy of Medical Sciences and Peking Union Medical College, Chengdu, China
	17:30-17:40	**Closing Remarks**
	18:00-19:00	Dinner/晚餐

From: Roberto Bruzzone
Sent: Wednesday, July 15, 2020 2:08 AM EDT
To:

Subject: ASCB/EMBO Online Meeting

Dear All,

I would like you to consider submitting abstracts to the 2020 ASCB/EMBO Meeting, which will go virtual.
https://www.ascb.org/cellbiovirtual2020/program/

I will be co-chairing a mini-symposium in the scientific track, Cells in Distress and Disease

My initial proposal focused on host-pathogen interactions at a molecular level.

We are currently accepting abstracts for consideration to give a talk in the 2020 Minisymposia.

The deadline for submission is July 30.
https://www.ascb.org/cellbiovirtual2020/abstracts

PLEASE SHARE THIS INFORMATION WITH OTHER COLLEAGUES WHO MAY BE INTERESTED. THANKS

All the best, Roberto

Professor Roberto Bruzzone
Co-Director
HKU-Pasteur Research Pole
School of Public Health
LKS Faculty of Medicine
The University of Hong Kong

7/F, HKJC Building for IR, 5 Sassoon Road, Pokfulam, Hong Kong

website: www.hkupasteur.hku.hk
http://isaric.tghn.org/

From: Lee, Benhur
Sent: Monday, March 02, 2020 7:51 PM EST
To: Schountz,Tony
CC: Jon Epstein ecohealthalliance.org>; Anthony, Simon J.
Subject: Bat Challenge

Hi Tony,

Sorry for late notice, but I didn't want to promise something this time without following through, so Simon (Anthony) can actually vouch for me.

STRICTLY CONFIDENTIAL-For your eyes (and ears) ONLY.
If you are free tomorrow at about 4 pm EST, can you Skype or Zoom in (I'm sure Jon Epstein can figure something out). I'm presenting data to relevant company at EcoHealth Alliance.

Anything bat-related is, of course, hot right now. So, this time, if you agree to help, yours will be the last experiment, not the first.

Meanwhile, if you get this message in time, can you let us know (Simon and Jon is CC-ed on this email) what species of bat you have in your colony? It's important for us to check something before hand.

Thanks! (Again, I apologize for the short notice, what's left of my life has been consumed by my second full-time job on Twitter)

Best regards,

Benhur

Benhur Lee, M.D.
Professor of Microbiology
Ward-Coleman Chair in Microbiology
Icahn School of Medicine at Mount Sinai
One Gustave L Levy Place #1124
New York, NY 10029

Lab Webpage: LeeLabVirus.Host |

From: Kendall,Lon >
Sent: Tuesday, March 17, 2020 1:25 PM EDT
To: Jon Epstein ecohealthalliance.org>; Richard Bowen >; Ebel,Greg ; Schountz,Tony
Subject: Bat housing

All,

Alan asked me to follow up on the renovations of the bull barn for bat holding. I did a quick space assessment of the building. It is approximately 2500 sf, including a 100 sf storage area. I am assuming of the 2500 sf we'll need about 500 sf for storage, feed prep and procedure space. The AZA recommendations for Pteropus giganteus is 15'x30' per 6 bats. With 2000 sf, that leave us holding for 24-29 bats. If there are some other housing guidelines someone has, please let me know.

On the call we discussed 40-60 bats. I'm looking for advice on how to proceed. We can look at extending the footprint to accommodate 40-60, but I'm not sure what the program needs will be.

Thanks,

Lon

Lon V. Kendall, DVM, PhD, DACLAM
Director, Laboratory Animal Resources and
Attending Veterinarian, Colorado State University
2007 Painter Center
Colorado State University
Fort Collins, CO 80523

From: Schountz,Tony <
Sent: Thursday, June 22, 2017 5:19 PM EDT
To:

<

Subject: Bat ID Symposium logistics
Attachment(s): "Campus map.pdf"

Dear Colleagues,

The symposium is one week away and I want to provide you with some logistical information for your arrival to Fort Collins.

1. Speakers. If you can email your presentation directly to me I will get it on the computer for the presentation**However, the file size must be less than 15 MB to accommodate our email server limit**. Otherwise, please bring your presentation on a USB drive if it is larger than 15 mb. We will have both Microsoft Power Point and Apple Keynote software for your presentations. **Bring your USB drive to the Thursday evening reception if you want to transfer it then.**

2. Poster presenters. The maximum size of the posters is 48” x 48” (120 cm x 120 cm). We will provide push pins to mount your poster on the easels. When you register, your poster will have a number assigned to it that corresponds to the easel number. Please mount your poster on that easel. **Bring your poster to the Thursday evening reception.**

3. Getting to Fort Collins. Those of you who are flying to Denver International Airport can schedule a ride with the **Green Ride Airport Shuttle** service. Please visit its web site (https://greenrideco.hudsonltd.net/) to make arrangements convenient for your flight schedules. There is a Green Ride desk in the main terminal at the airport with employees that can help you find the bus pickup. The bus ride is about 1 hour and 15 minutes. On the web site, in the box “Dropoff location” choose the appropriate destination from the pull-down menu. For those of you staying in the university dormitories it is “FC - Laurel Village”, the Hilton Hotel near campus is “FC - Hilton Ft Collins”, and the University Inn is “FC - Best Western University Inn”. And just to make you aware, afternoon and evening flights into Denver can be rather bumpy!

4. Weather and Climate. Fort Collins has lots of sunshine and is at 5000 ft/1500 meters. If you intend to be outdoors much you should bring sunscreen. We often get afternoon thunder showers in our otherwise dry climate but they are typically not more than an hour or two and it usually clears up afterwards. You may want to bring rain gear or a small umbrella. The current forecast is for the mid to high 80sF/low 30sC.

5. Getting to the UCA. The conference venue is the **University Center for the Arts (UCA)** (attached map, blue box, lower right). Oral and poster presentations will be in this building and directions will be posted inside. After you get settled in Thursday, please come to the UCA for the opening registration and social mixer by 5:30 PM. Walking paths (routes) are noted in blue hatched lines.

A. Laurel Village Alpine Dormitory. Those who are staying in campus housing, walk south to Plum Street and turn east to Meridian Avenue. Take Meridian Avenue south to Pitkin Street and take it east to Mason Street. Cross the railroad tracks and immediately turn right (south) just before the parking garage. Follow the path to just past the parking garage and turn left (east). This path leads to a **tunnel that passes under College Avenue** and comes out at the University Test Gardens (lots of flowers). Continue on this path and it will cross Remington Street to the UCA. **Allow 15-20 minutes to walk**.

B. Hilton Hotel. Proceed from the hotel to Prospect and Centre Avenue at the northwest corner of the Hilton Hotel parking lot. Cross Centre to the west and **take the tunnel under Prospect Avenue**. At Lake Street, turn right (east) to Mason Street. Cross the railroad tracks and immediately turn left (north). Just before the parking garage, turn right (east) and take the path that leads to a **tunnel that passes under College Avenue** and comes out at the University Test Gardens. Continue on this path and it will cross Remington Street to the UCA. **Allow 10 minutes to walk**.

C. University Inn Best Western Hotel. Take Elizabeth Street east to Remington Street (one block). Turn right (south) to Pitkin Street. Once you cross Pitkin Street, the University Center for the Arts is to your left. **Allow 5 minutes to walk.**

6. Registration packet. Your registration packet will include the program, name badge, water bottle and a pass for the Fort Collins MAX bus. The pass allows you to ride the bus through Saturday night. Registration also includes lunch for Friday and Saturday. If you are staying in the dorms you will also have breakfast provided at the dorm dining hall, Corbett Hall, which is just east of Alpine Hall where you are staying (please see the attached map).

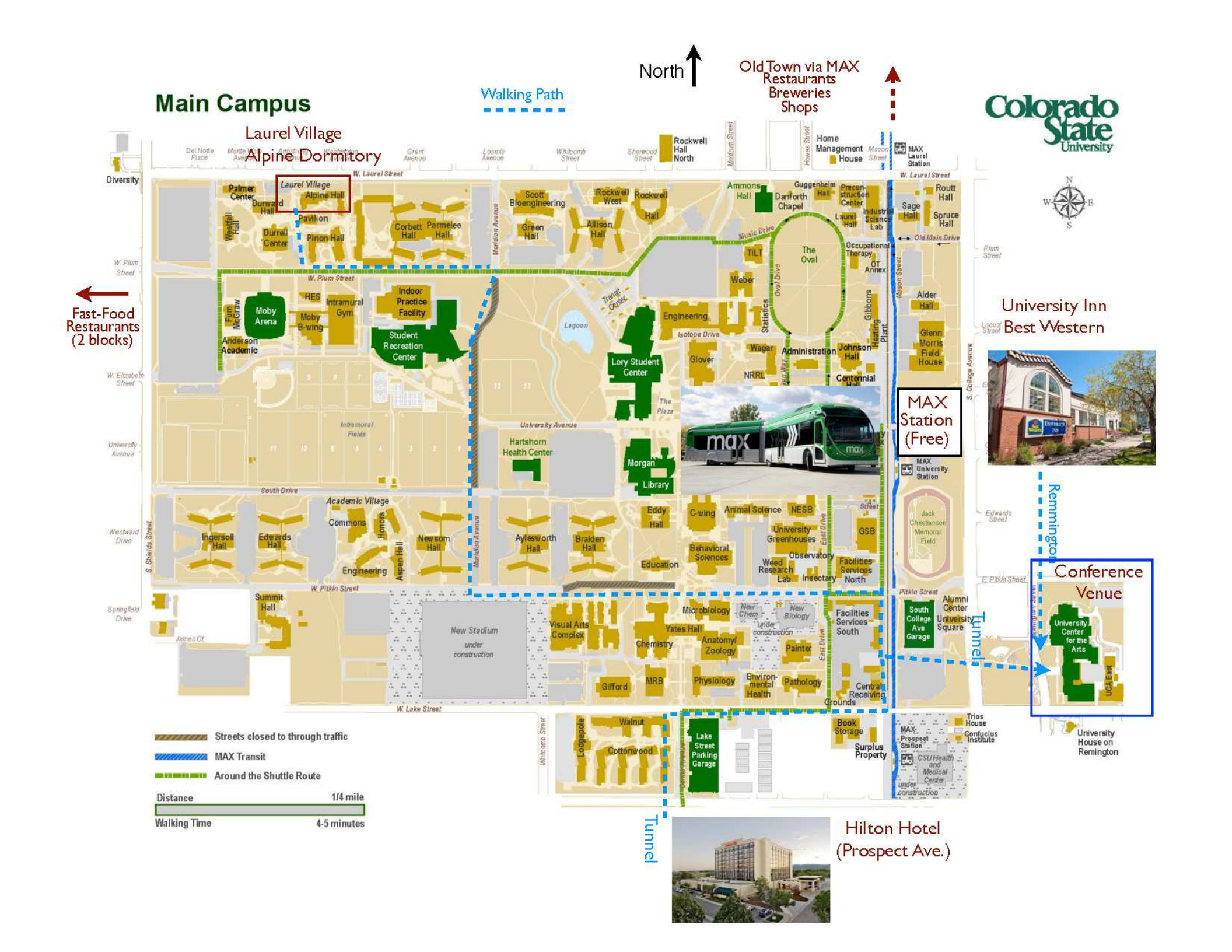
If you have questions, please contact me and I will address them. Finally, I will be at the American Society for Virology meeting Saturday through Wednesday so my email access may be intermittent.

Thanks and see you next week.

Tony

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University


Main Campus
North
Walking Path
Old Town via MAX
Restaurants
Breweries
Shops
Colorado State University
Laurel Village
Alpine Dormitory
Fast-Food Restaurants (2 blocks)
University Inn
Best Western
MAX Station (Free)
Conference Venue
Tunnel
Tunnel
Hilton Hotel (Prospect Ave.)
Remington
Streets closed to through traffic
MAX Transit
Around the Shuttle Route
Distance 1/4 mile
Walking Time 4-5 minutes

From: Kevin Olival, PhD ecohealthalliance.org>
Sent: Wednesday, March 29, 2017 4:40 PM EDT
To: Michaeleen Doucleff
CC: Jane Greenhalgh Schountz,Tony
Subject: Bat Infectious Disease meeting - Fort Collins, CO 29 June - 1 July

Dear Michaeleen,

I wanted to alert you to a conference on bat infectious diseases that's coming up this summer. Not sure if you had heard about it, or if it's something you're interested in attending or covering. I'm cc'ing my colleague Tony Schountz here who is the symposium organizer. I'll be there, along with a bunch of world-renouned bat disease nerds.

http://batid.org

Cheers,
Kevin

Kevin J. Olival, PhD

Associate Vice President for Research

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

From: Kevin Olival ecohealthalliance.org>
Sent: Tuesday, December 04, 2018 2:25 PM EST
To: Schountz,Tony >; Munster, Vincent (NIH/NIAID) [E] <
CC: Laing, Eric ; Chris Broder ; Luke Hamel ecohealthalliance.org>
Subject: Bat MERS-CoV sera for S protein luminex-based assay R&D

Dear Tony and Vincent,

Hope this finds you both well! I know Vincent is in the Congo, so his responses are delayed.

I'm working on a grant proposal (GHERI) with Chris Border and Eric Laing to do some serological screening and assay development for MERS-CoV and other CoVs using a Luminex-based platform. This builds off the work Broder and crew have already done, but will provide support for additional R&D for the MERS-CoV Spike assay, and for in-country capacity building and testing. The idea is to then use the multiplex CoV assays to screen bat sera that we are currently collecting under a DTRA supported project across Western Asia/Middle East (which I'm PI on, and Vincent is involved with).

In order to validate the MERS-CoV assay during the R&D phase,**it would be super helpful to have some confirmed MERS-CoV positive bat sera to work with**. Given that you guys have run MERS-CoV bat infection trials (and may be doing more?), I'm wondering what the possibility of getting some positive bat sera over to Chris' lab for validation? Also, in reading your paper again I remembered that you observed limited seroconversion in bats at 28 dpi… so maybe this is a moot question? Any additional evidence that supports seroconversion in bats?

The grant is due in a couple of weeks, so at this stage I'm just really looking for a general response if you think this is feasible, so we can throw a line in the proposal. i.e. "In collaboration with Vincent Munster (NIH) and Tony Schountz (CSU) we will validate our MERS S protein assay using positive control bat sera from previous experimental infection studies".

Please let me know your thoughts or any additional ideas.

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

www.ecohealthalliance.org

From: Jon Epstein < ecohealthalliance.org>
Sent: Thursday, August 03, 2017 5:42 PM EDT
To: Patricia (NIH/NIAID) Repik [E] ; Park, Eun-Chung (NIH/NIAID) [E]
CC: Schountz,Tony ; Munster, Vincent ; R. A. Bowen
>
Subject: Bat proposal
Attachment(s): "Establishing a bat colony in the US_Epstein_v3.docx","Pteropus bat model_research justification_2017.docx"

Dear Pat and Eun Chung,
It was wonderful to see you in Ft. Collins. I'm grateful that we had time to talk about this project and for your interest and support. Attached are two briefs which detail the scope of work and scientific rationale for setting up the Pteropus colony. Let's use this as a starting point for further discussion about a potential contract. I'd be happy to provide additional information as per your guidance.

Cheers,
Jon

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

)

web: ecohealthalliance.org

Draft: Pre-White paper for discussion
Epstein et al. 2016

Establishment of a pteropid bat colony (*Pteropus medius*) in the United States to study host-virus interactions, including the immune response, to Nipah virus and other zoonotic pathogens that threaten human health.

Prepared by
Jonathan Epstein, DVM, MPH, PhD, EcoHealth Alliance
Tony Schountz, PhD, Colorado State University
Dr. Vincent Munster, PhD, NIH NIAID Rocky Mountain Laboratories

Bats have been shown to carry more zoonotic pathogens than any other mammalian taxon (Olival et al, Nature 2017)**.**

Several emerging zoonotic pathogens associated with severe human disease originated, are hosted or suspected to be hosted by bats, including severe acute respiratory syndrome coronavirus (SARS-CoV), Middle East respiratory syndrome coronavirus (MERS CoV), Marburg virus, ebolaviruses, and a wide range of lyssaviruses. We recently found evidence of a SARS-like coronavirus in Chinese horseshoe bats that has the capability to transmit directly to people, which suggests that the original transmission of SARS may have been directly from bats, rather than via civets or other animal intermediate hosts. Recent studies have also found evidence that bats were reservoirs the ancestors of other human pathogens such as hantaviruses, hepatitis C, rubeola, mumps and rubella viruses. Much of this work arose from phylogenetic, epidemiological and virological studies of viruses identified in wild caught bats, including substantial work from our group. These findings have generated larger questions about how bats (the second largest group of mammals with more than 1,200 species) can host these viruses that without substantial pathology, yet they cause substantial disease in other species, including humans.

To determine whether bats have a specialized physiology or immune systems that permit viral infection with minimal disease requires development of bat models that can be used in laboratory experiments.

Bats of the genus *Pteropus* (family Pteropodidae) comprise more than 60 species that range from Madagascar eastward through most of Asia, Australia, and the Pacific islands. Several species of pteropid bats are natural reservoirs of NiV and other henipaviruses, including Hendra virus (HeV) and Cedar virus in Australia. Both Nipah and Hendra viruses are biosafety level 4 pathogens and select agents. Currently, the only captive colony of pteropid bats available for infectious disease research (to our knowledge) exists at the Australian Animal Health Laboratory (AAHL) in Geelong, Australia, which has BSL-4 small and large animal facilities. Although AAHL has developed and will collaboratively share cell lines derived from one species of pteropid bat (*P. alecto*), at present the bats are not available to researchers outside of AAHL. Thus, a significant need remains for a lab animal model that can be used to study NiV and HeV host-virus interactions and generate additional laboratory reagents and resources available to a broader research community.

Pteropus medius, in particular, is of special interest for viral research because it is has been found to carry Nipah virus and other viruses with potential human health impact, including filoviruses and other uncharacterized henipaviruses for which we have serological evidence. This species also carries a recently discovered virus called GBV-D, a flavivirus related to Hepatitis C virus. *The propensity for this particular species to carry a wide spectrum of viruses*

related to known human pathogens (without clinical affect) makes it an ideal candidate as a laboratory model to advance immunological and virological studies in bats.

The establishment of a research colony of Indian flying foxes (*Pteropus medius*) is critical to facilitate research in the United States that will test hypotheses related to the cellular mechanics of Nipah virus (NiV) and the host immune response, *in vivo,* in a wildlife reservoir species for Nipah virus. The Indian flying fox is endemic to the Indian subcontinent, and widely distributed throughout Bangladesh and India, where more than fifteen outbreaks of Nipah virus encephalitis have been reported since 2001. **There are no bats available in the United States for research related to *Pteropus* physiology, immunology, and viral pathophysiology.** NiV is an emerging, high consequence pathogen with 75% - 100% mortality in humans in Bangladesh, where is causes seasonal outbreaks of encephalitis. Currently, there is no effective treatment or vaccine for NiV. It is a highly communicable disease, including person-to-person and nosocomial transmission. Though the majority of outbreaks, to date, have occurred in rural villages, Bangladeshi patients are often transported to Dhaka for care. The introduction of NiV to Dhaka, a city of 12 million people with an international airport linking major cities, including New York, London, and Hong Kong, represents one of the most significant factors contributing to Nipah virus' pandemic potential.

Maintaining bat colonies requires many specialized husbandry facilities and resources. Indeed, insectivorous bats are notoriously difficult to keep, let alone breed in captivity. Frugivorous bats are much easier to maintain in captivity. They are typically robust and will eat a variety of fruits that are readily available in the United States. Their social structure and behavior is well understood, and zoological institutions have successfully kept and bred a variety of fruit bats species, including many different pteropid bat species. [Note: in the context of this proposal, zoological institutions are not a viable source of bats for founding a colony as biomedical research is generally considered "off mission" for zoological gardens focused on species conservation] The Indian flying fox is an attractive bat model because it is a reservoir host of NiV, its large body mass (~700-900g) allows for relatively large volumes of blood and lymphoid cells to be safely sampled to support clinical research, its conservation status is "non-threatened" (thus allowing wild founders to be more readily sourced), and it is easy to maintain and breed in captivity.

2) Who will establish the colony? Where would the bats come from and where would the colony be maintained?

Our group includes experts on the behavior and husbandry of bats, their ecology, the epidemiology of Nipah virus in wild populations, and the design and implementation of experiments involving non-traditional animal models.

Colorado State University is a registered NIAID contractor for establishing lab animal models and will be the location of the proposed bat colony. Tony Schountz, PhD is an Associate Professor in the Department of Microbiology, Immunology and Pathology, College of Veterinary Medicine at CSU. Dr. Schountz previously established a breeding colony of, Jamaican fruit bats *(Artibeus jamicensis)* that has been used for Tacaribe virus and MERS-CoV experimental research. CSU currently has the facilities to establish a colony of *Pteropus medius* and Dr. Schountz and Richard Bowen, DVM, PhD will be responsible for establishing and maintaining the research colony. The Director of Laboratory Animal Services at CSU is Lon Kendall, DVM, PhD, who has overseen the veterinary care of the Jamaican fruit bat colony. Thus, the facilities and staffing expertise are already in place at CSU for working with bat colonies.

Draft: Pre-White paper for discussion
Epstein et al. 2016

Dr. Jonathan Epstein, a veterinary epidemiologist at EcoHealth Alliance, has nearly 20 years of experience working with pteropid fruit bats in the wild. His research has focused on the epidemiology and ecology of Nipah virus and other zoonotic agents in bats. He directed the capture, quarantine and transport of live *Pteropus vampyrus* from Malaysia (another reservoir of Nipah virus) to AAHL as part of an NIH-funded long-term study of henipaviruses in bats in 2005. He has been working in Bangladesh since 2006, and has established strong collaboration with the government of Bangladesh, including the federal wildlife authority. Dr. Epstein, and his team in Bangladesh will be responsible for the capture, quarantine, and transportation of the bats from Bangladesh to CSU (Fort Collins, Colorado). He will also provide guidance for the facility at CSU (e.g., diurnal cycles, feeding, enrichment, etc.). Dr. Epstein is currently collaborating with Drs. Schountz and Munster on bat immunology studies and will continue to provide leadership and scientific engagement in this and future collaborative studies related to bat immunology and virology related to the imported *Pteropus* bats.

Dr. Vincent Munster is a senior scientist in the Laboratory of Virology, Rocky Mountain Laboratories, NIAID, (Hamilton, MT). His work has focused on experimental studies of bat-borne high containment pathogens such as Ebola virus, Nipah virus, SARS-CoV and MERS-CoV. Dr. Munster will facilitate the establishment of the colony, and will be the laboratory lead and co-investigator on all experimental studies utilizing these bats. We will have the support and use of the BSL 4 laboratory and veterinary personnel at RML for experimental work utilizing the bats.

Mr. Brian Pope, the Director of the Lubee Bat Conservancy in Gainesville Florida has more than 12 years of bat husbandry experience at zoological parks, including Disney World's Animal Kingdom, and will provide expert guidance on the regulatory aspects of bat importation and the development of the internal environment for the bat colony. He and his staff will provide training to the veterinary and animal care staff at CSU and RML on the husbandry and care of the bats. Mr. Pope and Dr. Epstein have collaborated for more than five years on bat immunology studies at the Lubee Bat Conservancy, and Dr. Epstein currently serves on Lubee's Scientific Advisory Board.

To found the colony, we propose to import 40 adult *P. medius* from Bangladesh, with the support of the Forestry Department – the federal wildlife agency. We will import 36 pregnant female bats, and 4 males - all seronegative for Nipah virus. A temporary quarantine facility will be constructed by the Forest Department at the Dhaka zoo, where veterinary and animal care staff are available. Bats will be sampled (blood and urine) every three weeks and samples will be sent to RML laboratories and tested for Nipah virus antibodies and RNA using ELISA, SNT, and PCR.. Bats that have three consecutive negative tests will be shipped to CSU. Our group previously transported pteropid bats from Malaysia to Australia for research purposes. *P. medius* is a seasonal breeder, and females within a colony tend to be pregnant all at once, so capturing 35 pregnant females is achievable. The gestation period is six months, and the timing of transport will be such that the bats will be in the fourth month of pregnancy to maximize the safety to the fetus during transport. We expect 80-90% of pregnancies to be maintained during quarantine and shipment, such that the colony will immediately provide about 30 juveniles that could be used for experimental work within 12 months of birth or to continue breeding after 30 months when they reach sexual maturity. The adults will be bred every year (one breeding cycle per year), which will generate a cohort of 20-35 bats each season. Over a period of 3-5 years, we expect to have generated a colony of more than 200 bats that will be available for experimental studies.

3) Long-term sustainability.

Use of the bat colony as well as cell lines derived from bat tissues will be made available to the scientific community. We expect that cell lines will be the most frequently requested products that could be readily shared among the scientific community. Have a supply of primary and immortalized (e.g., large T, hTERT) cell lines in the US will rapidly facilitate research because it will obviate the need for CITES and other import permits when reagents are shipped to other US-based labs. The colony will also benefit conservation efforts by providing genetic material to zoological institutions that have breeding programs for *P. medius* now or in the future.

Support from NIAID will be required to establish and expand the colony over an initial 5-year period. Once the colony is established, we will generate reagents and cell lines that will be made available to other researchers upon request. After the completion of the contract and to support the maintenance of the colony and associated resources, we will establish a modest fee structure for use of the bats and materials derived from the bats, which will be channeled directly back into colony maintenance costs. We will also consider experiments that require the use of bats and will include budget in each proposal that will be used to support maintenance costs. The fee structure could be modeled from the one used by the Lubee Bat Conservancy, or a de novo fee-for-service system will be developed.

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CC: Kingston, Tigga ; Rodrigo Medellin < ; Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Isabella Mandl
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure
Attachment(s): "IUCN infographic wildlife version.png"

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Take care, and I'll look forward to your feedback.

Best,
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https://twitter.com/rodrigomedellin

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<PastedGraphic-3.png>

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Preventing transmission of SARS-CoV-2 from humans to wild mammals

Exposure Risks

Contact exposure
Mammals coming into contact with contaminated hands or equipment

Aerosol exposure
Infectious droplets from handlers holding mammals in close proximity

Environmental exposure
Sharing enclosed, poorly-ventilated spaces with mammals, where virus may persist in the air or on surfaces

MAP your plan to prevent transmission to mammals!

Mitigation Strategies

Minimize

Delay, prioritize, or avoid handling mammals when possible, i.e. collect environmental samples

Assess

Postpone handling mammals if there is a probability that you have been exposed to SARS-CoV-2 or if you have symptoms

Protect

Adopt practices that reduce exposure, i.e. face covering, gloves, disinfection procedures

From: Kading,Rebekah on behalf of Kading,Rebekah <
Sent: Tuesday, August 11, 2020 6:31 PM EDT
To: Kendra Phelps ecohealthalliance.org>
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Hi Kendra -

Thank you! I'm glad you like it! I have a subscription to BioRender for my lab...well worth the investment...so we get unlimited images, don't have the watermark on it, and can export high resolution for use in publications, grants, presentations etc. I started playing around with the free version though just to be sure I liked it, and its been a huge hit with my lab!

Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kendra Phelps ecohealthalliance.org>
Sent: Tuesday, August 11, 2020 2:49 PM
To: Kading,Rebekah
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Hi Rebekah,

Wow, that is amazing! The environmental sampling icons are perfect!

I was checking into BioRender today to make a schematic for a publication, do you use the free version?

Cheers,
Kendra

P.S. Fingers and toes crossed for Anna's interview with EHA this Friday:)

Kendra Phelps, PhD
Research Scientist

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<IUCN infographic wildlife version.png>

From: Kading,Rebekah on behalf of Kading,Rebekah < >
Sent: Tuesday, August 25, 2020 12:35 PM EDT
To: William B. Karesh ecohealthalliance.org>
CC: Dr. Melinda Rostal ecohealthalliance.org>; Kevin Olival ecohealthalliance.org>; Tigga.Kingston_
; Rodrigo Medellin >; Kendra Phelps ecohealthalliance.org.test-google-a.com>; Isabella Mandl
-to-bat transmission of SARS-CoV-2 Figure
Attachment(s): "IUCN BSG MAP TRANSLATION SHEET.docx","IUCN infographic wildlife version_cc.pdf"

Hi Billy,

The pdf version should be editable, so they should be able to work directly on that and then re-save as an image file. As an alternative, if anyone in your working group or OIE has a BioRender license, I can share the infographic file directly with that person through BioRender to edit. Third option - I'm attaching a translation sheet that could be used as a template. It still has the bat infographic language on it, but if this is updated with the French and Spanish translations for the wildlife infographic, feel free to send those translations back to me and I'd be happy to update the infographic.

Hope that helps, and just let me know how you'd like to proceed.

Best regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: William B. Karesh ecohealthalliance.org>
Sent: Tuesday, August 25, 2020 9:22 AM
To: Kading,Rebekah >
Cc: Dr. Melinda Rostal ecohealthalliance.org>; Kevin Olival ecohealthalliance.org>; Tigga.Kingston
>; Rodrigo Medellin ; Kendra Phelps ecohealthalliance.org.test-google-a.com>; Isabella Mandl

Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Hi Rebekah and all.

Thanks again for the graphic.

OIE is distributing our joint WHSG/OIE guidelines and also translating it to French and Spanish as they normally do. They would like to change the language in the graphic also but need either the editable file or at least the background images on which they can overlay the French and Spanish. Are either of those something you could provide?

Thanks,

Billy

William B. Karesh, D.V.M
Executive Vice President for Health and Policy

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018 USA

www.ecohealthalliance.org

President, OIE Working Group on Wildlife

Co-chair, IUCN Species Survival Commission - Wildlife Health Specialist Group

EPT Partners Liaison, USAID Emerging Pandemic Threats - PREDICT-2 Program

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

On Aug 20, 2020, at 10:43 AM, Kading,Rebekah > wrote:

Hi everyone -

So sorry for the delay! I'm attaching the Infographic -- a pdf version with clickable links and a png version which may be easier for social media postings. Just let me know if you have any final suggestions. We are very happy to collaborate with you on aligning the messaging coming from our working groups on this issue - thank you again very much for reaching out about this!

Kind regards,
Rebekah

Rebekah C. Kading, PhD

Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Dr. Melinda Rostal ecohealthalliance.org>
Sent: Tuesday, August 18, 2020 8:29 AM
To: Dr. Kevin Olival ecohealthalliance.org>
Cc: Kading,Rebekah >; Tigga Kingston >; Rodrigo Medellin >; Billy Karesh ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Isabella Mandl
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Dear Tigga and Rodrigo,
Attached is the figure with the acknowledgment. The WHSG would prefer not to include logos on the figure if possible as it is positioned in the middle of our text. However, I want to ensure you are satisfied with it. So if you have any concerns about the acknowledgement, please let me know by Thursday Aug 20.

Thanks very much!

And thanks again to you and Rebekah for letting us modify your great figure:)

Best,

Mindy

Melinda Rostal DVM, MPH, PhD
Principal Scientist, Vector-Borne Diseases

Rift Valley Fever Virus Project Manager

EcoHealth Alliance
520 Eighth Ave, Ste. 1200
New York, NY 10018

)
www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.
EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

On Aug 12, 2020, at 2:49 PM, Kevin Olival <

a wider distribution.

Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org
EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

On Aug 11, 2020, at 9:47 AM, Kading,Rebekah < wrote:

Hi Mindy, Billy, Kevin, and Kendra -

I hope your week has gotten off to a good start!

I'm attaching a draft infographic for your review. I've modified the current BSG MAP infographic per your suggestions for a wildlife version. I can also add a logo, QR, and/or website at the bottom if you'd like. Not sure of exactly the best way to portray environmental samples...I was assuming this will comprise activities like passive fecal sample collections...so please let me know if this captures what you had in mind or if there is something else you're envisioning and I can revise accordingly! (BioRender does have an amusing variety of poo icons, but I was trying to keep it classy and professional.) ��

Take care, and I'll look forward to your feedback.

Best,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Dr. Melinda Rostal ecohealthalliance.org>
Sent: Friday, August 7, 2020 2:16 PM

To: Kading,Rebekah <
Cc: Kingston, Tigga ; Rodrigo Medellin ; Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Isabella Mandl >
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

That's great Rebekah!

Thanks! I'm happy to chat more with you about it, if that's helpful:)

~ Mindy

Melinda Rostal DVM, MPH, PhD
Principal Scientist, Vector-Borne Diseases

Rift Valley Fever Virus Project Manager

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New York, NY 10018

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460 West 34th Street – 17th floor
New York, NY 10001

On Aug 7, 2020, at 3:22 PM, Kading,Rebekah < > wrote:

Hi everyone,

Just chiming in to say thank you for the discussion and interest in the Infographic! I'm so glad it has been a good communication tool - the suggested modifications would be very easy to make.

Kind regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kingston, Tigga >
Sent: Friday, August 7, 2020 10:04 AM
To: Dr. Melinda Rostal ecohealthalliance.org>; Rodrigo Medellin
Cc: Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival cohealthalliance.org>; Kendra Phelps < ecohealthalliance.org>; Kading,Rebekah < >; Isabella Mandl >
Subject: RE: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Dear Melinda
That sounds appropriate to me. Our group meets early on Tuesday morning, so I'd like to run this by them then for final agreement, if that's OK, but I don't imagine any objections.

Best
Tigga

From: Dr. Melinda Rostal ecohealthalliance.org>
Sent: Friday, August 7, 2020 10:39 AM
To: Rodrigo Medellin
Cc: Kingston, Tigga ; Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>; Kading,Rebekah >; Isabella Mandl
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Dear Rodrigo and Tigga,

I spoke to my colleagues and we would propose to change "bats" to either "mammals" or "wild mammals", change the graphic in the center to include a smaller version of the bat that is there as well as an ape and a mustelid, change the example in the Minimize box from "i.e. implement acoustic surveys" to "i.e. collect environmental samples", and change the figure of the bat calling to a figure of collecting an environmental sample.

The risks and mitigation strategies are really nicely laid out as you originally made it so we wouldn't need to change that or the rest of the text/figures. We support your MAP plan.

Do you think that would be acceptable? We think it remains very consistent with your message.

If yes, what is the best way to proceed with the modification?

Kind regards,

Mindy

Melinda Rostal DVM, MPH, PhD
Principal Scientist, Vector-Borne Diseases

Rift Valley Fever Virus Project Manager

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New York, NY 10018

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New York, NY 10001

On Aug 4, 2020, at 5:14 PM, Rodrigo Medellin > wrote:

Hi everyone

Thank you Tigga for copying me with the good email address. Mindy good talking to you again. I fully concur with Tigga about being mindful of the brains behind the infographic, and of course about any changes. If at all possible Mindy we would rather have it presented with due credits verbatim. Multiple version will be confusing, regardless of whether the different versions clash with each other. Stay safe.

--

Dr. Rodrigo A. Medellin
Instituto de Ecología, UNAM
Ap. Postal 70-275
04510 Ciudad Universitaria, D. F.
MEXICO

DIRECCION FISICA (STREET ADDRESS):

Dr. Rodrigo A. Medellín
Instituto de Ecologia, UNAM
Circuito Exterior s/n junto al Jardín Botánico Exterior
04510 Ciudad Universitaria, D. F.
MEXICO

https://www.facebook.com/rodrigo.a.medellin
https://www.instagram.com/rodrigomedellin1223/
https://twitter.com/rodrigomedellin

Check out our YouTube channel with dozens of cool, short videos on bats:https://www.youtube.com/user/RMedellinbats
http://web.ecologia.unam.mx/medellin/

On Tue, Aug 4, 2020 at 9:22 AM Kingston, Tigga < wrote:

> Dear Mindy
>
> The infographic was constructed in BioRender by Dr Rebekah Kading, so they would probably need to be manipulated in that environment. I've copied Rebekah and Dr Bella Mandl – who is also leading our graphics – on this email.
>
> They have also worked up infographics for rehabbers and cavers and the original is now in a number of languages. Rebekah is a whizz at adapting the base design, but we of course need to be mindful of her time.
>
> **Critically, we would need to review and sanction any changes because we don't want any messages to conflict with our own.** It would be confusing to have essentially the same graphic circulating saying different things. Our messaging is organized around the MAP concept so we don't want that disrupted, for example.
>
> Do you have a clearer idea of how you would use the infographic?
>
> Caveats aside, happy to work with you of course!!
>
> Best wishes
> Tigga
>
> P.S. I copied Rodrigo with his current email.

From: Melinda Rostal ecohealthalliance.org>
Sent: Monday, August 3, 2020 8:41 PM
To: Kingston, Tigga ; Rodrigo A. Medellín

Cc: Billy Karesh ecohealthalliance.org>; Dr. Kevin Olival ecohealthalliance.org>; Kendra Phelps ecohealthalliance.org>
Subject: Re: Preventing human-to-bat transmission of SARS-CoV-2 Figure

Dear Tigga,
I just wanted to let you know that I've sent this to 2 email addresses for Rodrigo and it seems they have bounced back. I am not sure if he has seen my request.

I hope to hear from you soon about whether the Wildlife Health Specialist Group can use or modify your infographic (with the appropriate credit).

Best,
Mindy

Sent from my iPhone

On Jul 29, 2020, at 3:11 PM, Dr. Melinda Rostal ecohealthalliance.org> wrote:

> Dear Rodrigo and Tigga,
>
> Rodrigo, it's been several years since we have spoken and I hope you are well.
> I hope you are both managing to stay safe during the pandemic.
>
> I have been working with Billy Karesh, some folks from the Wildlife Health Specialist Group and the OIE to come up with some recommendations for working with free-living, wild mammals during the pandemic. We thought that the documents that the Bat Specialist Group wrote were great and we certainly refer anyone working with bats to review your guidelines as well.
>
> We really liked the figure you used (pasted below) and were wondering if we could reproduce it and/or modify it slightly in our document. We would certainly credit your group with creating it.
>
> If it is ok to modify it, would it be possible to get a powerpoint slide or photoshop document to allow for easy modification?
>
> I look forward to hearing from you and we would be happy to promote your work.
>
> Kind regards,
>
> Mindy

<PastedGraphic-3.png>
Melinda Rostal DVM, MPH, PhD
Principal Scientist, Vector-Borne Diseases

Rift Valley Fever Virus Project Manager

EcoHealth Alliance
520 Eighth Ave, Ste. 1200
New York, NY 10018

www.ecohealthalliance.org

<IUCN infographic wildlife version.png>

<IUCN infographic wildlife version_cc.pdf><IUCN infographic wildlife version_cc.png>

Translation Sheet. Please translate the English to your language as closely as possibly and use the same format for the section. If you can retain the “MAP” – Minimize, Assess, Protect that is ideal, but it of course depends on the translation.
Example

Section	**English**	
Title	**Preventing human-to-bat transmission of SARS-CoV-2**	
Tagline	MAP your plan to prevent transmission to bats	
Heading 1	**Exposure Risk**	
Heading 2	*Contact exposure*	
	Bats coming into contact with contaminated hands or equipments	
Heading 2	*Aerosol exposure*	
	Infectious droplets from handler holding bats in close proximity	
Heading 2	*Environmental exposure*	
	Sharing enclosed, poorly ventilated spaces with bats, where virus may persist in the air or on surface	
Heading 1	**Mitigation strategies**	
Heading 2	*Minimize*	
	Delay, prioritize, or avoid handling bats when possible, i.e. implement acoustic surveys	
Heading 2	*Assess*	
	Postpone handling bats if there is probability that you have been exposed to SARS-CoV-2 or if you have to symptoms	
Heading 2	*Protect*	
	Adopt practices that reduce exposure, i.e. face covering, gloves, disinfection procedures	

EXAMPLE

Section	English	LANGUAGE
Title	**Preventing human-to-bat transmission of SARS-CoV-2**	**Cegah Penularan SARS-CoV-2 dari manusia-ke-kelelawar**
Tagline	MAP your plan to prevent transmission to bats	**KENAL**[1] dan rencanakan pencegahan penularan ke kelelawar [1]KENAL: Kurangi, Nilai dan Lindungi Note: Kenal in Indonesia means know, be familiar
Heading 1	**Exposure Risk**	**Risiko Paparan**
Heading 2	*Contact exposure*	*Paparan kontak*
	Bats coming into contact with contaminated hands or equipments	Kelelawar kontak langsung dengan tangan atau peralatan yang terkontaminasi
Heading 2	*Aerosol exposure*	*Paparan aerosol*
	Infectious droplets from handler holding bats in close proximity	Droplet infeksius dari pemegang kelelawar dalam jarak dekat
Heading 2	*Environmental exposure*	*Paparan lingkungan*
	Sharing enclosed, poorly ventilated spaces with bats, where virus may persist in the air or on surface	Berada satu tempat dengan kelelawar di ruang tertutup, dan minim ventilasi dimana virus dapat bertahan di udara atau di permukaan benda
Heading 1	**Mitigation strategies**	**Strategi mitigasi**
Heading 2	*Minimize*	*Kurangi*
	Delay, prioritize, or avoid handling bats when possible, i.e. implement acoustic surveys	Menunda, memprioritaskan, atau sebisa mungkin hindari memegang kelelawar, misalnya menerapkan survei akustik

Heading 2	*Assess*	*Nilai*
	Postpone handling bats if there is probability that you have been exposed to SARS-CoV-2 or if you have to symptoms	Tidak memegang kelelawar jika anda merasa ada kemungkinan terinfeksi SARS-CoV-2 atau memiliki gejala
Heading 2	*Protect*	*Lindungi*
	Adopt practices that reduce exposure, i.e. face covering, gloves, disinfection procedures	Lakukan tindakan yang dapat mengurangi paparan, seperti menggunakan pelindung wajah, masker, sarung tangan, dan langkah desinfeksi

Preventing transmission of SARS-CoV-2 from humans to wild mammals

Exposure Risks

Contact exposure
Mammals coming into contact with contaminated hands or equipment

Aerosol exposure
Infectious droplets from handlers holding mammals in close proximity

Environmental exposure
Sharing enclosed, poorly-ventilated spaces with mammals, where virus may persist in the air or on surfaces

MAP your plan to prevent transmission to mammals!

Mitigation Strategies

Minimize

Delay, prioritize, or avoid handling mammals when possible, i.e. collect environmental samples

Assess

Postpone handling mammals if there is a probability that you have been exposed to SARS-CoV-2 or if you have symptoms

Protect

Adopt practices that reduce exposure, i.e. face covering, gloves, disinfection procedures

This figure was adapted in collaboration with the IUCN Bat Specialist group.

From: Kading,Rebekah on behalf of Kading,Rebekah
Sent: Monday, August 31, 2020 12:15 AM EDT
To: Aleksei Chmura ecohealthalliance.org>
CC: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Re: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

Hi Aleksei,

This is wonderful news!! I'm thrilled for Anna. She really is a shining star and I will be sad to see her go when that time comes, but I know she has an amazing future ahead of her and its been exciting to see her career blossom already. I'd be happy to put my thoughts into a letter of recommendation this week if that's what you prefer? Otherwise Tuesday and Friday are my most open days this week for a phone call; I could talk Tuesday anytime between 1-5 Eastern time or Friday is wide open.

Best regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Aleksei Chmura ecohealthalliance.org>
Sent: Sunday, August 30, 2020 4:26 PM
To: Kading,Rebekah >
Cc: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

Dear Dr. Kading,

We just interviewed Anna Fagre for a position here at EcoHealth Alliance as a Research Scientist and Project Manager. Our hiring committee thought she was terrific with the right background and attitude for our team. Anna listed you as a reference. If you would be willing to send some comments about Anna, that would be terrific!

I have attached our position advertisement, so you may know more about the position - though based on her skillset, the specifics would evolve a bit. This position would focus primarily on our emerging infectious disease projects based in Southeast Asia including our recently awarded, NIAID funded EID-SEARCH program:

- https://www.ecohealthalliance.org/program/south-east-asia-research-collaboration-hub

I look forward to your reply and should a phone call be more convenient, we could do that as well.

On behalf of our whole committee, I sincerely appreciate your time.

-Aleksei

Aleksei Chmura, PhD
Chief of Staff

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-4182

www.ecohealthalliance.org

From: Kading,Rebekah on behalf of Kading,Rebekah
Sent: Tuesday, September 01, 2020 3:57 PM EDT
To: Aleksei Chmura ecohealthalliance.org>
CC: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Re: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

Dear Aleksei, Peter, and Hongying,

I enthusiastically recommend Dr. Anna Fagre for the Research Scientist and Project Manager position at EcoHealth Alliance.

To speak to Anna's **research experience and capability**: I've known Anna since I joined the CSU faculty in 2016, when she arranged to a rotation as part of her microbiology residency. Anna formally joined my laboratory as a PhD student in July 2017. Her dissertation is focused on the role of bats as reservoirs of emerging arboviruses, and she has made significant progress on both *in vitro* and *in vivo* studies involving bat-associated orbiviruses. The primary emphasis of these studies is on characterization of Bukakata orbivirus, a novel virus that I isolated from a fruit bat in Uganda in 2013. Bukakata orbivirus is putatively tick-borne, based on the phylogenetic analyses we have conducted. To study this virus in the broader context of other orbiviruses that have been isolated from naturally-infected bats, we acquired all three of the remaining bat-associated orbiviruses from the CDC reference collection as well as Chobar Gorge virus, a tick-borne orbivirus to which Bukakata appears to be closely related. Anna's molecular and phylogenetic characterization of Bukakata and other bat-associated orbiviruses was published in a special collection on bat viruses, in the journal Viruses (PMID: 30832334) along with a comprehensive review of the potential for bats to serve as reservoirs for arboviruses (PMID: 30832426). Since the time these papers were completed, Anna has also put significant effort into investigating the use of subgenomic RNA derived from the 3'UTR of flaviviruses to look for evidence of past infection in archived tissue samples. Because of the complex hairpin structure of the viral RNA in the 3'UTR, it is protected from RNA degradation by the exonuclease XRN1, so we hypothesized that we would find residual viral RNA that could be amplified and sequenced. After optimizing this methodology, Anna screened all of our remaining bat tissue samples from Uganda, going back 10 years, and discovered that 4 bats between 2009 – 2013 had been infected with Zika virus. Moreover, this Zika virus sequence was most similar to the Asian lineage, suggesting either diversification of Zika virus strains prior to the virus expanding into Asian in the ~1960s or spillback into Africa of the epidemic strain much earlier than we have appreciated. This manuscript is currently in review. All in all, Anna's work in my lab has been top-notch. She is meticulous and hard-working and has an excellent grasp of the molecular methodologies and big picture of how they can be applied innovatively in an ecological context. In each of these projects, she has done an excellent job leading, and taken initiatives beyond the original study scope that have made the work much stronger in the end. Her **background in veterinary medicine** has also added valuable perspective, and been very much in-demand as she has helped other laboratories on campus during this pandemic with *in vivo* studies involving SARS-CoV-2.

Other key attributes relevant to the current opportunity:

Anna is highly **collaborative,** personable, and very proactive in seeking these collaborations. This year she has re-connected with a former CSU graduate school colleague who is now in Bangladesh, and has been actively developing some research ideas and using her own funding to generate preliminary data. She also joined the VERENA consortium and has been working on a review paper with collaborators in that group. She works very well with others, as a leader of diverse teams as well as a contributing member. She has had the opportunity to contribute to a number of **international projects** both as part of my lab and during her previous experience, and is very adaptable, capable, and enthusiastic about working internationally. Over the past year she has been an invaluable member of an global initiative led by the CSU Office of the Vice President for Research, and has earned the respect of the highest CSU leadership for her contributions to this team.

Anna has been successful at **securing extramural funding**, of her own initiative. Since joining my lab, she has been awarded three highly-competitive fellowships and grants: An NIH TL1 fellowship through the Colorado Clinical and Translational Science Institute, a spot on the NIH T32 award to CSU, and the 2019 Robert E. Shope International Fellowship in Infectious Diseases through ASTMH/ACAV.

Anna is an excellent writer and **science communicator**, and also publishes frequently on blogs and other social media platforms in addition to her prolific peer-reviewed publications. She is the literature watchdog of the lab, and somehow seems to know about every relevant paper or report that is published within a half hour of it hitting the press. Anna has excellent soft skills when interacting with other professionals. She was featured in a documentary video made by CSU, and had a very natural presence and ability to clearly explain her research and general principles of disease ecology in lay terms.

In conclusion, I give Anna my highest recommendation and think she would be a fantastic addition to your team. Anna is extremely proactive, self-motivated, skilled, and has brought a wonderful energy and work ethic to my laboratory. She is an up-and-coming leader in the field, and I am thrilled to have her as part of my team. This turned out to be not-so-brief a recommendation, but I hope was a useful assessment! If you have any questions or if I can be of any additional assistance, please do not hesitate to contact me.

Best regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Aleksei Chmura ecohealthalliance.org>
Sent: Sunday, August 30, 2020 10:25 PM
To: Kading,Rebekah >
Cc: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Re: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

Dear Rebekah,

Thanks for your quick reply and it is good to read your enthusiasm about Anna! An informal, brief, and detailed email reply-to-all will be splendid - any time this week.

Much appreciated!

-Aleksei

On Aug 31, 2020, at 00:15, Kading,Rebekah > wrote:

Hi Aleksei,

This is wonderful news!! I'm thrilled for Anna. She really is a shining star and I will be sad to see her go when that time comes, but I know she has an amazing future ahead of her and its been exciting to see her career blossom already. I'd be happy to put my thoughts into a letter of recommendation this week if that's what you prefer? Otherwise Tuesday and Friday are my most open days this week for a phone call; I could talk Tuesday anytime between 1-5 Eastern time or Friday is wide open.

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Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Aleksei Chmura ecohealthalliance.org>
Sent: Sunday, August 30, 2020 4:26 PM
To: Kading,Rebekah >
Cc: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

Dear Dr. Kading,

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I have attached our position advertisement, so you may know more about the position - though based on her skillset, the specifics would evolve a bit. This position would focus primarily on our emerging infectious disease projects based in Southeast Asia including our recently awarded, NIAID funded EID-SEARCH program:

- https://www.ecohealthalliance.org/program/south-east-asia-research-collaboration-hub

I look forward to your reply and should a phone call be more convenient, we could do that as well.

On behalf of our whole committee, I sincerely appreciate your time.

-Aleksei

Aleksei Chmura, PhD
Chief of Staff

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-4182

)

From: Kading,Rebekah on behalf of Kading,Rebekah >
Sent: Monday, August 31, 2020 12:36 AM EDT
To: Aleksei Chmura ecohealthalliance.org>
CC: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Re: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

Ok sounds good - I'll follow up this week.
Thanks!
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Aleksei Chmura ecohealthalliance.org>
Sent: Sunday, August 30, 2020 10:25 PM
To: Kading,Rebekah >
Cc: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Re: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

Dear Rebekah,

Thanks for your quick reply and it is good to read your enthusiasm about Anna! An informal, brief, and detailed email reply-to-all will be splendid - any time this week.

Much appreciated!

-Aleksei

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>
> **Rebekah C. Kading, PhD**
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> Department of Microbiology Immunology and Pathology
> Colorado State University
>
> ---
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> **From:** Aleksei Chmura ecohealthalliance.org>
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funded EID-SEARCH program:

- https://www.ecohealthalliance.org/program/south-east-asia-research-collaboration-hub

I look forward to your reply and should a phone call be more convenient, we could do that as well.

On behalf of our whole committee, I sincerely appreciate your time.

-Aleksei

Aleksei Chmura, PhD
Chief of Staff

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-4182

www.ecohealthalliance.org

From: Kading,Rebekah on behalf of Kading,Rebekah
Sent: Tuesday, June 02, 2020 5:25 PM EDT
To: Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) >; Grant, Evan H >; Gilbert, Amy T - APHIS >; Kevin Castle ; Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) >; epstein ecohealthalliance.org>; dreeder >; Daniel Streicker kate.e.jones Plowright, Raina wfrick ; a.peel >; Christine Kreuder Johnson
Subject: Re: SARS expert judgement - final report on the risk assessment

Thank you very much, Evan and Mike, and congratulations on completing such a tremendous amount of work! It was a pleasure to be involved in this process, and have such thorough and insightful discussions with all of you. I learned a lot, and look forward to future interactions.
Kind regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP)
Sent: Tuesday, June 2, 2020 1:26 PM
To: Grant, Evan H >; Gilbert, Amy T - APHIS >; Kevin Castle ; Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) ; epstein ecohealthalliance.org>; dreeder >; Daniel Streicker >; kate.e.jones ; Kading,Rebekah ; Plowright, Raina >; wfrick >; a.peel Christine Kreuder Johnson >
Subject: RE: SARS expert judgement - final report on the risk assessment

Nice report! It was a really interesting and informative process. Many thanks for including me.
Best wishes,
Jon

Jonathan S. Towner, PhD
Lead, Virus Host Ecology Team
Viral Special Pathogens Branch
Centers for Disease Control and Prevention

From: Grant, Evan H >
Sent: Tuesday, June 2, 2020 1:39 PM
To: Gilbert, Amy T - APHIS ; Kevin Castle Amman, Brian R. (CDC/DDID/NCEZID/DHCPP) Jon Epstein ecohealthalliance.org>; dreeder Daniel Streicker ; kate.e.jones ; Kading,Rebekah >; Towner, Jonathan (Jon) (CDC/DDID/NCEZID/DHCPP) ; Plowright, Raina wfrick ; a.peel Christine Kreuder Johnson >
Subject: SARS expert judgement - final report on the risk assessment

SARS-bat Experts,
Thanks again for lending your expertise to this risk assessment. I attach here the report from this work.
Kindest regards,
Evan and Mike

From: Kading,Rebekah on behalf of Kading,Rebekah
Sent: Wednesday, April 15, 2020 10:43 AM EDT
To: Kingston, Tigga ; Cryan, Paul
CC: olival ecohealthalliance.org>
Subject: Re: SARS-CoV-2 spillback risk to North American bats

Hi Paul, Kevin, Tigga,

I'll just reply to this thread. Yes, I'd be happy to take a look at the paper as well -- thank you very much for spearheading that effort! As Tigga mentioned we're working on something as well that we'll reach out to you guys separately about. Seems like BOHRN is mobilizing on multiple fronts, which is great to see.

Take care and talk to you soon -
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Kingston, Tigga
Sent: Wednesday, April 15, 2020 7:52 AM
To: Cryan, Paul ; Kading,Rebekah >
Cc: olival ecohealthalliance.org>
Subject: RE: SARS-CoV-2 spillback risk to North American bats

Hi Paul
Very interested to see the MS. Rebekah and I have been working on something that arose out of BOHRN that would be very complementary and might be worth trying to coordinate dissemination in some way. We are meeting today and will take stock of where we are at.

I just started an email to you and Kevin about the state of affairs as we Rodrigo and I are getting quite a bit of push-back on the IUCN BSG recommendation to suspend field studies while further data are gathered (primarily from western scientists with access to PPE). It would be good to hear what those committees are finding sooner rather than later.

Best wishes
Tigga

From: Cryan, Paul >
Sent: Tuesday, April 14, 2020 2:16 PM
To: Kingston, Tigga >
Cc: ecohealthalliance.org
Subject: SARS-CoV-2 spillback risk to North American bats

Hi Tigga,

Sorry for the silence since my call for help about the risks of humans potentially infecting bats in North America with the SARS-CoV-2 virus. Thanks for your patience and willingness to get involved in what we're hoping can be another disease response where scientists coming at disparate aspects of bats and pathogens can help each other. Those of us in the bat research world that focused most of our past efforts in the U.S. on conservation and management of bat populations can certainly use your expertise and help adjusting to the new situation.

A lot happened during my silence. Another group in USGS has been working at the behest of decision makers across federal and state natural resource management agencies to pull off a formal risk assessment by querying a subset of the experts we've reached out to. You lucked out and were not chosen for that exercise (yet), but we will keep you posted on the outcomes of that rapid assessment.

The other thing keeping me silent over the past couple of weeks is a short manuscript (currently 5 pages single spaced) that Kevin Olival and I drafted to articulate the potential risks of humans infecting North American temperate-zone bats with SARS-CoV-2, potentially relevant patterns we observed in bat-CoV distributions at a global scale, and the likely benefits of

disease and bat researchers working together to draw on the strengths of our various disciplines. We hope to have a draft to circulate by tomorrow and would appreciate input and feedback from any of you willing to read it and help us stress test the concepts and assertions therein. Please let me know if you are interested.

Thanks again for your help and patience.

All the best,
Paul

Paul Cryan
Research Biologist
USGS Fort Collins Science Center

Web Page and Contact Info

From: Kading,Rebekah on behalf of Kading,Rebekah >
Sent: Friday, May 22, 2020 1:32 PM EDT
To: GSE Events < ; kityrob < ; abelwade >; epstein ecohealthalliance.org>; Tigga.Kingston < >; spwa >; ian.mendenhall
CC: Stokes, Martha M CIV (USA) Jamechia Hoyle >; Katie Leahy >; Aleman, Nicki D CTR DTRA COOP THRT REDUCT (USA) >
Subject: Re: World One Health Congress and BTRP TRN Side Meeting - BOHRN

Greetings everyone! Thank you for the update - I will stay tuned to see how the situation unfolds. I am available on those dates should that work out. We could try a Zoom meeting sometime in the interim, if that would be helpful to get everyone "together"? I know many BOHRN members have been collaborating and contributing to the pandemic response in a variety of ways, which I think represents some successful grassroots mobilization of the network. Might be encouraging to have something of a group call to hear about what folks have been up to and if there's anything we can band together more formally to accomplish despite being scattered. Just an idea to throw out there!
Kind regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: GSE Events
Sent: Friday, May 22, 2020 10:51 AM
To: kityrob >; abelwade >; epstein ecohealthalliance.org>; Tigga.Kingston < ; Kading,Rebekah >; spwa >; ian.mendenhall

Cc: Stokes, Martha M CIV (USA) ; Jamechia Hoyle ; Katie Leahy ; Aleman, Nicki D CTR DTRA COOP THRT REDUCT (USA)
Subject: Re: World One Health Congress and BTRP TRN Side Meeting - BOHRN

Dear BOHRN TRN Steering Committee Members,

We hope you have been able to remain safe during these times and that this email finds you well. As you may already know, the World One Health Congress has been rescheduled to take place on October 30 - November 3 in response to worldwide travel restrictions and to coincide with International One Health Day on November 3rd. We wanted to inform you that the BTRP TRN side meetings have been rescheduled in tandem with the Congress, now aiming to take place on November 3 - 4. This is a change we are trying to implement, however, we understand the current scope of world events and anticipate further changes as we go forward. Our utmost priority is everyone's safety and we will continue to monitor the situation to act accordingly. We will be sure to keep you informed of all updates.

Please let us know if you have any questions and stay safe.

Kind Regards,

GSE Logistics Team

Global Systems Engineering, LLC
A Certified HUBZone Company
www.globalsyseng.com
signature_1234061396

From: Caitlin Devaney >
Date: Tuesday, March 10, 2020 at 2:30 PM
To: "kityrob "abelwade < >, "epstein " ecohealthalliance.org>, "Tigga.Kingston >, "Rebekah.Kading < , "spwa >, "ian.mendenhall "
Cc: "Stokes, Martha M CIV (USA)" Hoyle Katie Leahy >, Megan Hudson >, "Aleman, Nicki D CTR DTRA COOP THRT REDUCT (USA)" >

Subject: World One Health Congress and BTRP TRN Side Meeting - BOHRN

Dear BOHRN TRN Steering Committee Members,

On behalf of Dr. Martha Stokes, please accept this Save the Date to attend the World One Health Congress in Edinburgh, Scotland 15-17 June 2020 and participate in side meetings on BTRP's Threat Reduction Networks and planning for BOHRN.

Tentatively, we plan to hold two sessions at the end of the week: Thursday, 18 June - an afternoon TRN session that will include a wide group of BTRP-funded participants from its other research networks to discuss network metrics for sustainability; Friday, 19 June - a side meeting for BOHRN to map out its schedule and strategy, aligning with funding opportunities from BTRP and other entities. Attached is a tentative schedule for the week, for your reference. Due to travel and budgetary constraints we are unable to invite the entire steering committee, but intend to have productive discussions and meet objectives with the smaller group on this Save the Date email.

Please let us know if you will be able to attend the WOHC and side meetings on 18-19 June. Official invitation with travel instructions, details on arrangements, and more formal agenda will be forthcoming. Please note that there is a potential for the WOHC and BTRP side meetings to be postponed, given the current travel uncertainties related to COVID-19. We will be monitoring the status of the conference, and will keep you apprised of any cancellations should they occur. As always, let us know if you have any questions!

We hope to see you in Edinburgh!!

V/r,
Caitlin Devaney

CAITLIN DEVANEY | ***Program Manager***
Global Systems Engineering, LLC
A Certified HUBZone Company
www.globalsyseng.com

From: Kading,Rebekah on behalf of Kading,Rebekah >
Sent: Wednesday, March 11, 2020 4:25 PM EDT
To: Caitlin Devaney < >; kityrob >;
abelwade >; epstein ecohealthalliance.org>;
Tigga.Kingston >; spwa >; ian.mendenhall

CC: Stokes, Martha M CIV (USA) ; Jamechia Hoyle >; Katie Leahy
>; Megan Hudson >; Aleman, Nicki D CTR DTRA
COOP THRT REDUCT (USA) >
Subject: Re: World One Health Congress and BTRP TRN Side Meeting - BOHRN

Dear Caitlin, and hello everyone,

Thank you very much for the invitation! I would very much like to attend and participate in these discussions regarding BOHRN, but I have a couple of complications. Colorado State University currently has a restriction on international travel until further notice, but it's hard to know what things will be like in June. Hopefully that would be lifted by then. These dates also overlap with the Infectious Diseases of Bats Symposium being held at CSU June 17-19 after the American Society for Virology meeting, and I confirmed awhile ago I would participate in the bat meeting here. I think I should honor that existing commitment, which means I will not be able to attend the BOHRN steering committee meeting in Edinburgh. If this affects more steering committee members than just me, would having the BOHRN meeting in conjuction with the bat ID be a possibility? I understand if not, and I will look forward to catching up with everyone at the next opportunity!

Best regards,
Rebekah

http://www.batid.org/

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Caitlin Devaney < >
Sent: Tuesday, March 10, 2020 12:30 PM
To: kityrob ; abelwade ; epstein
ecohealthalliance.org>; Tigga.Kingston ; Kading,Rebekah
; spwa >; ian.mendenhall
>
Cc: Stokes, Martha M CIV (USA) ; Jamechia Hoyle ; Katie Leahy
; Megan Hudson < >; Aleman, Nicki D CTR DTRA COOP THRT
REDUCT (USA) >
Subject: World One Health Congress and BTRP TRN Side Meeting - BOHRN

Dear BOHRN TRN Steering Committee Members,

On behalf of Dr. Martha Stokes, please accept this Save the Date to attend the World One Health Congress in Edinburgh, Scotland 15-17 June 2020 and participate in side meetings on BTRP's Threat Reduction Networks and planning for BOHRN.

Tentatively, we plan to hold two sessions at the end of the week: Thursday, 18 June - an afternoon TRN session that will include a wide group of BTRP-funded participants from its other research networks to discuss network metrics for sustainability; Friday, 19 June - a side meeting for BOHRN to map out its schedule and strategy, aligning with funding opportunities from BTRP and other entities. Attached is a tentative schedule for the week, for your reference. Due to travel and budgetary constraints we are unable to invite the entire steering committee, but intend to have productive discussions and meet objectives with the smaller group on this Save the Date email.

Please let us know if you will be able to attend the WOHC and side meetings on 18-19 June. Official invitation with travel instructions, details on arrangements, and more formal agenda will be forthcoming. Please note that there is a potential for the WOHC and BTRP side meetings to be postponed, given the current travel uncertainties related to COVID-19. We will be monitoring the status of the conference, and will keep you apprised of any cancellations should they occur. As always, let us know if you have any questions!

We hope to see you in Edinburgh!!

V/r,
Caitlin Devaney

CAITLIN DEVANEY | ***Program Manager***
Global Systems Engineering, LLC

From: Kading,Rebekah
Sent: Tuesday, November 13, 2018 10:35 AM EST
To: Stokes, Martha M CIV (US) katie.leahy ; Megan Hudson ; Jon Epstein ecohealthalliance.org>; Kingston, Tigga >
Subject: thank you!

Dear Marty, Katie, Megan, Jon, and Tigga -

I just wanted to send a quick message to thank you for all your hard work on our BOHRN meeting last week! I know that took an amazing amount of coordination to get so many more people there, and I thought it was a very productive time! It was nice to have formal talks from some folks, and the white paper exercise was a great way to get people working together. I appreciate all the time and energy you each put into BOHRN -- it is a unique group with an important purpose and I am excited about the trajectory we are on so far! I'll look forward to touching base again soon about planning the Uganda meeting in the spring.

Take care and have a great week -

Best regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Katie Leahy
Sent: Tuesday, December 12, 2017 10:41 AM EST
To: Keti Sidamonidze < >; Robert Kityo ; Ian Mendenhall ; Joram Buza >; Vivek Kapur < ; Kevin Olival ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>; Kading,Rebekah >; Lela Urushadaze Lela Urushadaze >; Tamar Kutateladze ; Supaporn Wacharapluesadee < >; Abel Wade ; Catalino Demetria ; Tigga Kingston >; Paul Cryan >; DeeAnn Reeder >; Gavin Smith >; Nisreen Alhmoud
CC: Stokes, Martha M CIV (US) >; Megan Hudson >; Lancaster, Mary J CIV (US) >; Aleman, Nicki D CTR DTRA J3-7 (US) >
Subject: BPERNet Side Meeting / PMAC

All,

By now you should have received a letter of invitation from the PMAC Organizing Committee. Please log-on and sign up to the sessions that you can attend. Our side meeting will be on the 30th at Chula Hospital. If you have confirmed attendance with us, then you should have already contacted Nicki Aleman (copied). If not, and you require travel assistance, please email me and her.

CBEP is still covering your air travel, transport to and from the airport, and hotel arrangements, so please ignore those instructions in your PMAC invitation.

Please let me know if you have any questions.

V/r,

Katie Leahy

Katie Leahy
Program Manager | Global Systems Engineering
6303 Little River Turnpike, Suite 208
Alexandria, VA 22305

http://globalsyseng.com

From: Kading,Rebekah on behalf of Kading,Rebekah >
Sent: Wednesday, January 10, 2018 10:38 AM EST
To: Katie Leahy >; lance.r.brooks >; Newman, Carl I CIV DTRA J3-7 (US) >; christopher.r.lewis ; mary.j.lancaster BounheuangK >; cryanp >; vkapur >; olival ecohealthalliance.org>; epstein ecohealthalliance.org>; ian.mendenhall ; l.urushadze >; gavin.smith abelwade >; c_demetria ; spwa >; kityrob ; tamar_kutateladze ; nisreen.hmoud >; joram.buza ; Tigga Kingston >; DeeAnn Reeder < >; Keti Sidamonidze >
CC: martha.m.stokes.civ ; Megan Hudson <
Subject: Re: Reception at U.S. Embassy (Context)

Thank you very much, Katie, for providing this context to the event. It is an honor to be invited, and I'm very much looking forward to it! A sincere thank you to CBEP as well, for all your excellent work in promoting cooperation on health issues in this region and globally. I'm looking forward to seeing all of you very soon and continuing development of the BPERNet.

Kind regards,
Rebekah

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

From: Katie Leahy
Sent: Wednesday, January 10, 2018 4:07:37 AM
To: lance.r.brooks . Newman, Carl I CIV DTRA J3-7 (US); christopher.r.lewis ; mary.j.lancaster BounheuangK ; cryanp ; Kading,Rebekah; vkapur ; ecohealthalliance.org; ecohealthalliance.org; ian.mendenhall l.urushadze gavin.smith abelwade ; c_demetria ; spwa kityrob tamar_kutateladze ; nisreen.hmoud ; joram.buza Tigga Kingston; DeeAnn Reeder; Keti Sidamonidze
Cc: martha.m.stokes. ; Megan Hudson
Subject: Reception at U.S. Embassy (Context)

All,

You likely received an invitation from “Protocol Bangkok” inviting you to a Prince Mahidol Award Reception at the U.S. Ambassador’s residence on Thursday, February 1 from 1800 – 2000.

Here is a bit of context about the event: this year, the United States became the first country to receive awards in all categories of the Prince Mahidol Awards, which are awarded annually under patronage of the Thai Royal Family to individuals and organizations that have made outstanding contributions to medicine and public health. Historically, winners have been forerunners to Nobel prizes. This year’s American awardees include the Human Genome Project and a team of researchers who developed a vaccine against Haemophilus influenza.

The U.S. Ambassador is not only proud of this historic American accomplishment, but would also like to use the opportunity to highlight the U.S. Government’s long history of military and civilian cooperation on health issues in Thailand and the greater region. The 60-year history of U.S. – Thai health cooperation is one of the lesser told success stories of the long-standing relationship with a close regional ally; and further, an alignment with the 200-year anniversary of U.S. – Thai friendship, which also occurs in 2018.

CBEP is very much a contributor to U.S.-Thai military and civilian cooperation and accomplishment on health issues; therefore, Dr. Stokes and her colleagues are co-sponsoring the celebration at the Ambassador’s residence and provided your names as their guests to the event. On behalf of her and the CBEP delegation, we very much hope you will attend.

Please let me know **if you did not receive an invitation**. Please also let me know if you have any questions. Otherwise, please follow the instructions in your invitation for favorable response.

Thank you!

V/r,

Katie Leahy

Katie Leahy
Program Manager | Global Systems Engineering
6303 Little River Turnpike, Suite 208
Alexandria, VA 22305

http://globalsyseng.com

Subject: Bat Facility meeting
Location: Microsoft Teams Meeting

Start: Tuesday, March 31, 2020 12:00 PM EDT
End: Tuesday, March 31, 2020 1:00 PM EDT
Show Time As: Tentative

Recurrence: None

Meeting Status: Not yet responded

Organizer: Kendall,Lon
Required Attendees: Kendall,Lon ; Angela Bosco-Lauth >; Bowen,Richard ; Dean,Gregg ; epstein ecohealthalliance.org>; Schountz,Tony >; Szalai,Edit >; bpope jean.patterson >; mchallberg < ; Ebel,Greg >; Cassetti, Cristina (NIH/NIAID) [E]

Here is tomorrow's agenda. Talk to you all tomorrow. You should be able to join by clicking the link below.
Introduction
Lon- why meeting was initially organized, then turf to Jon (I won't be long)
Jon- provide background about program discussions with CSU and NIAID and why we are here (Jon really sparked this discussion, and is probably best to lead)
Jean- Discuss NIAID possibilities and expectations and what's needed from CSU (Thought Jean should go sooner to help frame discussion below. I will send her agenda once we get it finalized)
Ebel- Discuss CVID abilities, and possibilities related to emerging disease, prior C06
Tony- Discuss current research and potential needs
Bowen/Angela- Discuss current research and potential needs
Determine next steps

_____
Join Microsoft Teams Meeting<https://nam01.safelinks.protection.outlook.com/ap/t-59584e83/?url=https%3A%2F%2Fteams.microsoft.com%2Fl%2Fmeetup-join%2F19%253ameeting_NzEwNWQwYWEtZDA3Yi00OTczLTgzNGMtY2Y4MGU4MWRiNDYw%2540thread.v2%2F0%3Fcontext%3D%257b%2522Tid%2522%253a%2522afb58802-ff7a-4bb1-ab21-367ff2ecfc8b%2522%252c%2522Oid%2522%253a%2522c577d4c0-7b31-47d8-891c-90b281bca62b%2522%257d&data=02%7C01%7CRichard.Bowen%40ColoState.EDU%7Ca716e5dffcb2409d015008d7d5195d2e%7Cafb58802ff7a4bb1ab21367ff2ecfc8b%7C0%7C0%7C637212177216827495
Learn more about Teams<https://nam01.safelinks.protection.outlook.com/?url=https%3A%2F%2Faka.ms%2FJoinTeamsMeeting&data=02%7C01%7CRichard.Bowen%40ColoState.EDU%7Ca716e5dffcb2409d015008d7d5195d2e%7Cafb58802ff7a4bb1ab21367ff2ecfc8b%7C0%7C0 | Meeting options<https://nam01.safelinks.protection.outlook.com/?url=https%3A%2F%2Fteams.microsoft.com%2FmeetingOptions%2F%3ForganizerId%3Dc577d4c0-7b31-47d8-891c-90b281bca62b%26tenantId%3Dafb58802-ff7a-4bb1-ab21-367ff2ecfc8b%26threadId%3D19_meeting_NzEwNWQwYWEtZDA3Yi00OTczLTgzNGMtY2Y4MGU4MWRiNDYw%40thread.v2%26messageId%3D0%26language%3Den-US&data=02%7C01%7CRichard.Bowen%40ColoState.EDU%7Ca716e5dffcb2409d015008d7d5195d2e%7Cafb58802ff7a4bb1ab21367ff2ecfc8b%7C0%7C0%7C637212177216827495&sdata=2GJzTgA9u
_____

From: Tony Schountz > on behalf of Schountz,Tony >
Sent: Wednesday, October 21, 2020 3:33 PM EDT
To: epstein ecohealthalliance.org>
Subject: Genome paper

Jon, I suspect you've seen this?

https://www.frontiersin.org/articles/10.3389/fmicb.2020.01807/full

Should be quite helpful for the grant.

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Tony Schountz > on behalf of Schountz,Tony <
Sent: Monday, October 19, 2020 4:27 PM EDT
To: epstein ecohealthalliance.org>
Subject: Monoclonal antibodies

Jon, I think a really important part of the grant will be to make monoclonal antibodies to various proteins (e.g., CD antigens, cytokines) and cytokines as reagents. If you agree, I'd like to approach a colleague of my, Brian Geiss, to see if he is willing to be on the grant. Recombinant protein expression is his "thing" and he would be a great asset for the grant.

I also think we should get as many letters of support that we can get. I can probably get at least 10 from people we've helped over the years (provided tissues and cells, conducted experimental infections, etc.).

Let me know what you think.

Just moved into our new building. It is really sweet. :)

Thanks,

T.

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Tony Schountz on behalf of Schountz,Tony <
Sent: Wednesday, October 21, 2020 4:28 PM EDT
To: epstein ecohealthalliance.org>
Subject: Re: Genome paper

Yes, I'd like to start on it next week. I have some grading to do this week plus interviews for DVM/PhD candidates for our program, so calendar is quite full. Next week is pretty good for me except (MST) Monday 2-3, Tues 12-2, Wed 3-5. Any of those work for you?

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Oct 21, 2020, at 2:05 PM, Jon Epstein ecohealthalliance.org> wrote:

Yes! I agree.

Should we schedule a time to talk? So we can start to organize for writing this thing?

On Wed, Oct 21, 2020 at 3:33 PM Schountz,Tony > wrote:

> Jon, I suspect you've seen this?
>
> https://www.frontiersin.org/articles/10.3389/fmicb.2020.01807/full
>
> Should be quite helpful for the grant.
>
> T.
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

)

web: ecohealthalliance.org

From: Tony Schountz on behalf of Schountz,Tony >
Sent: Monday, October 19, 2020 4:40 PM EDT
To: epstein ecohealthalliance.org>
Subject: Re: Monoclonal antibodies

It would be a great idea to have another building in-country for housing and staging bats for quarantine before shipping to USA.

Getting on a call with DARPA in a few minutes, so won't be responsive for an hour or so.

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Oct 19, 2020, at 2:38 PM, Jon Epstein ecohealthalliance.org> wrote:

Awesome - and agree.
I would like to brainstorm together for the letters before we approach anyone. I'll start a google doc and we can live edit it.
Let's think about who the 'dream team' will be for this.
It also occurred to me - what do you think about building in a facility in Bangladesh where we keep a captive breeding colony, that would serve as a feeder if we need more bats along the way? We could develop and fund a closed colony there, like what Cambridge did in Ghana, and we'd know the status of each bat. Brian Pope would be great at helping set this up. And it would allow the colony at CSU to fluctuate a bit in size, and we could pull in new bats as needed. I think it's a nice insurance policy to support the colony in CO as we develop it. This could be something I would manage - but I think we could convince the govt and if we provide all the funding for construction and upkeep, it could really happen.

Thoughts?

On Mon, Oct 19, 2020 at 4:27 PM Schountz,Tony wrote:

> Jon, I think a really important part of the grant will be to make monoclonal antibodies to various proteins (e.g., CD antigens, cytokines) and cytokines as reagents. If you agree, I'd like to approach a colleague of my, Brian Geiss, to see if he is willing to be on the grant. Recombinant protein expression is his "thing" and he would be a great asset for the grant.
>
> I also think we should get as many letters of support that we can get. I can probably get at least 10 from people we've helped over the years (provided tissues and cells, conducted experimental infections, etc.).
>
> Let me know what you think.
>
> Just moved into our new building. It is really sweet. :)
>
> Thanks,
>
> T.
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

web: ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

From: Tony Schountz > on behalf of Schountz,Tony < >
Sent: Wednesday, October 07, 2020 3:58 PM EDT
To: Woodson, Sara (NIH/NIAID) [E] >
CC: epstein ecohealthalliance.org>; Schountz,Tony ; Ebel,Greg >; jean.patterson ; Challberg, Mark (NIH/NIAID) [E]

Subject: Re: R24 Discussion

Yes, thanks much, Sara. I appreciate that you, Jean and Mark chatted with us today.

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Oct 7, 2020, at 1:51 PM, Woodson, Sara (NIH/NIAID) [E] wrote:

Hi Tony, Jon, and Greg;
Here are the example R24's you may want to look up in NIH Reporter:

R24AI059830 PI: Jacques Robert (University of Rochester, animal model containing)
R24AI120942 PI: Scott Weaver (University of Texas Medical Branch, WRCEVA—no model development but may be relevant if thinking about including training; may also be good to link in with them for potential distribution of critical reagents along with BEI Resources)

As Mark mentioned on the phone, NIAID doesn't allow a lot of R24 grants and thus not many are funded, so there aren't many relevant examples to what you would be putting forth in your R24. Please let me know if you have other questions or concerns!
Happy writing 😊
Sincerely, Sara

-----Original Appointment-----
From: Woodson, Sara (NIH/NIAID) [E]
Sent: Wednesday, September 30, 2020 1:22 PM
To: Woodson, Sara (NIH/NIAID) [E]; ecohealthalliance.org; Schountz, Tony; Ebel,Greg; Patterson, Jean (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Beaubien, Candice (NIH/NIAID) [E]
Subject: R24 Discussion
When: Wednesday, October 7, 2020 3:00 PM-3:30 PM (UTC-05:00) Eastern Time (US & Canada).
Where: Skype Meeting

Please use this Zoom link for our meeting this afternoon instead…..

https://www.zoomgov.com/j/1614258516?pwd=bGVHUDFrbHVxWm91M2ZGUEdWcXF4QT09

Sincerely, Sara

From: Tony Schountz
Sent: Tuesday, March 07, 2017 7:05 AM EST
To: peng.zhou
CC: Schountz,Tony >
Subject: Bat ID Abstract Submission

Thank you for submitting an abstract to the Bat ID Symposium. A decision on its disposition will be made in May.

Bat ID Abstract Submission

Presenting author email address *	
Presentation Type *	Oral Presentation
Please choose ONE or TWO categories for your abstract *	• Immunology
Title *	Dampening of STING-dependent IFN production: an implication of virus tolerance in bats?
Authors *	Xie J, Ma C, Li Y, Cui J, Wang L-F, Shi Z, Zhou P*
Institutions *	Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan 430071, China; Emerging Infectious programme, Singapore Duke-NUD Medical School, Singapore 169857, Singapore
Upload your abstract *	us_bat_conference_peng_zhou_oral1.docx 14.40 KB · DOCX

From: Tony Schountz
Sent: Wednesday, March 29, 2017 9:37 AM EDT
To: zlshi <
CC: Schountz,Tony
Subject: Bat ID Abstract Submission

Thank you for submitting an abstract to the Bat ID Symposium. A decision on its disposition will be made in May.

Bat ID Abstract Submission

Presenting author email address *	
Presentation Type *	Oral Presentation
Please choose ONE or TWO categories for your abstract *	• Coronaviruses
Title *	SARS coronavirus may have originated from frequent recombination events between SARS-like coronaviruses in a single horseshoe bat habitat
Authors *	Hu B, Zeng L-P, Yang X-L, Ge X-Y, Zhang W, Li B, Luo D-S, Zhang Y-Z, Wang M-N, Daszak P, Wang L-F, Cui J, Shi Z-L.
Institutions *	CAS Key Laboratory of Special Pathogens and Biosafety, Center for Emerging Infectious Diseases of Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China; Yunnan Institute of Endemic Diseases Control and Prevention, Dali, China; EcoHealth Alliance, New York, New York, USA; Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore
Upload your abstract *	us_bat_conference_zhengli_shi_oral.docx 16.38 KB · DOCX

From: Tony Schountz >
Sent: Saturday, April 01, 2017 9:20 PM EDT
To: huben >
CC: Schountz,Tony
Subject: Bat ID Abstract Submission

Thank you for submitting an abstract to the Bat ID Symposium. A decision on its disposition will be made in May.

Bat ID Abstract Submission

Presenting author email address *	
Presentation Type *	Poster Presentation
Please choose ONE or TWO categories for your abstract *	• Coronaviruses
Title *	Genomic characterization of diverse BatCoV HKU10 and three novel alphacoronaviruses
Authors *	Wang N, Luo CM, Yang XL, Liu HZ, Zhang W, Li B, Ge XY, Hu B, Zhu Y, Peng C, Shi ZL
Institutions *	Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan 430071, China.
Upload your abstract *	us_bat_conference_ben_hu_poster.docx 17.15 KB · DOCX

From: Tony Schountz >
Sent: Saturday, April 01, 2017 3:51 AM EDT
To: yangx
CC: Schountz,Tony
Subject: Bat ID Abstract Submission

Thank you for submitting an abstract to the Bat ID Symposium. A decision on its disposition will be made in May.

Bat ID Abstract Submission

Presenting author email address *	
Presentation Type *	Poster Presentation
Please choose ONE or TWO categories for your abstract *	• Filoviruses
Title *	Genetically Diverse Filoviruses in Rousettus and Eonycteris spp. Bats, China, 2009 and 2015
Authors *	Xing-Lou Yang, Yun-Zhi Zhang, Ren-Di Jiang, Hua Guo, Wei Zhang, Bei-Li, Ning Wang, Li-Wang, Cecilia Waruhiu, Ji-Hua Zhou, Shi-Yue Li, Peter Daszak, Lin-Fa Wang, Zheng-Li Shi
Institutions *	Wuhan Institute of Virology, Chinese Academy of Sciences
Upload your abstract *	abstract_for_bat_virus_meeting.docx 19.29 KB · DOCX

From: Schountz,Tony
Sent: Thursday, April 27, 2017 12:58 PM EDT
To: Schountz,Tony
CC: huben >
Subject: Re: Bat ID Abstract Submission

Dear Ben,

Your abstract submission has been accepted for a **POSTER** presentation. The session is **Friday, April 30 from 12:00 to 2:00 PM** in the University Center for the Arts. The maximum size of your poster **should not exceed 122 cm/48 inches height and width**. We will provide push pins for mounting your poster on the easel. If you have questions, please feel free to contact me.

Thank you and we look forward to your presentation.

Tony Schountz

On Apr 1, 2017, at 7:20 PM, Tony Schountz > wrote:

Thank you for submitting an abstract to the Bat ID Symposium. A decision on its disposition will be made in May.

Bat ID Abstract Submission

Presenting author email address *	
Presentation Type *	Poster Presentation
Please choose ONE or TWO categories for your abstract *	• Coronaviruses
Title *	Genomic characterization of diverse BatCoV HKU10 and three novel alphacoronaviruses
Authors *	Wang N, Luo CM, Yang XL, Liu HZ, Zhang W, Li B, Ge XY, Hu B, Zhu Y, Peng C, Shi ZL
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Upload your abstract *	us_bat_conference_ben_hu_poster.docx 17.15 KB · DOCX

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony >
Sent: Thursday, April 27, 2017 12:47 PM EDT
To: Schountz,Tony
CC: yangxl >
Subject: Re: Bat ID Abstract Submission

Dear Xing-Lou,

Your abstract submission has been accepted for a **POSTER** presentation. The session is **Friday, April 30 from 12:00 to 2:00 PM** in the University Center for the Arts. The maximum size of your poster **should not exceed 122 cm/48 inches height and width**. We will provide push pins for mounting your poster on the easel. If you have questions, please feel free to contact me.

Thank you and we look forward to your presentation.

Tony Schountz

> On Apr 1, 2017, at 1:51 AM, Tony Schountz > wrote:
>
> Thank you for submitting an abstract to the Bat ID Symposium. A decision on its disposition will be made in May.
>
> ## Bat ID Abstract Submission
>
> | | |
> |---|---|
> | **Presenting author email address** * | |
> | **Presentation Type** * | Poster Presentation |
> | **Please choose ONE or TWO categories for your abstract** * | • Filoviruses |
> | **Title** * | Genetically Diverse Filoviruses in Rousettus and Eonycteris spp. Bats, China, 2009 and 2015 |
> | **Authors** * | Xing-Lou Yang, Yun-Zhi Zhang, Ren-Di Jiang, Hua Guo, Wei Zhang, Bei-Li, Ning Wang, Li-Wang, Cecilia Waruhiu, Ji-Hua Zhou, Shi-Yue Li, Peter Daszak, Lin-Fa Wang, Zheng-Li Shi |
> | **Institutions** * | Wuhan Institute of Virology, Chinese Academy of Sciences |
> | **Upload your abstract** * | abstract_for_bat_virus_meeting.docx
19.29 KB · DOCX |

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: 石正丽 <zlshi >
Sent: Wednesday, April 26, 2017 8:32 PM EDT
To: Schountz,Tony
Subject: Re: Re: Bat ID Abstract Submission

Dear Tony,

Thank you very much for your information and organising the meeting!

Looking forward to meeting you!

Best regards,

Zhengli,

-----原始邮件-----
发件人: "Schountz,Tony"
发送时间: 2017年4月27日 星期四
收件人: "Schountz,Tony"
抄送: "zlshi
主题: Re: Bat ID Abstract Submission

Dear Dr. Shi,

We have you scheduled to give a 15 min talk (12 minutes plus 3 minutes for questions) at the bat infectious diseases symposium, probably Friday morning, June 30. I should have the program draft up next week.

Thanks,

Tony

On Mar 29, 2017, at 7:37 AM, Tony Schountz > wrote:

Thank you for submitting an abstract to the Bat ID Symposium. A decision on its disposition will be made in May.

Bat ID Abstract Submission

Presenting author email address *	
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Institutions *	CAS Key Laboratory of Special Pathogens and Biosafety, Center for Emerging Infectious Diseases of Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China; Yunnan Institute of Endemic Diseases Control and Prevention, Dali, China; EcoHealth Alliance, New York, New York, USA; Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore
Upload your abstract *	us_bat_conference_zhengli_shi_oral.docx 16.38 KB · DOCX

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: zlshi >
Sent: Wednesday, July 12, 2017 9:39 PM EDT
To: Schountz,Tony >
CC: 周鹏 <peng.zhou linfa.wang
Subject: 回复: Re: Bat ID Abstract Submission

Dear Tony,

Thank you for your organizing the nice bat ID symposium. We enjoy very much th discussion with the scientists of different speciality.

Thank you for your considering to participate in the meeting "8th International symposium on emerging viral dieases" to be held in Wuhan in Ocotber, 2018. We will add you at the email distribution list and let you know as soon as we have a fixed date. Usually, the meeting will be held at the 4th week with the duration of 3 days (with 2 days of scientifc activity).

Looking forward to meeting you again,

Best regards,
Zhengli,

发件人： Schountz,Tony
发送时间： 2017-07-13 08:16
收件人： 石正丽
主题： Re: Re: Bat ID Abstract Submission

Hi Zhengli,

I hope your travel home was peaceful. I wanted to thank you for your attendance and presentation at the bat ID symposium. I think it was a very good meeting and I hope others benefited from it. We are already planning to host it again in 2020.

If you have an email distribution list for the conference you're hosting next year, could you please add me to it? It looks like a great meeting and if I can get travel arranged I would like to come.

Thank you,

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: 石正丽 <zlshi >
Sent: Wednesday, April 26, 2017 6:32 PM
To: Schountz,Tony
Subject: Re: Re: Bat ID Abstract Submission

Dear Tony,
Thank you very much for your information and organising the meeting!
Looking forward to meeting you!
Best regards,

Zhengli,

-----原始邮件-----
发件人: "Schountz,Tony"
发送时间: 2017年4月27日 星期四
收件人: "Schountz,Tony"
抄送: "zlshi "
主题: Re: Bat ID Abstract Submission

Dear Dr. Shi,

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Thanks,

Tony

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Thank you for submitting an abstract to the Bat ID Symposium. A decision on its disposition will be made in May.

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Institutions *	CAS Key Laboratory of Special Pathogens and Biosafety, Center for Emerging Infectious Diseases of Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China; Yunnan Institute of Endemic Diseases Control and Prevention, Dali, China; EcoHealth Alliance, New York, New York, USA; Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore
Upload your abstract *	us_bat_conference_zhengli_shi_oral.docx 16.38 KB · DOCX

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

Subject: Bat Facility meeting
Location: Microsoft Teams Meeting

Start: Tuesday, March 31, 2020 12:00 PM EDT
End: Tuesday, March 31, 2020 1:00 PM EDT
Show Time As: Busy

Recurrence: None

Meeting Status: Not yet responded

Organizer: Kendall,Lon
Required Attendees: Kendall,Lon >; Angela Bosco-Lauth < >; Bowen,Richard < ; Dean,Gregg ; epstein ecohealthalliance.org>; Schountz,Tony >; Szalai,Edit bpope < >; jean.patterson ; mchallberg >; Ebel,Greg >; Cassetti, Cristina (NIH/NIAID) [E]

Here is tomorrow's agenda. Talk to you all tomorrow. You should be able to join by clicking the link below.
Introduction
Lon- why meeting was initially organized, then turf to Jon (I won't be long)
Jon- provide background about program discussions with CSU and NIAID and why we are here (Jon really sparked this discussion, and is probably best to lead)
Jean- Discuss NIAID possibilities and expectations and what's needed from CSU (Thought Jean should go sooner to help frame discussion below. I will send her agenda once we get it finalized)
Ebel- Discuss CVID abilities, and possibilities related to emerging disease, prior C06
Tony- Discuss current research and potential needs
Bowen/Angela- Discuss current research and potential needs
Determine next steps

Join Microsoft Teams Meeting<https://nam01.safelinks.protection.outlook.com/ap/t-59584e83/?url=https%3A%2F%2Fteams.microsoft.com%2Fl%2Fmeetup-join%2F19%253ameeting_NzEwNWQwYWEtZDA3Yi00OTczLTgzNGMtY2Y4MGU4MWRiNDYw%2540thread.v2%2F0%3Fcontext%3D%257b%2522Tid%2522%253a%2522afb58802-ff7a-4bb1-ab21-367ff2ecfc8b%2522%252c%2522Oid%2522%253a%2522c577d4c0-7b31-47d8-891c-90b281bca62b%2522%257d&data=02%7C01%7CTony.Schountz%40colostate.edu%7Ca716e5dffcb2409d015008d7d5195d2e%7Cafb58802ff7a4bb1ab21367ff2ecfc8b%7C0%7C0%7C637212177217988770
Learn more about Teams<https://nam01.safelinks.protection.outlook.com/?url=https%3A%2F%2Faka.ms%2FJoinTeamsMeeting&data=02%7C01%7CTony.Schountz%40colostate.edu%7Ca716e5dffcb2409d015008d7d5195d2e%7Cafb58802ff7a4bb1ab21367ff2ecfc8b%7C0%7C0 | Meeting options<https://nam01.safelinks.protection.outlook.com/?url=https%3A%2F%2Fteams.microsoft.com%2FmeetingOptions%2F%3ForganizerId%3Dc577d4c0-7b31-47d8-891c-90b281bca62b%26tenantId%3Dafb58802-ff7a-4bb1-ab21-367ff2ecfc8b%26threadId%3D19_meeting_NzEwNWQwYWEtZDA3Yi00OTczLTgzNGMtY2Y4MGU4MWRiNDYw%40thread.v2%26messageId%3D0%26language%3Den-US&data=02%7C01%7CTony.Schountz%40colostate.edu%7Ca716e5dffcb2409d015008d7d5195d2e%7Cafb58802ff7a4bb1ab21367ff2ecfc8b%7C0%7C0%7C637212177217988770&sdata=wiFrH%2Fv

---

From: jid_oup o>
Sent: Monday, January 13, 2020 1:01 AM EST
To: vincent.munster >; jnls.author.support ;
jonathan.schulz >; stephanie.seifert < ;
jthompson >; victoria.avanzato
lianying.yan. >; spencer.sterling.ctr
; michael.letko ; matthew.matson
; fischerro < >; atremeau
; jseetahal ; vernie.ramkisson
>; jerome.foster >; tgoldstein
; sja ; epstein
ecohealthalliance.org>; eric.laing ; christopher.broder
; christine.carrington >; Schountz,Tony

Subject: Action needed: check your proof 10.1093/infdis/jiz648

Dear Dr. Vincent Munster,

You must check your proof now to avoid delaying publication.

What you need to do now:

1. Access your proof https://pubkit.newgen.co/auth_token_login/af89fcf9-b35f-40b5-a782-420952f1a4a4

2. Respond on the proof to any copyeditor queries.

3. Approve your proof for publication or submit minor formatting corrections within one working day.

Please note that this is causing a delay to the publication of your manuscript. Please contact us if you need any help.

Best wishes,

The Journal of Infectious Diseases production team

Oxford University Press

From: 胡犇 <huben >
Sent: Friday, September 28, 2018 11:17 PM EDT
To: Schountz,Tony >
Subject: Agenda of the 8th International Symposium of Emerging Viral Diseases
Attachment(s): "Program of the 8th ISEVD.pdf"

Dear speaker:

We have made the program for our emerging virus symposium. Your presentation is scheduled in the afternoon of 21st October, in the session "emerging viral pathogens".

I have attached the program for your information.

We have reserved accommodation for you at the conference venue, Optic Valley Plaza hotel. Please provide me your flight information once it is available, and we will arrange pick-up service at the airport.

Also, please send me your update CV by 7th October, as we would like to include the CV of our speakers together with the abstracts in the conference proceedings.

Thank you!

Best wishes

Ben Hu Ph.D

Wuhan Institute of Virology, CAS
Secretary of the 8th ISEVD

Program of
The 8th International Symposium on Emerging Viral Diseases

Date 日期	Time 时间	Content 议程
Saturday 星期六 Oct. 20, 2018 10 月 20 日	**Venue 地点** 09:00-21:00	**Registration**/报到注册 Ground Floor, Optics Valley Kingdom Plaza Hotel/光谷金盾大酒店一楼大厅
Sunday 星期日 Oct. 21, 2018 10 月 21 日	**Day 1, Morning Session /第一天上午**	
	Venue 地点	Banquet Hall of Optics Valley Kingdom Plaza 3nd floor of the hotel 光谷金盾大酒店三楼宴会厅
	08:30-08:40	**Opening Address/开幕式致词**
	08:40-11:50	**Session 1: Antiviral Immunity** **Session Chairs: Peng ZHOU, Linfa WANG**
	08:40-09:10 Keynote Speech S-01	**Title:** Holy immune balance, batman! **Speaker: Linfa Wang** Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore
	09:10-09:30 S-02	**Title: To be determined** **Speaker: Yanyi Wang** Wuhan Institute of Virology, Chinese Academy of Sciences
	09:30-09:50	Group Photo of Symposium Participants/与会代表合影 Coffee Break /茶歇
	09:50-10:10 S-03	**Title:** Recent advances in developing therapeutics monoclonal antibodies Against Ebola Virus Infection **Speaker: Xiangguo Qiu** Special Pathogens Program, National Microbiology laboratory, Public Health Agency of Canada
	10:10-10:30 S-04	**Title:** Nipah virus and Hendra Virus: Basic Science to Global Countermeasures **Speaker: Christopher Broder** Department of Microbiology, Uniformed Services University, Bethesda, MD, USA
	10:30-10:50 S-05	**Title:** Immunopathogenesis of Nipah virus infection **Speaker: Branka Horvat** International Center for Infectiology Research - CIRI, INSERM U1111, University Lyon 1, France
	10:50-11:10 S-06	**Title:** Incorporation of NS1 and PrM/M confer more effective protection for ZIKA virus vaccine **Speaker: Ling Chen** Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences, Guangzhou, China

11:10-11:30 S-07	**Title:** Antiviral RNAi immunity – from basic to translation **Speaker: Xi Zhou** Wuhan Institute of Virology, Chinese Academy of Sciences
11:30-11:50 S-08	**Title:** To be determined **Speaker: Shi Liu** Wuhan University, China
11:50-12:05 Sponsor Presentation	Newly Technology development of Cryo TEM by JEOL **By Jianzhong Yuan** TEM product manager of JEOL in China
12:05-14:00	Lunch/午餐
Day 1, Afternoon Session /第一天下午	
14:00-17:30	**Session 2: Emerging viral pathogens** **Session Chairs: Zhengli SHI, Peter DASZAK**
14:00-:14:30 Keynote Speech S-09	**Title:** To be determined **Speaker: Hualan Chen** Harbin Veterinary Research Institute, Chinese Academy of Agricultural Sciences, Harbin, China
14:30-14:50 S-10	**Title:** Forecasting future viral pandemics and the Global Virome Project **Speaker: Peter Daszak** EcoHealth Alliance, New York, USA
14:50-15:10 S-11	**Title:** Infection and Immune Responses of Jamaican Fruit Bats (*Artibeus jamaicensis)* Experimentally Challenged with a Bat HL18NL11 Influenza A Virus **Speaker: Tony Schountz** Department of Microbiology, Immunology and Pathology, College of Veterinary Medicine and Biomedical Sciences, Colorado State University
15:10-15:30 S-12	**Title:** To be determined **Speaker: Di Liu** Wuhan Institute of Virology, Chinese Academy of Sciences
15:30-15:50	Coffee Break and Poster Presentation/茶歇和展板
15:50-16:10 S-13	**Title:** Risks of MERS-cluster coronaviruses in China **Speaker: Peng Zhou** Wuhan Institute of Virology, Chinese Academy of Sciences
16:10-16:30 S-14	**Title:** Molecular mechanisms for cross-species transmissions of SARS and MERS coronaviruses **Speaker: Fang Li** Department of Veterinary and Biomedical Sciences, University of Minnesota
16:30-16:50 S-15	**Title:** Human coronavirus OC43 (HCoV-OC43) and bovine coronavirus (BCoV) **Speaker: Astrid Vabret** Laboratory of Virology, University Hospital of Caen, France

	16:50-17:10 S-16	**Title:** Origin and cross-species transmission of bat coronaviruses in China **Speaker: Alice Latine** EcoHealth Alliance, New York, USA
	17:10-17:30 S-17	**Title:** Coronaviruses phylogenetics and intra-colony evolution of the SARS-CoV sister-clade Betacoronavirus in bats in western Palearctics **Speaker: Meriadeg Ar Gouilh** Groupe de Recherche sur l'Adaptation Microbienne, Normandy University, France
	18:00-20:00	Banquet 会议晚宴

Program of
The 8th International Symposium on Emerging Viral Diseases

Date 日期	Time 时间	Content 议程
Monday 星期一 Oct. 22, 2018 10 月 22 日		**Day 2, Morning Session /第二天上午**
	08:30-12:10	**Session 3: Virus-Host Interaction** **Session Chair: Xi ZHOU, Ralph BARIC**
	08:30-09:00 Keynote Speech S-18	**Title:** To be determined **Speaker: Ralph Baric** Department of Epidemiology, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA
	09:00-09:30 Keynote Speech S-19	**Title:** Peptide-based Virus Entry Inhibitors against Class I and II Enveloped Viruses **Speaker: Shibo Jiang** Basic Medical College, Fudan University, Shanghai, China
	09:30-09:50 S-20	**Title:** Small molecules as filoviral entry inhibitors and chemical probes **Speaker: Lijun Rong** Department of Microbiology and Immunology, College of Medicine, University of Illinois at Chicago, Chicago, IL, USA
	09:50-10:10 S-21	**Title:** Entry mechanisms of highly pathogenic coronaviruses: MERS-CoV and SARS-CoV **Speaker: Yi Shi** CAS Key Laboratory of Pathogenic Microbiology and Immunology, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China
	10:10-10:30	Coffee Break and Poster Presentation/茶歇和展板
	10:30-10:50 S-22	**Title:** Pathology of and development of antiviral therapy with favipiravir for severe fever with thrombocytopenia syndrome **Speaker: Masayuki Saijo** Department of Virology, National Institute of Infectious Diseases, Tokyo, Japan
	10:50-11:10 S-23	**Title:** Epistasis and complementation contribute to the evolution of the Rabies virus phosphoprotein in the face of severe functional constraints within the replication complex **Speaker: Hervé Bourhy** Institut Pasteur, Unit of Lyssavirus Dynamics and Host Adaptation, Paris, France
	11:10-11:30 S-24	**Title:** Influenza A virus-derived siRNAs increase in the absence of NS1 yet fail to inhibit virus replication **Speaker: Kevin Tsai** Department of Molecular Genetics and Microbiology, Duke University Medical Center, Durham, North Carolina, USA

	11:30-11:50 S-25	**Title:** Mechanisms of Herpesvirus capsid assembly and maturation **Speaker: Xiangxi Wang** Institute of Biophysics, Chines Academy of Sciences, Beijing, China
	11:50-12:10 S-26	**Title:** To be determined **Speaker: Yu Chen** Wuhan University, China
	12:10-13:40	Lunch/午餐
	Day 2, Afternoon Session /第二天下午	
	13:40-17:30	**Session 4: Arbovirus** **Session Chairs: Zhihong HU, Pei-Yong SHI**
	13:40-14:10 Keynote Speech S-27	**Title:** Zika Virus: Emergence and Vaccine Development **Speaker: Pei-Yong Shi** University of Texas Medical Branch, Galveston, Texas, USA
	14:10-14:30 S-28	**Title:** Replicase Proteins of Alphaviruses as Determinants of Viral Pathogenesis and Vector Transmission **Speaker: Andres Merits** Institute of Technology, University of Tartu, Estonia
	14:30-14:50 S-29	**Title:** Identification of prognostic biomarkers for Dengue disease severity through an integrated 'omics analysis of patient serum **Speaker: Andrew Davidson** University of Bristol, Bristol, United Kingdom
	14:50-15:10 S-30	**Title:** Zika virus tropism for neural stem cells: the bad and the good **Speaker: Cheng-Feng Qin** Beijing Institute of Microbiology and Epidemiology, Academy of Military Medical Sciences, Beijing, China
	15:10-15:30 S-31	**Title:** A gut commensal bacterium promotes mosquito permissiveness to arboviruses **Speaker: Gong Cheng** Tsinghua-Peking Center for Life Sciences, School of Medicine, Tsinghua University, Beijing, China
	15:30-15:50	Coffee Break 茶歇
	15:50-16:10 S-32	**Title:** The fabulous NSs protein of Rift Valley fever virus **Speaker: Pierre-Yves Lozach** Cluster of Excellence and Center for Integrative Infectious Disease Research, University Hospital Heidelberg, Germany
	16:10-16:30 S-33	**Title:** Novel delivery of a live-attenuated chikungunya virus vaccine candidate **Speaker: Adam Taylor** Griffith University, Southport, Queensland, Australia

	16:30-16:50 S-34	**Title:** To be determined **Speaker: Fei Deng** Wuhan Institute of Virology, Chinese Academy of Sciences
	16:50-17:10 S-35	**Title:** Species-specific disruption of STING-dependent antiviral cellular defenses by the Zika virus NS2B3 protease **Speaker: Qiang Ding** School of Medicine, Tsinghua University, Beijing, China
	17:10-17:30 S-36	**Title:** ISG15 regulates Zika Virus Replication through Jak/STAT Signaling pathway and its ISGylation **Speaker: Yancui Wang** Institute of Blood Transfusion, Chinese Academy of Medical Sciences and Peking Union Medical College, Chengdu, China
	17:30-17:40	**Closing Remarks**
	18:00-19:00	Dinner/晚餐

From: Roberto Bruzzone
Sent: Wednesday, July 15, 2020 2:08 AM EDT
To:

Subject: ASCB/EMBO Online Meeting

Dear All,

I would like you to consider submitting abstracts to the 2020 ASCB/EMBO Meeting, which will go virtual.
https://www.ascb.org/cellbiovirtual2020/program/

I will be co-chairing a mini-symposium in the scientific track, Cells in Distress and Disease

My initial proposal focused on host-pathogen interactions at a molecular level.

We are currently accepting abstracts for consideration to give a talk in the 2020 Minisymposia.

The deadline for submission is July 30.
https://www.ascb.org/cellbiovirtual2020/abstracts

PLEASE SHARE THIS INFORMATION WITH OTHER COLLEAGUES WHO MAY BE INTERESTED. THANKS

All the best, Roberto

Professor Roberto Bruzzone
Co-Director
HKU-Pasteur Research Pole
School of Public Health
LKS Faculty of Medicine
The University of Hong Kong

7/F, HKJC Building for IR, 5 Sassoon Road, Pokfulam, Hong Kong

website: www.hkupasteur.hku.hk
http://isaric.tghn.org/

From: Lee, Benhur
Sent: Monday, March 02, 2020 7:51 PM EST
To: Schountz,Tony
CC: Jon Epstein ecohealthalliance.org>; Anthony, Simon J.
Subject: Bat Challenge

Hi Tony,

Sorry for late notice, but I didn't want to promise something this time without following through, so Simon (Anthony) can actually vouch for me.

STRICTLY CONFIDENTIAL-For your eyes (and ears) ONLY.
If you are free tomorrow at about 4 pm EST, can you Skype or Zoom in (I'm sure Jon Epstein can figure something out). I'm presenting data to relevant company at EcoHealth Alliance.

Anything bat-related is, of course, hot right now. So, this time, if you agree to help, yours will be the last experiment, not the first.

Meanwhile, if you get this message in time, can you let us know (Simon and Jon is CC-ed on this email) what species of bat you have in your colony? It's important for us to check something before hand.

Thanks! (Again, I apologize for the short notice, what's left of my life has been consumed by my second full-time job on Twitter)

Best regards,

Benhur

Benhur Lee, M.D.
Professor of Microbiology
Ward-Coleman Chair in Microbiology
Icahn School of Medicine at Mount Sinai
One Gustave L Levy Place #1124
New York, NY 10029

Lab Webpage: LeeLabVirus.Host |

From: Kendall,Lon >
Sent: Tuesday, March 17, 2020 1:25 PM EDT
To: Jon Epstein ecohealthalliance.org>; Richard Bowen >; Ebel,Greg ; Schountz,Tony
Subject: Bat housing

All,

Alan asked me to follow up on the renovations of the bull barn for bat holding. I did a quick space assessment of the building. It is approximately 2500 sf, including a 100 sf storage area. I am assuming of the 2500 sf we'll need about 500 sf for storage, feed prep and procedure space. The AZA recommendations for Pteropus giganteus is 15'x30' per 6 bats. With 2000 sf, that leave us holding for 24-29 bats. If there are some other housing guidelines someone has, please let me know.

On the call we discussed 40-60 bats. I'm looking for advice on how to proceed. We can look at extending the footprint to accommodate 40-60, but I'm not sure what the program needs will be.

Thanks,

Lon

Lon V. Kendall, DVM, PhD, DACLAM
Director, Laboratory Animal Resources and
Attending Veterinarian, Colorado State University
2007 Painter Center
Colorado State University
Fort Collins, CO 80523

From: Schountz,Tony <
Sent: Thursday, June 22, 2017 5:19 PM EDT
To:

<

Subject: Bat ID Symposium logistics
Attachment(s): "Campus map.pdf"

Dear Colleagues,

The symposium is one week away and I want to provide you with some logistical information for your arrival to Fort Collins.

1. Speakers. If you can email your presentation directly to me I will get it on the computer for the presentation**However, the file size must be less than 15 MB to accommodate our email server limit**. Otherwise, please bring your presentation on a USB drive if it is larger than 15 mb. We will have both Microsoft Power Point and Apple Keynote software for your presentations. **Bring your USB drive to the Thursday evening reception if you want to transfer it then.**

2. Poster presenters. The maximum size of the posters is 48” x 48” (120 cm x 120 cm). We will provide push pins to mount your poster on the easels. When you register, your poster will have a number assigned to it that corresponds to the easel number. Please mount your poster on that easel. **Bring your poster to the Thursday evening reception.**

3. Getting to Fort Collins. Those of you who are flying to Denver International Airport can schedule a ride with the **Green Ride Airport Shuttle** service. Please visit its web site (https://greenrideco.hudsonltd.net/) to make arrangements convenient for your flight schedules. There is a Green Ride desk in the main terminal at the airport with employees that can help you find the bus pickup. The bus ride is about 1 hour and 15 minutes. On the web site, in the box “Dropoff location” choose the appropriate destination from the pull-down menu. For those of you staying in the university dormitories it is “FC - Laurel Village”, the Hilton Hotel near campus is “FC - Hilton Ft Collins”, and the University Inn is “FC - Best Western University Inn”. And just to make you aware, afternoon and evening flights into Denver can be rather bumpy!

4. Weather and Climate. Fort Collins has lots of sunshine and is at 5000 ft/1500 meters. If you intend to be outdoors much you should bring sunscreen. We often get afternoon thunder showers in our otherwise dry climate but they are typically not more than an hour or two and it usually clears up afterwards. You may want to bring rain gear or a small umbrella. The current forecast is for the mid to high 80sF/low 30sC.

5. Getting to the UCA. The conference venue is the **University Center for the Arts (UCA)** (attached map, blue box, lower right). Oral and poster presentations will be in this building and directions will be posted inside. After you get settled in Thursday, please come to the UCA for the opening registration and social mixer by 5:30 PM. Walking paths (routes) are noted in blue hatched lines.

A. Laurel Village Alpine Dormitory. Those who are staying in campus housing, walk south to Plum Street and turn east to Meridian Avenue. Take Meridian Avenue south to Pitkin Street and take it east to Mason Street. Cross the railroad tracks and immediately turn right (south) just before the parking garage. Follow the path to just past the parking garage and turn left (east). This path leads to a **tunnel that passes under College Avenue** and comes out at the University Test Gardens (lots of flowers). Continue on this path and it will cross Remington Street to the UCA. **Allow 15-20 minutes to walk**.

B. Hilton Hotel. Proceed from the hotel to Prospect and Centre Avenue at the northwest corner of the Hilton Hotel parking lot. Cross Centre to the west and **take the tunnel under Prospect Avenue**. At Lake Street, turn right (east) to Mason Street. Cross the railroad tracks and immediately turn left (north). Just before the parking garage, turn right (east) and take the path that leads to a **tunnel that passes under College Avenue** and comes out at the University Test Gardens. Continue on this path and it will cross Remington Street to the UCA. **Allow 10 minutes to walk**.

C. University Inn Best Western Hotel. Take Elizabeth Street east to Remington Street (one block). Turn right (south) to Pitkin Street. Once you cross Pitkin Street, the University Center for the Arts is to your left. **Allow 5 minutes to walk.**

6. Registration packet. Your registration packet will include the program, name badge, water bottle and a pass for the Fort Collins MAX bus. The pass allows you to ride the bus through Saturday night. Registration also includes lunch for Friday and Saturday. If you are staying in the dorms you will also have breakfast provided at the dorm dining hall, Corbett Hall, which is just east of Alpine Hall where you are staying (please see the attached map).

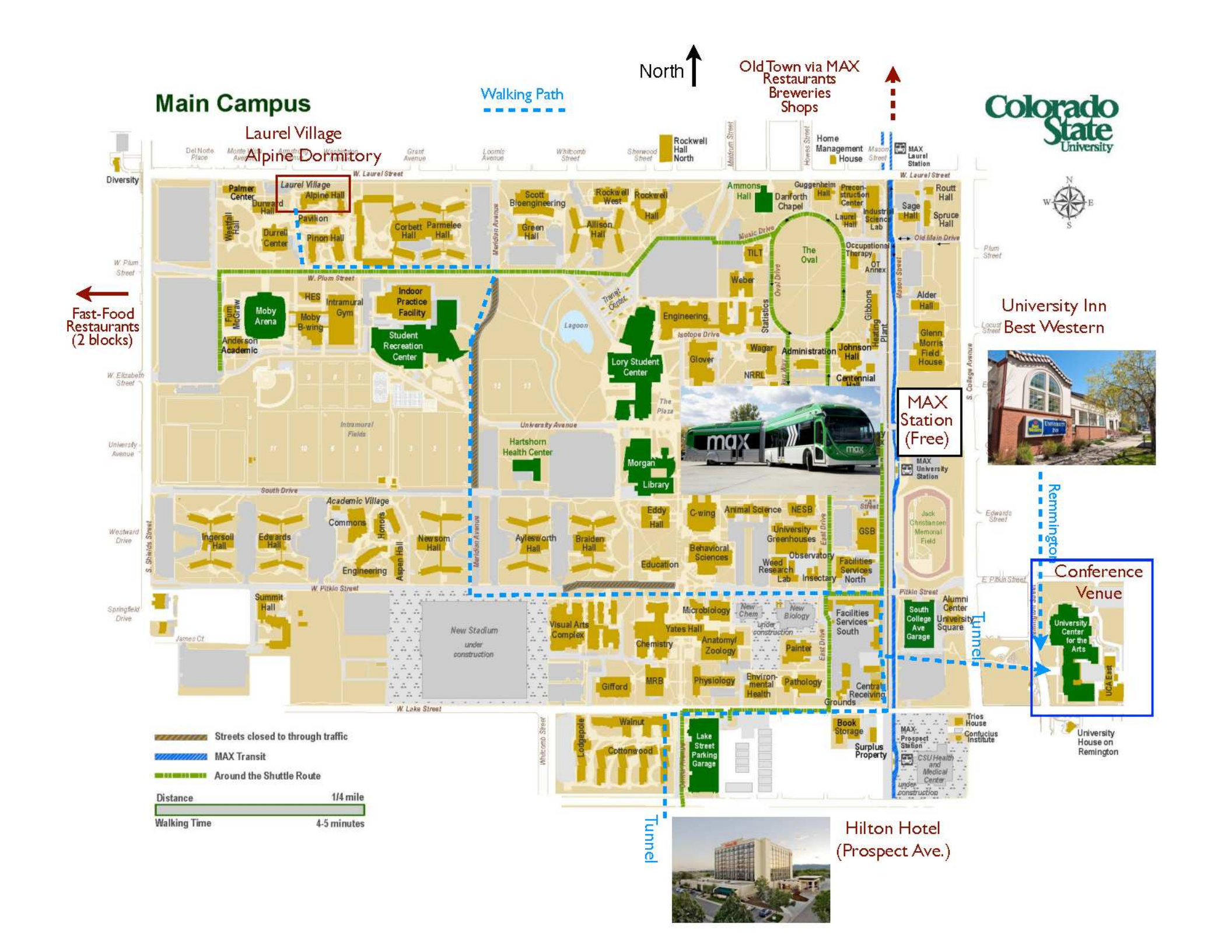
If you have questions, please contact me and I will address them. Finally, I will be at the American Society for Virology meeting Saturday through Wednesday so my email access may be intermittent.

Thanks and see you next week.

Tony

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University


Main Campus
North
Walking Path
Old Town via MAX
Restaurants
Breweries
Shops
Colorado State University
Laurel Village
Alpine Dormitory
Fast-Food Restaurants (2 blocks)
University Inn
Best Western
MAX Station (Free)
Conference Venue
Tunnel
Tunnel
Hilton Hotel (Prospect Ave.)
Remington
Streets closed to through traffic
MAX Transit
Around the Shuttle Route
Distance 1/4 mile
Walking Time 4-5 minutes

From: Kevin Olival, PhD ecohealthalliance.org>
Sent: Wednesday, March 29, 2017 4:40 PM EDT
To: Michaeleen Doucleff
CC: Jane Greenhalgh Schountz,Tony
Subject: Bat Infectious Disease meeting - Fort Collins, CO 29 June - 1 July

Dear Michaeleen,

I wanted to alert you to a conference on bat infectious diseases that's coming up this summer. Not sure if you had heard about it, or if it's something you're interested in attending or covering. I'm cc'ing my colleague Tony Schountz here who is the symposium organizer. I'll be there, along with a bunch of world-renouned bat disease nerds.

http://batid.org

Cheers,
Kevin

Kevin J. Olival, PhD

Associate Vice President for Research

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

From: Kevin Olival ecohealthalliance.org>
Sent: Tuesday, December 04, 2018 2:25 PM EST
To: Schountz,Tony >; Munster, Vincent (NIH/NIAID) [E] <
CC: Laing, Eric ; Chris Broder ; Luke Hamel ecohealthalliance.org>
Subject: Bat MERS-CoV sera for S protein luminex-based assay R&D

Dear Tony and Vincent,

Hope this finds you both well! I know Vincent is in the Congo, so his responses are delayed.

I'm working on a grant proposal (GHERI) with Chris Border and Eric Laing to do some serological screening and assay development for MERS-CoV and other CoVs using a Luminex-based platform. This builds off the work Broder and crew have already done, but will provide support for additional R&D for the MERS-CoV Spike assay, and for in-country capacity building and testing. The idea is to then use the multiplex CoV assays to screen bat sera that we are currently collecting under a DTRA supported project across Western Asia/Middle East (which I'm PI on, and Vincent is involved with).

In order to validate the MERS-CoV assay during the R&D phase,**it would be super helpful to have some confirmed MERS-CoV positive bat sera to work with**. Given that you guys have run MERS-CoV bat infection trials (and may be doing more?), I'm wondering what the possibility of getting some positive bat sera over to Chris' lab for validation? Also, in reading your paper again I remembered that you observed limited seroconversion in bats at 28 dpi… so maybe this is a moot question? Any additional evidence that supports seroconversion in bats?

The grant is due in a couple of weeks, so at this stage I'm just really looking for a general response if you think this is feasible, so we can throw a line in the proposal. i.e. "In collaboration with Vincent Munster (NIH) and Tony Schountz (CSU) we will validate our MERS S protein assay using positive control bat sera from previous experimental infection studies".

Please let me know your thoughts or any additional ideas.

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

www.ecohealthalliance.org

From: Jon Epstein < ecohealthalliance.org>
Sent: Thursday, August 03, 2017 5:42 PM EDT
To: Patricia (NIH/NIAID) Repik [E] ; Park, Eun-Chung (NIH/NIAID) [E]
CC: Schountz,Tony ; Munster, Vincent ; R. A. Bowen
>
Subject: Bat proposal
Attachment(s): "Establishing a bat colony in the US_Epstein_v3.docx","Pteropus bat model_research justification_2017.docx"

Dear Pat and Eun Chung,
It was wonderful to see you in Ft. Collins. I'm grateful that we had time to talk about this project and for your interest and support. Attached are two briefs which detail the scope of work and scientific rationale for setting up the Pteropus colony. Let's use this as a starting point for further discussion about a potential contract. I'd be happy to provide additional information as per your guidance.

Cheers,
Jon

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

)

web: ecohealthalliance.org

Draft: Pre-White paper for discussion
Epstein et al. 2016

Establishment of a pteropid bat colony (*Pteropus medius*) in the United States to study host-virus interactions, including the immune response, to Nipah virus and other zoonotic pathogens that threaten human health.

Prepared by
Jonathan Epstein, DVM, MPH, PhD, EcoHealth Alliance
Tony Schountz, PhD, Colorado State University
Dr. Vincent Munster, PhD, NIH NIAID Rocky Mountain Laboratories

Bats have been shown to carry more zoonotic pathogens than any other mammalian taxon (Olival et al, Nature 2017)**.**

Several emerging zoonotic pathogens associated with severe human disease originated, are hosted or suspected to be hosted by bats, including severe acute respiratory syndrome coronavirus (SARS-CoV), Middle East respiratory syndrome coronavirus (MERS CoV), Marburg virus, ebolaviruses, and a wide range of lyssaviruses. We recently found evidence of a SARS-like coronavirus in Chinese horseshoe bats that has the capability to transmit directly to people, which suggests that the original transmission of SARS may have been directly from bats, rather than via civets or other animal intermediate hosts. Recent studies have also found evidence that bats were reservoirs the ancestors of other human pathogens such as hantaviruses, hepatitis C, rubeola, mumps and rubella viruses. Much of this work arose from phylogenetic, epidemiological and virological studies of viruses identified in wild caught bats, including substantial work from our group. These findings have generated larger questions about how bats (the second largest group of mammals with more than 1,200 species) can host these viruses that without substantial pathology, yet they cause substantial disease in other species, including humans.

To determine whether bats have a specialized physiology or immune systems that permit viral infection with minimal disease requires development of bat models that can be used in laboratory experiments.

Bats of the genus *Pteropus* (family Pteropodidae) comprise more than 60 species that range from Madagascar eastward through most of Asia, Australia, and the Pacific islands. Several species of pteropid bats are natural reservoirs of NiV and other henipaviruses, including Hendra virus (HeV) and Cedar virus in Australia. Both Nipah and Hendra viruses are biosafety level 4 pathogens and select agents. Currently, the only captive colony of pteropid bats available for infectious disease research (to our knowledge) exists at the Australian Animal Health Laboratory (AAHL) in Geelong, Australia, which has BSL-4 small and large animal facilities. Although AAHL has developed and will collaboratively share cell lines derived from one species of pteropid bat (*P. alecto*), at present the bats are not available to researchers outside of AAHL. Thus, a significant need remains for a lab animal model that can be used to study NiV and HeV host-virus interactions and generate additional laboratory reagents and resources available to a broader research community.

Pteropus medius, in particular, is of special interest for viral research because it is has been found to carry Nipah virus and other viruses with potential human health impact, including filoviruses and other uncharacterized henipaviruses for which we have serological evidence. This species also carries a recently discovered virus called GBV-D, a flavivirus related to Hepatitis C virus. *The propensity for this particular species to carry a wide spectrum of viruses*

related to known human pathogens (without clinical affect) makes it an ideal candidate as a laboratory model to advance immunological and virological studies in bats.

The establishment of a research colony of Indian flying foxes (*Pteropus medius*) is critical to facilitate research in the United States that will test hypotheses related to the cellular mechanics of Nipah virus (NiV) and the host immune response, *in vivo,* in a wildlife reservoir species for Nipah virus. The Indian flying fox is endemic to the Indian subcontinent, and widely distributed throughout Bangladesh and India, where more than fifteen outbreaks of Nipah virus encephalitis have been reported since 2001. **There are no bats available in the United States for research related to *Pteropus* physiology, immunology, and viral pathophysiology.** NiV is an emerging, high consequence pathogen with 75% - 100% mortality in humans in Bangladesh, where is causes seasonal outbreaks of encephalitis. Currently, there is no effective treatment or vaccine for NiV. It is a highly communicable disease, including person-to-person and nosocomial transmission. Though the majority of outbreaks, to date, have occurred in rural villages, Bangladeshi patients are often transported to Dhaka for care. The introduction of NiV to Dhaka, a city of 12 million people with an international airport linking major cities, including New York, London, and Hong Kong, represents one of the most significant factors contributing to Nipah virus' pandemic potential.

Maintaining bat colonies requires many specialized husbandry facilities and resources. Indeed, insectivorous bats are notoriously difficult to keep, let alone breed in captivity. Frugivorous bats are much easier to maintain in captivity. They are typically robust and will eat a variety of fruits that are readily available in the United States. Their social structure and behavior is well understood, and zoological institutions have successfully kept and bred a variety of fruit bats species, including many different pteropid bat species. [Note: in the context of this proposal, zoological institutions are not a viable source of bats for founding a colony as biomedical research is generally considered "off mission" for zoological gardens focused on species conservation] The Indian flying fox is an attractive bat model because it is a reservoir host of NiV, its large body mass (~700-900g) allows for relatively large volumes of blood and lymphoid cells to be safely sampled to support clinical research, its conservation status is "non-threatened" (thus allowing wild founders to be more readily sourced), and it is easy to maintain and breed in captivity.

2) Who will establish the colony? Where would the bats come from and where would the colony be maintained?

Our group includes experts on the behavior and husbandry of bats, their ecology, the epidemiology of Nipah virus in wild populations, and the design and implementation of experiments involving non-traditional animal models.

Colorado State University is a registered NIAID contractor for establishing lab animal models and will be the location of the proposed bat colony. Tony Schountz, PhD is an Associate Professor in the Department of Microbiology, Immunology and Pathology, College of Veterinary Medicine at CSU. Dr. Schountz previously established a breeding colony of, Jamaican fruit bats *(Artibeus jamicensis)* that has been used for Tacaribe virus and MERS-CoV experimental research. CSU currently has the facilities to establish a colony of *Pteropus medius* and Dr. Schountz and Richard Bowen, DVM, PhD will be responsible for establishing and maintaining the research colony. The Director of Laboratory Animal Services at CSU is Lon Kendall, DVM, PhD, who has overseen the veterinary care of the Jamaican fruit bat colony. Thus, the facilities and staffing expertise are already in place at CSU for working with bat colonies.

Draft: Pre-White paper for discussion
Epstein et al. 2016

Dr. Jonathan Epstein, a veterinary epidemiologist at EcoHealth Alliance, has nearly 20 years of experience working with pteropid fruit bats in the wild. His research has focused on the epidemiology and ecology of Nipah virus and other zoonotic agents in bats. He directed the capture, quarantine and transport of live *Pteropus vampyrus* from Malaysia (another reservoir of Nipah virus) to AAHL as part of an NIH-funded long-term study of henipaviruses in bats in 2005. He has been working in Bangladesh since 2006, and has established strong collaboration with the government of Bangladesh, including the federal wildlife authority. Dr. Epstein, and his team in Bangladesh will be responsible for the capture, quarantine, and transportation of the bats from Bangladesh to CSU (Fort Collins, Colorado). He will also provide guidance for the facility at CSU (e.g., diurnal cycles, feeding, enrichment, etc.). Dr. Epstein is currently collaborating with Drs. Schountz and Munster on bat immunology studies and will continue to provide leadership and scientific engagement in this and future collaborative studies related to bat immunology and virology related to the imported *Pteropus* bats.

Dr. Vincent Munster is a senior scientist in the Laboratory of Virology, Rocky Mountain Laboratories, NIAID, (Hamilton, MT). His work has focused on experimental studies of bat-borne high containment pathogens such as Ebola virus, Nipah virus, SARS-CoV and MERS-CoV. Dr. Munster will facilitate the establishment of the colony, and will be the laboratory lead and co-investigator on all experimental studies utilizing these bats. We will have the support and use of the BSL 4 laboratory and veterinary personnel at RML for experimental work utilizing the bats.

Mr. Brian Pope, the Director of the Lubee Bat Conservancy in Gainesville Florida has more than 12 years of bat husbandry experience at zoological parks, including Disney World's Animal Kingdom, and will provide expert guidance on the regulatory aspects of bat importation and the development of the internal environment for the bat colony. He and his staff will provide training to the veterinary and animal care staff at CSU and RML on the husbandry and care of the bats. Mr. Pope and Dr. Epstein have collaborated for more than five years on bat immunology studies at the Lubee Bat Conservancy, and Dr. Epstein currently serves on Lubee's Scientific Advisory Board.

To found the colony, we propose to import 40 adult *P. medius* from Bangladesh, with the support of the Forestry Department – the federal wildlife agency. We will import 36 pregnant female bats, and 4 males - all seronegative for Nipah virus. A temporary quarantine facility will be constructed by the Forest Department at the Dhaka zoo, where veterinary and animal care staff are available. Bats will be sampled (blood and urine) every three weeks and samples will be sent to RML laboratories and tested for Nipah virus antibodies and RNA using ELISA, SNT, and PCR.. Bats that have three consecutive negative tests will be shipped to CSU. Our group previously transported pteropid bats from Malaysia to Australia for research purposes. *P. medius* is a seasonal breeder, and females within a colony tend to be pregnant all at once, so capturing 35 pregnant females is achievable. The gestation period is six months, and the timing of transport will be such that the bats will be in the fourth month of pregnancy to maximize the safety to the fetus during transport. We expect 80-90% of pregnancies to be maintained during quarantine and shipment, such that the colony will immediately provide about 30 juveniles that could be used for experimental work within 12 months of birth or to continue breeding after 30 months when they reach sexual maturity. The adults will be bred every year (one breeding cycle per year), which will generate a cohort of 20-35 bats each season. Over a period of 3-5 years, we expect to have generated a colony of more than 200 bats that will be available for experimental studies.

3) Long-term sustainability.

Use of the bat colony as well as cell lines derived from bat tissues will be made available to the scientific community. We expect that cell lines will be the most frequently requested products that could be readily shared among the scientific community. Have a supply of primary and immortalized (e.g., large T, hTERT) cell lines in the US will rapidly facilitate research because it will obviate the need for CITES and other import permits when reagents are shipped to other US-based labs. The colony will also benefit conservation efforts by providing genetic material to zoological institutions that have breeding programs for *P. medius* now or in the future.

Support from NIAID will be required to establish and expand the colony over an initial 5-year period. Once the colony is established, we will generate reagents and cell lines that will be made available to other researchers upon request. After the completion of the contract and to support the maintenance of the colony and associated resources, we will establish a modest fee structure for use of the bats and materials derived from the bats, which will be channeled directly back into colony maintenance costs. We will also consider experiments that require the use of bats and will include budget in each proposal that will be used to support maintenance costs. The fee structure could be modeled from the one used by the Lubee Bat Conservancy, or a de novo fee-for-service system will be developed.

Critical research to understand emerging zoonotic viruses requires a US-based captive bat colony

Prepared by Jonathan Epstein, DVM MPH; Tony Schountz, PhD; Judith Mandl, PhD; Richard Bowen, DVM, and Vincent Munster, DVM, PhD.

There is a growing consensus among the scientific community studying high consequence zoonotic viruses, that in order to understand why these viruses are lethal in people it is necessary not only to study their basic structure and function; their pathogenesis; their epidemiology and host ecology; but it is also vital to understand how these viruses behave in their hosts, which appear to be infected without signs of clinical disease. Of particular concern to the global health community are a suite of zoonotic viruses that cause high mortality in people and that are believed to originate in bats: SARS coronavirus, Ebola virus, Marburg virus, Nipah virus, Hendra virus, and Middle East respiratory syndrome coronavirus (MERS CoV). Further, there is increasing evidence that groups of established human pathogens originated in bats, including measles, mumps, hepatitis C virus, and potentially influenza viruses. An important and frequently asked scientific question is whether bats are better hosts for lethal viruses than other mammals. A bat animal model that can be used in controlled experiments is essential for developing a better understanding of basic bat immunology and will allow for sophisticated viral infection studies which may ultimately answer this question and lead to new approaches in antiviral therapeutics for people affected by diseases like Ebola virus disease, Nipah virus encephalitis, and Marburg Hemorrhagic fever.

We propose to establish a sustainable, *Pteropus giganteus* colony in the United States that will allow research requiring bats and bat-derived reagents such as cell lines to be conducted. We propose *Pteropus giganteus* as a model species because it is the natural reservoir for Nipah virus in South Asia, a virus with pandemic potential that causes near-annual outbreaks of fatal encephalitis in humans in Bangladesh with case fatality rates averaging 75% and that have reached 100%. Nipah virus is categorized as a category C select agent and biosafety level 4 pathogen. *Pteropus giganteus* is also host to more than 50 other viruses that have been identified (Anthony S, Epstein JH, et al., *mBio* 2013). Serological evidence suggests it also carries a yet unidentified filovirus (Epstein et al., unpublished). This species is robust and easily adapted to captivity compared to other bat species. Our group has extensive expertise with pteropid bat husbandry; experimental studies of Nipah virus and other BSL 4 viral pathogens, and studying viral epizootiology and bat ecology in wild populations in Asia. We have access to founder bats and facilities where a colony could be established and sustainably maintained (Colorado State University) and where research on select agents and high consequence viral pathogens could be conducted (NIH Rocky Mountain Laboratories).

The following is a list of research questions and ideas we have developed to illustrate the need for establishing a colony of *Pteropus giganteus* at a qualified research institute in the United States.

***In vivo* studies: Functional bat immunology / physiology / viral evolution**

- Characterizing the innate immune system of pteropid bats. This requires access to primary cells and hence a live, infection-free, colony from which, for example, blood can be taken on a regular basis for *in vitro* testing. A live colony will also allow controlled *in vivo* experiments where their innate immune response can be interrogated using the administration of defined stimuli that have been used in humans, primates, and mice.

- Characterizing the innate and adaptive immune response of pteropid bats to infection with viruses for which they are known reservoirs. A key question remains whether bats develop significant pathology from infection with the viruses for which they are natural hosts. It has been hypothesized that bats are distinct from humans in specific immune pathways as a result of having evolved to fly and hence having adapted to repair DNA damage that is the result of acute oxidative stress and inflammation caused by flight. This research was done using pteropid bat cell lines in Australia. A live *Pteropus* colony will enable us to determine whether pathology occurs following infection with Nipah virus, and whether reduced/absence of disease is also seen with other RNA viruses that are harbored by other bat species (eg. Ebola, MERS Cov). Experiments in controlled conditions will also enable us to address whether there are indeed aspects of bat physiology which impact their immune response as a result of their ability to fly. It will also be important to compare the components of the bat innate immune response to viral infection with an agent originating in pteropid and non-pteropid bats (Ebola virus, Nipah virus, Marburg virus, SARS CoV) to viral infection with a non-bat virus (e.g. Rift Valley Fever virus, HPAI H5N1 influenza virus, etc…).

- Kinetics of antibody production in NIPV-infected *P. giganteus*. When do IgM and IgG appear? When does neutralizing antibody appear? How long do neutralizing and non-neutralizing (e.g., N protein) persist?

- Lymphocyte responses during infection. What are the temporal and kinetic transcriptional profiles of *P. giganteus* lymphoid responses? RNA-Seq and qPCR could be used here.

- What occurs in immunosuppressed *P. giganteus* infected with NiV?

- Do bats get sick from the above viral infections? A bat model is necessary to determine the pathology that occurs during infection and whether clinical signs occur that would allow one to observe disease in bats. Pathogens of high importance include Nipah virus, Ebola, MERS CoV. Can we appreciate clinical

signs when bats have been infected with viruses associated with different but related bat hosts? For example, what if one pteropid species infects another pteropid species with its particular henipavirus? What clinical signs can be observed in the recipient host? What mutations occur in the viral genome following interspecific transmission? What about transmission to another bat species within the same family (e..g from *Pteropus giganteus* to *Rousettus aegyptiacus.*) In nature, multiple species often share habitat and may exchange viruses, assisting in viral persistence in a geographic area. **This would help understand viral evolution when multiple hosts are involved – as is the case with Nipah virus in Southeast Asia, Hendra virus in Australia, and Ebola virus in Central Africa**)

- Characterizing the complete genome of *Pteropus* with >50x coverage to look at the presence/absence and actual nucleotide sequences of genes responsible for innate immune function. Comparison to other species (particularly humans) will enable probing for different types of selection pressures, which may provide clues as to which genes have changed due to specific adaptations (positive selection) versus which genes have been under strong selection pressure to remain conserved to maintain their function.

- What mutations occur following conspecific bat to bat transmission of Nipah virus?

Specific viral pathogen research: Henipaviruses (Nipah virus, Hendra virus, Cedar virus); Filoviruses (Zaire ebolavirus, Marburg virus, Reston ebolavirus); and Coronaviruses (SARS and MERS).

- Characterizing Nipah virus transmission and replication in pteropid bats. Controlled experiments where the dose, route and time of virus exposure is precisely known will enable us to determine: by what route virus shed, what the extent is of viral replication (timing, magnitude) in different tissues, what the timing and magnitude is of viral shedding. Answering such questions will be essential to determining how Nipah virus is transmitted between bats and how Nipah virus is transmitted from bats to other animals. It will also reveal what the highest risk tissues are for transmission to humans, e.g. during butchering, whether virus can be transmitted through blood contact, through urine/feces, etc.

- How does Nipah virus infection / transmission differ from other henipaviruses like Hendra and Cedar virus? Can differences in pathogenesis among these viruses provide insight into immunity and potential therapeutic approaches? How do henipavirus infections compare to filovirus and coronavirus infections?

- Are there molecules or compound in existing libraries that can block or limit Nipah virus shedding/transmission in host species? How do these mechanisms

work? Could this be applied to other animal models and ultimately used to reduce viremia in people?

- What are the highest risk tissues in bats that may results in Ebola transmission during butchering? What are the peak viremic levels during acute Ebola infection? Nipah virus? Could Nipah virus be transmitted to humans through contact with blood (e.g. during butchering process)?

- Are there mechanisms within the bat's innate immune system that can be mimicked by therapeutic agents to reduce pathology during human infection?

***In Vitro* Studies**

- A *Pteropus giganteus* colony will allow for the development of immortalized cell lines for use in *in vitro* experiments (these are a product from this colony that could be disseminated to other research groups in the United States to support research requiring bat cell lines).

- Are *P. giganteus* dendritic cells (pDC, cDC) and macrophages susceptible to NiV infection? How do the viral proteins affect the responses of these cells? A lot has been done in non-bat cells, but nothing has been done in *P. giganteus*. Are the STAT1 or MDA5 pathways similarly targeted in *P. giganteus* cells as they are in human cells?

- Are *P. giganteus* endothelial cells susceptible to NiV? If so, how does the virus affect those cells (e.g., lytic, non-lytic, suppression of type I/III IFN pathways)?

- Are infected *P. giganteus* cells susceptible to CTL-mediated lysis?

- What are the profiles of helper T cells from NIPV-infected bats?

- Are there commercially available antibodies that are cross-reactive with *P. giganteus* proteins? Many of the antiviral protein Abs should be cross reactive, but less so for cell surface proteins or cytokines. We may find anti-CD4 and anti-CD8, which could lead to depletion studies *in vivo*.

Ultimately, such studies will collectively reveal whether there mechanisms within the bat's innate or adaptive immune system that can be mimicked by therapeutic agents to reduce pathology during human infection with zoonotic viruses originating from bat species.

From: Ebel,Greg
Sent: Tuesday, June 02, 2020 6:44 PM EDT
To: epstein ecohealthalliance.org>
CC: Schountz,Tony < >
Subject: Bat space at CSU

Hi Jon,

Here's what we know about our "barn" space, per Lon Kendall, our lab vet here at CSU, and someone I very much trust. Pasted from various emails that have been flying around today:

If it is the Pteropus, a renovated barn could hold approximately 25 bats. Maybe good for some short term studies, but insufficient for a breeding colony.

There is not an existing building that would meet the space requirements of the Pteropus. The barn is about 2500 sf, and we would need 7500 sf for a 60 bat breeding colony, plus support space, so about 10000 sf. I can't think of another space that large that could be renovated.

This puts us in a position where we're seeking funds to construct/add on to a facility *in order to be able to apply for funds to renovate that facility*. I think this is more than I can ask, and think our best course is to move on. I'll reach out one last time to our NIH contacts, but this seems like a dead end to me if the really can't find a way to fund the C06 (which seems very off to me – if they want to fund it they should be able to do so in my opinion).

Sorry not to have better news.

Greg

Gregory D. Ebel
Professor, Department of Micribiology, Immunology and Pathology
Director, Arthropod-Borne and Infectious Diseases Laboratory
College of Veterinary Medicine and Biomedical Sciences
Colorado State University

Ft. Collins CO 80526

From: Jon Epstein ecohealthalliance.org>
Sent: Friday, May 19, 2017 9:48 AM EDT
To: Schountz,Tony
CC: Munster, Vincent
Subject: Bat tissue

Tony,
I just heard that Lubee's P. giganteus recently died and I think they've harvested tissue. Were you aware? Did you get any samples?
-Jon

From: Ebel,Greg < >
Sent: Wednesday, May 20, 2020 4:27 PM EDT
To: Schountz,Tony >; epstein ecohealthalliance.org>; Challberg, Mark (NIH/NIAID) [E] ; jean.patterson
Subject: C06 check in call

Hi all,

Here is the zoom invitation for the call to discuss the status of the CSU C06 proposal. The meeting is Thursday, 28-May at 2:00 Mountain, 4:00 eastern.

Best,

Greg

Gregory Ebel is inviting you to a scheduled Zoom meeting.

Topic: C06 Check In
Time: May 28, 2020 02:00 PM Mountain Time (US and Canada)

Join Zoom Meeting
https://zoom.us/j/91750793084?pwd=dTNXZWxpcXlkUGZtVHlsdTZNUll0dz09

Meeting ID: 917 5079 3084
Password: 4fGZUC

From: Ebel,Greg >
Sent: Thursday, April 02, 2020 12:12 PM EDT
To: jean.patterson >; Challberg, Mark (NIH/NIAID) [E] <
CC: epstein ecohealthalliance.org>; Schountz,Tony ; Dean,Gregg >; Kendall,Lon ; Szalai,Edit
Subject: C06 update documents
Attachment(s): "C06 Update 2020_clean.docx","Munster LoS_Ebel_signed.pdf"

Dear Jean and Mark,

As promised, I'm attaching a two page update on the C06.

It highlights (a) the overall rationale for the project, (b) our vision for how it would be used, and (c) a summary of current bat-focused experimental research that it would support.

The overall picture that I would like to convey is that CSU is an ideal environment for locating a bat facility due to our longstanding interest in emerging zoonotic and vector-borne infections and our commitment to developing infrastructure to support research in this area. I very much hope that this comes through. If you think that there are points that are being missed, please let me know and I can edit further.

I'm also attaching a letter of support from Dr. Vincent Munster at RML. If you think it would be helpful in moving this forward, we can also obtain a letter from EcoHealth alliance supporting the project.

Thanks so much for your attention and do let me know how I can further help move this project forward.

Best regards,

Greg

Pathogens transmitted by bat and arthropod vectors continue to significantly threaten the health of humans and domestic animals around the world. Bat-associated pathogens, such as coronaviruses, including the currently circulating SARS-CoV-2; filoviruses (e.g. Ebola and Marburg viruses), and henipaviruses (e.g. Nipah virus), are among the most impactful and dreaded viruses known. Malaria is perhaps the most deadly infection in the tropics. West Nile, chikungunya and Zika viruses also have emerged as major global pathogens. Tick-transmitted infections such as Lyme disease and Powassan virus continue to emerge in temperate regions as climate change expands the range tick vectors. Agents hosted by bats and vector-borne pathogens thus constitute some of the most feared, difficult and persistent problems affecting human health.

To meet this challenge, Colorado State University (CSU) established the Arthropod-borne and Infectious Disease Laboratory (AIDL) in 1984 to counter these emerging threats. One of the many unique aspects of AIDL includes housing one of the only captive breeding colonies of bats for use in infectious disease research. One of the major challenges for studying the origins, transmissibility and pathogenesis of emerging bat-borne viruses is the lack of bat animal models. The species diversity of bats is second only to rodents among mammals, however, there are key species that have been associated with important groups of zoonotic viruses such as Ebola and Marburg virus, Nipah virus, and SARS and SARS-CoV2-related coronaviruses, and there is growing evidence that bats are physiologically and immunologically unique in their ability to tolerate viral infection, resist cancer, and have disproportionately long lifespans for their size. All of this makes the dearth of facilities capable of housing bats for basic research and the lack of available bat colonies in the United States for use in biomedical investigations a major impediment to basic infectious disease and translational medicine research. The current COVID-19 pandemic highlights the national need for the proposed facility as a scientific resource, and the central role that CSU now occupies in the ability of the US to study and design countermeasures against emerging viral threats.

To support research into significant known and unknown emerging diseases, including those listed by the WHO R&D Blueprint as the ten most significant infectious disease threats to global health (half of which are bat-associated or vector borne viruses), CSU committed $22M in 2019 to construct a new building, the Center for Vector-Borne Infectious Diseases (CVID), to replace aging AIDL infrastructure. CVID construction is ongoing and we anticipate moving in in late 2020.

While CSU's commitment of $22M is laudable, it has proven insufficient to provide adequate housing for the additional bat colonies needed to address the urgent need for research into the biology and emergence of SARS-CoV-2, MERS CoV, Nipah virus, Ebola and yet-to-be discovered viral agents which are most likely to emerge from bat reservoirs. Further, additional infrastructure within the CVID is required in order to ensure that research focusing on bat-borne diseases is paired with adequate BSL2 and BSL-3 lab, tissue culture and other support space.

This proposal, which scored well in 2019 but was not selected for funding, represents a unique opportunity to rapidly accelerate US capacity for housing, breeding and using bats in biomedical research. In particular, we propose to:

- **Develop a state-of-the art facility to house a breeding colony of *Pteropus* fruit bats** known to be natural reservoirs for henipaviruses, filoviruses, and coronaviruses. This will be the first of its kind in the world, and will be a critically important resource for:
    - **Developing and generating reagents** including cell lines, validated serology and PCR assays, etc.

- **Studying basic genomics.** Groundbreaking work has begun in Singapore and Australia on bat viral tolerance using an Australian *Pteropus* species. The proposed facility will allow the US to actively accelerate this area of research by focusing on a natural reservoir for Nipah virus, filoviruses, and coronaviruses.
- **Build on the existing immunology and genomics work, and develop new lines of cancer and aging related research** by engaging investigators from various centers at NIH, CSU, EcoHealth Alliance, and around the world.
- **Experimental work involving high containment pathogens** (Nipah virus, Ebola, etc..) will be conducted through a partnership with EcoHealth Alliance, and NIAID Rocky Mountain Labs (see Munster letter of support) in Hamilton, MT.

- **Develop facilities to permit the importation of other key bat species** (e.g. *Rhinlophus affinis*) and house native North American bat species for use in coronavirus research, including SARS CoV-2 within CVID.

Current Bat Research at CSU

Colorado State University has a breeding colony of Jamaican fruit bats (*Artibeus jamaicensis*), one of the most common and largest fruit bats in the New World. This colony was established in 2005 with funds from the NIAID Emerging Virus Disease Unit contract (AI25489) after it was determined that SARS-CoV was a bat-borne virus. Currently funded bat projects are to study SARS-CoV (CSU VPR funding), MERS-CoV (AI140442), bat influenza A viruses (AI134768), henipaviruses (DARPA G228-19-W7329) and rabies virus (DOE B634747). Our long-term goal for this colony is to make it the “bat version” of the laboratory mouse so that we can conduct experimental infections for other researchers, or provide bats to those who may need them for experiments at their institutions.

Our progress with these bats thus far has been remarkable. We have determined they are susceptible to several viruses, including Zika virus, H18N11 bat influenza A virus, MERS-CoV, Cedar henipavirus, Tacaribe virus and Bukakata virus, the last two of which cause fatal diseases in the bats. We also have established primary bat cell lines that are susceptible to MERS-CoV, Zaire ebolavirus, and Nipah, Hendra and Cedar henipaviruses. We have generated a number of reagents, including monoclonal antibodies and recombinant cytokines, virological and immunological methods, large transcriptome data sets, basic physiological parameters. Our work has demonstrated that it can serve as a surrogate bat model organism for the study of bat-borne viruses. Importantly, a genome assembly to 30x coverage is available (NCBI PVKR01). These bats already have been used to address SARS-CoV-2 infection. We performed an initial susceptibility study of three Jamaican fruit bats and found that all had low levels of viral RNA in oral swabs within a few days after intranasal inoculation. By day 14, all three bats had seroconverted by ELISA to recombinant SARS-CoV-2 nucleoprotein and by day 24 the titers had increased at least 4-fold for each bat, with titers up to 1:6400. Thus we are confident that we have established a surrogate bat model for the study of SARS-CoV-2 in bats. We currently have 27 bats enrolled in a challenge and transmission study and are performing serial euthanasia to determine virus kinetics, tissue tropism, host response and transmission dynamics. Our productivity with our existing bats, and committed partnerships with Rocky Mountain Labs and EcoHealth Alliance who are invested in emerging disease research, clearly demonstrates their importance as research resources and our ability to productively engage with a wide array of projects and partners, indicating the suitability of CSU as a home for new bat housing and laboratory support facilities.

National Institute of Allergy and Infectious Diseases

ROCKY MOUNTAIN LABORATORIES

Division of Intramural Research
National Institute of Allergy
and Infectious Diseases
Laboratory of Virology
Virus Ecology Section

April 1st, 2020

Dear Dr. Auchincloss,

It is with utmost pleasure to be able to provide a letter of support for the CSU bat research center. Past outbreaks of bat-borne zoonotic viruses such as coronaviruses, henipaviruses and filoviruses, have had an enormous impact on human and wildlife health. The unpredictability of the zoonotic introductions of these bat-borne limits the potential for effective intervention strategies. Within my research at the NIAIDs Rocky Mountain Laboratories, I have directly focussed on bat-borne viruses such as Nipah virus, Ebola virus, MERS-CoV and now SARS-CoV-2. In particular we have extensive knowledge of bat infection models of ß-coronaviruses (MERS-CoV and WIV-1, in *Artibeus* and *Rousettus* bats) and Nipah virus (*Rousettus* bats) and are one of the few facilities which are completely set-up to perform bat studies in high and maximum containment (including long-term husbandry and on-site veterinary staff) and complete downstream immunological, genetic and virological analyses. In the absence of suitable breeding facilities at intramural NIAID, the addition of a centre focussed on *in vivo* bat research at CSU deserves the NIAIDs unconditional support.

I am underwriting my enthusiasm to continue to collaborate on the development of a bat resource center including breeding colonies of key bat species, at CSU. Having access to natural hosts for coronaviruses, henipaviruses and filoviruses would significantly advance research in infectious disease undertaken by my group and others at RML, and I am committed to working with Drs. Bowen and Schountz at CSU (long standing research collaboration on MERS-CoV) and Dr. Epstein of EcoHealth Alliance (long standing collaboration on the underlying ecological changes driving spillover events of Nipah virus) to develop and use the resources generated through this C06 proposal. The SARS-CoV-2 pandemic marks an occasion which should put renewed focus on detailed studies of bats as reservoirs of emerging diseases. After SARS-CoV-1, MERS-CoV and Ebola virus in West Africa, we have yet another high impact (both from public health as economic perspective) bat-borne disease which justifies the urgent need for facilities in the US for advanced bat infectious disease studies.

Please feel free to contact me with any remaining questions,

Sincerely,

Vincent Munster
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Kendall,Lon >
Sent: Friday, April 10, 2020 12:07 PM EDT
To: epstein ecohealthalliance.org>; jean.patterson
CC: Ebel,Greg ; Schountz,Tony >
Subject: CO6 follow up

Jean and Jon,

I can't recall, what are the next steps with the C06?

I know Greg is really busy, and just wanted to keep this momentum.

Lon

Lon V. Kendall, DVM, PhD, DACLAM
Director, Laboratory Animal Resources and
Attending Veterinarian, Colorado State University

From: 罗波 <luob
Sent: Thursday, March 26, 2020 3:47 AM EDT
To:

Subject: Could you please fill in this questionnaire concerning bat conservation in China?

Dear Bat Researchers,

Good day! More than 130 bat species have been recorded in China. None of them are included in the List of Chinese State Key Protected Wildlife, although some bat species are in rapid decline in recent decades. Many Chinese people experience intense panic at the thought of bats and some even propose to kill bats since the outbreak of novel coronavirus (COVID-19). In this case, we are dedicated to gathering researchers' opinions on the major threats and conservation strategies of bats in China. We restricted the population surveyed to researchers and students worldwide that have research experience on bats. Through this brief survey, your answers may be helpful in improving the conservation status of bats in China. There is no right or wrong answer to the question. Your response will only be used for survey purposes. Thank you very much for your valuable time and suggestions! Could you please also send this email to your colleagues and students?

Here is the network link of our self-designed questionnaire: https://www.wjx.cn/jq/66714439.aspx

Best,

Bo Luo, PhD
Key Laboratory of Southwest China Wildlife Resources Conservation (Ministry of Education), China West Normal University 1# Shida Road, Nanchong 637002, China
Jilin Provincial Key Laboratory of Animal Resource Conservation and Utilization, Northeast Normal University, 2555 Jingyue Street, Changchun 130117, China

From: Kendall,Lon
Sent: Friday, March 20, 2020 3:59 PM EDT
To: Bowen,Richard >; Angela Bosco-Lauth ;
Schountz,Tony ; Ebel,Greg >; Jon Epstein
ecohealthalliance.org>
Subject: CSU Bat Facility

All,

Just following up to schedule a meeting to start discussions on the bat facility. Please respond to the doodle poll and I'll let everyone know the date. I've also added everyone to the MS Team VPR Bat Facility

Jon- I don't have Brian's contact information. Can you please forward this to him and provide me his email so I can add him to the team.

https://doodle.com/poll/tgswptaa4295tae5

Thanks,

Lon

Lon V. Kendall, DVM, PhD, DACLAM
Director, Laboratory Animal Resources and
Attending Veterinarian, Colorado State University

From: Ebel,Greg
Sent: Thursday, August 13, 2020 1:21 PM EDT
To: jean.patterson >
CC: epstein ecohealthalliance.org>; Schountz,Tony
Subject: CSU Bat space

Dear Jean,

I'm writing to let you know that as of this AM, we are seeing some traction toward renovation funds for a bat facility at CSU. I think it makes sense to discuss next steps as long as interest remains at NIAID in moving forward with this effort.

Thank you,

Greg

Gregory D. Ebel
Professor, Department of Microbiology, Immunology and Pathology
Director, Arthropod-Borne and Infectious Diseases Laboratory
College of Veterinary Medicine and Biomedical Sciences
Colorado State University

Ft. Collins CO 80526

From: Jon Epstein ecohealthalliance.org>
Sent: Wednesday, December 19, 2018 6:10 PM EST
Subject: EcoHealthNet 2019 application deadline extended to Dec 31st
Attachment(s): "EHN_Flyer_2019_deadlineDec31.pdf"

Dear colleagues,
We have extended the EcoHealthNet application deadline to December 31st. Please spread the word and encourage your graduate and undergraduate students to apply to this fully funded research opportunity!

Happy Holidays,

-Jon

P.S. attached is a flyer with details about the June 2019 workshop in Washington. Please distribute.

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street, Ste. 1701

New York, NY 10001

)

web: ecohealthalliance.org

EcoHealth Alliance

EcoHealthNet 2019

EcoHealthNet (EHN) is an undergraduate and graduate-level global research coordination network, funded by the National Science Foundation, to bring together world-class research scientists from medical, ecology, veterinary, epidemiology, virology, anthropology, climate science, data science, and economics that will advance One Health research and education. Advancements will take place through three activities: 1) create a peer network of undergraduate and graduate STEM students from various disciplines via 1-week workshops that teach applied skills and provide in-person contact time with scientists actively conducting research related to anthropogenic environmental change, economics, and emerging diseases, which will also be delivered live as an interactive webinar to university students globally; 2) develop the next generation of One Health practitioners through mentored research projects that reflect One Health principles; 3) link participants to professional science and policy associations. This project will develop and deliver live online content to thousands of students on a global scale. This project will inspire broad, One Health research, which will create lasting connectivity among scientists from different disciplines as they advance in their careers.

The online application for 2019 are now open until December 31st!

The 2019 Workshop, **Emerging Threats to Global Health**, will be held at George Mason University in Virginia from June 2-8th, in collaboration with Johns Hopkins University and the Smithsonian Institute. Research Exchange projects can take place between May and August 2019.

EcoHealthNet is made possible through a partnership among EcoHealth Alliance, Harvard School of Public Health, Tufts University, University of California - Davis, Chittagong Veterinary and Animal Sciences University of Bangladesh, George Mason University, Columbia University, Johns Hopkins B SPH, Agriculture and Forest University of Nepal, University of Wyoming, Royal Veterinary College, London, University of Wisconsin Madison, Wuhan Institute of Virology China, National Wildlife Health Center, Universidad National Autonoma de Mexico, Chulalongkorn University Thailand, University of Georgia, and a number of other partners.

For more information and to submit an application, check out our webpage:
https://www.ecohealthalliance.org/program/ecohealthnet
Or email us: ecohealthnet@ecohealthalliance.org

EHN research exchange participant working on the Orangutan Fecal Pathogen Study in Borneo.

EcoHealthNet workshop participants visiting the Massachusetts State Laboratory Institute, USA while attending the 2017 EHN Workshop co-hosted by Tufts Cummings School of Veterinary Medicine and Harvard University School of Public Health in Medford/Boston, MA, USA.

Support for EcoHealthNet is provided by a National Science Foundation Research Coordination Network Grant awarded to EcoHealth Alliance.

Local conservation.
Global health.

EcoHealth Alliance
460 West 34th Street, 17th Floor
New York, NY 10001-2320
212.380.4460

EcoHealthAlliance.org

From: 胡犇 <huben
Sent: Monday, October 15, 2018 9:14 AM EDT
To: Schountz,Tony
Subject: Final Program of the 8th International Symposium on Emerging Viral Diseases
Attachment(s): "Program of the 8th ISEVD_Final.pdf"

Dear speaker:

We will have the 8th International Symposium on Emerging Viral Diseases in Wuhan soon this weekend.

Please find enclosed the final program of the meeting, as minor changes have been made compared with the version that I previously sent to you.

You will be accommodated in the venue hotel of the symposium, the Optics Valley Kingdom Plaza. Our student volunteers or myself will pick you up at Wuhan airport or Wuhan railway station when you arrive.

We look forward to meeting you soon.

Sincerely

Ben Hu Ph.D
Wuhan Institute of Virology, CAS
Secretary of the 8th ISEVD

Program of
The 8th International Symposium on Emerging Viral Diseases

Date 日期	Time 时间	Content 议程
Saturday **星期六** **Oct. 20, 2018** **10 月 20 日**	**Venue** **地点** 09:00-21:00	**Registration**/报到注册 Ground Floor, Optics Valley Kingdom Plaza Hotel/光谷金盾大酒店一楼大厅
Sunday **星期日** **Oct. 21, 2018** **10 月 21 日**	**Day 1, Morning Session /第一天上午**	
	Venue **地点**	Banquet Hall of Optics Valley Kingdom Plaza 3nd floor of the hotel 光谷金盾大酒店三楼宴会厅
	09:00-09:10	**Opening Address/开幕式致词**
	09:10-12:00	**Session 1: Antiviral Immunity** **Session Chairs: Peng ZHOU, Linfa WANG**
	09:10-09:40 Keynote Speech S-01	**Title:** Holy immune balance, batman! **Speaker: Linfa Wang** Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore
	09:40-10:00 S-02	**Title:** Recent advances in developing therapeutics monoclonal antibodies Against Ebola Virus Infection **Speaker: Xiangguo Qiu** Special Pathogens Program, National Microbiology laboratory, Public Health Agency of Canada
	10:00-10:20	Group Photo of Symposium Participants/与会代表合影 Coffee Break /茶歇
	10:20-10:40 S-03	**Title:** Nipah virus and Hendra Virus: Basic Science to Global Countermeasures **Speaker: Christopher Broder** Department of Microbiology, Uniformed Services University, Bethesda, MD, USA
	10:40-11:00 S-04	**Title:** Immunopathogenesis of Nipah virus infection **Speaker: Branka Horvat** International Center for Infectiology Research - CIRI, INSERM U1111, University Lyon 1, France
	11:00-11:20 S-05	**Title:** Incorporation of NS1 and PrM/M confer more effective protection for ZIKA virus vaccine **Speaker: Ling Chen** Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences, Guangzhou, China
	11:20-11:40 S-06	**Title:** Antiviral RNAi immunity – from basic to translation **Speaker: Xi Zhou** Wuhan Institute of Virology, Chinese Academy of Sciences

	11:40-12:00 S-07	**Title:** The role of MVP in viral infection **Speaker: Shi Liu** College of Life Sciences, Wuhan University, China
	12:00-12:15 Sponsor Presentation	Newly Technology development of Cryo TEM by JEOL **By Jianzhong Yuan** TEM product manager of JEOL in China
	12:15-14:00	Lunch/午餐
	Day 1, Afternoon Session /第一天下午	
	14:00-17:30	**Session 2: Emerging viral pathogens** **Session Chairs: Zhengli SHI, Peter DASZAK**
	14:00-14:30 Keynote Speech S-08	**Title:** Forecasting future viral pandemics and the Global Virome Project **Speaker: Peter Daszak** EcoHealth Alliance, New York, USA
	14:30-14:50 S-09	**Title:** Infection and Immune Responses of Jamaican Fruit Bats (*Artibeus jamaicensis)* Experimentally Challenged with a Bat HL18NL11 Influenza A Virus **Speaker: Tony Schountz** Department of Microbiology, Immunology and Pathology, College of Veterinary Medicine and Biomedical Sciences, Colorado State University
	14:50-15:10 S-10	**Title:** PLSCR1 negatively regulates influenza A virus replication by targeting the nuclear import of viral NP protein **Speaker: Chengjun Li** Harbin Veterinary Research Institute, Chinese Academy of Agricultural Sciences, Harbin, China
	15:10-15:30 S-11	**Title:** Inter-host and intra-host evolution of Ebola virus **Speaker: Di Liu** Wuhan Institute of Virology, Chinese Academy of Sciences
	15:30-15:50	Coffee Break and Poster Presentation/茶歇和展板
	15:50-16:10 S-12	**Title:** Risks of MERS-cluster coronaviruses in China **Speaker: Peng Zhou** Wuhan Institute of Virology, Chinese Academy of Sciences
	16:10-16:30 S-13	**Title:** Molecular mechanisms for cross-species transmissions of SARS and MERS coronaviruses **Speaker: Fang Li** Department of Veterinary and Biomedical Sciences, University of Minnesota
	16:30-16:50 S-14	**Title:** Human coronavirus OC43 (HCoV-OC43) and bovine coronavirus (BCoV) **Speaker: Astrid Vabret** Laboratory of Virology, University Hospital of Caen, France

	16:50-17:10 S-15	**Title:** Origin and cross-species transmission of bat coronaviruses in China **Speaker: Alice Latinne** EcoHealth Alliance, New York, USA
	17:10-17:30 S-16	**Title:** Coronaviruses phylogenetics and intra-colony evolution of the SARS-CoV sister-clade Betacoronavirus in bats in western Palearctics **Speaker: Meriadeg Ar Gouilh** Groupe de Recherche sur l'Adaptation Microbienne, Normandy University, France
	18:00-20:00	Banquet 会议晚宴

Program of
The 8th International Symposium on Emerging Viral Diseases

Date 日期	Time 时间	Content 议程
Monday 星期一 Oct. 22, 2018 10 月 22 日	Day 2, Morning Session /第二天上午	
	08:30-12:10	**Session 3: Virus-Host Interaction** **Session Chairs: Xi ZHOU, Ralph BARIC**
	08:30-09:00 Keynote Speech S-17	**Title**: Genetic Regulation of Host Susceptibility to Emerging Virus Infections **Speaker**: **Ralph Baric** Department of Epidemiology, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA
	09:00-09:30 Keynote Speech S-18	**Title:** Peptide-based Virus Entry Inhibitors against Class I and II Enveloped Viruses **Speaker: Shibo Jiang** Basic Medical College, Fudan University, Shanghai, China
	09:30-09:50 S-19	**Title:** Small molecules as filoviral entry inhibitors and chemical probes **Speaker: Lijun Rong** Department of Microbiology and Immunology, College of Medicine, University of Illinois at Chicago, Chicago, IL, USA
	09:50-10:10 S-20	**Title:** Entry mechanisms of highly pathogenic coronaviruses: MERS-CoV and SARS-CoV **Speaker: Yi Shi** CAS Key Laboratory of Pathogenic Microbiology and Immunology, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China
	10:10-10:30	Coffee Break and Poster Presentation/茶歇和展板
	10:30-10:50 S-21	**Title:** Pathology of and development of antiviral therapy with favipiravir for severe fever with thrombocytopenia syndrome **Speaker: Masayuki Saijo** Department of Virology, National Institute of Infectious Diseases, Tokyo, Japan
	10:50-11:10 S-22	**Title:** Epistasis and complementation contribute to the evolution of the Rabies virus phosphoprotein in the face of severe functional constraints within the replication complex **Speaker: Hervé Bourhy** Institut Pasteur, Unit of Lyssavirus Dynamics and Host Adaptation, Paris, France
	11:10-11:30 S-23	**Title:** Influenza A virus-derived siRNAs increase in the absence of NS1 yet fail to inhibit virus replication **Speaker: Kevin Tsai** Department of Molecular Genetics and Microbiology, Duke University Medical Center, Durham, North Carolina, USA

	11:30-11:50 S-24	**Title:** Mechanisms of Herpesvirus capsid assembly and maturation **Speaker: Xiangxi Wang** Institute of Biophysics, Chines Academy of Sciences, Beijing, China
	11:50-12:10 S-25	**Title:** From the functional-structure of coronavirus methyltransferase to anti-viral drug development **Speaker: Yu Chen** College of Life Sciences, Wuhan University, China
	12:10-14:00	Lunch/午餐
	Day 2, Afternoon Session /第二天下午	
	14:00-17:30	**Session 4: Arbovirus** **Session Chairs: Zhihong HU, Pei-Yong SHI**
	14:00-14:30 Keynote Speech S-26	**Title:** Zika Virus: Emergence and Vaccine Development **Speaker: Pei-Yong Shi** University of Texas Medical Branch, Galveston, Texas, USA
	14:30-14:50 S-27	**Title:** Replicase Proteins of Alphaviruses as Determinants of Viral Pathogenesis and Vector Transmission **Speaker: Andres Merits** Institute of Technology, University of Tartu, Estonia
	14:50-15:10 S-28	**Title:** Identification of prognostic biomarkers for Dengue disease severity through an integrated ‘omics analysis of patient serum **Speaker: Andrew Davidson** University of Bristol, Bristol, United Kingdom
	15:10-15:30 S-29	**Title:** Zika virus tropism for neural stem cells: the bad and the good **Speaker: Cheng-Feng Qin** Beijing Institute of Microbiology and Epidemiology, Academy of Military Medical Sciences, Beijing, China
	15:30-15:50	Coffee Break 茶歇
	15:50-16:10 S-30	**Title:** A gut commensal bacterium promotes mosquito permissiveness to arboviruses **Speaker: Gong Cheng** Tsinghua-Peking Center for Life Sciences, School of Medicine, Tsinghua University, Beijing, China
	16:10-16:30 S-31	**Title:** The fabulous NSs protein of Rift Valley fever virus **Speaker: Pierre-Yves Lozach** Cluster of Excellence and Center for Integrative Infectious Disease Research, University Hospital Heidelberg, Germany
	16:30-16:50 S-32	**Title:** Novel delivery of a live-attenuated chikungunya virus vaccine candidate **Speaker: Adam Taylor** Griffith University, Southport, Queensland, Australia

	16:50-17:10 S-33	**Title:** Viromes of ticks reveals highly potential risks of tick-borne viral diseases in Xinjiang, China **Speaker: Fei Deng** Wuhan Institute of Virology, Chinese Academy of Sciences
	17:10-17:30 S-34	**Title:** Species-specific disruption of STING-dependent antiviral cellular defenses by the Zika virus NS2B3 protease **Speaker: Qiang Ding** School of Medicine, Tsinghua University, Beijing, China
	17:30-17:40	**Closing Remarks**
	18:00-19:00	Dinner/晚餐

From: Ebel,Greg
Sent: Wednesday, May 20, 2020 1:50 PM EDT
To: epstein ecohealthalliance.org>; Schountz,Tony >
Subject: FW: C06 check in

Tony and Jon,

See below. I can do Thursday, May 28th at 4:00 EST (2:00 mountain). Can you please rearrange your schedules to accommodate this call? Let' hope for some good news.

Greg

From: Patterson, Jean (NIH/NIAID) [E] >
Sent: Wednesday, May 20, 2020 11:38 AM
To: Ebel,Greg >
Subject: RE: C06 check in

Morning, Greg. Why don't we try to get on a call with you all next week? Mark and I are available Wed. May 27th: 2-3:30pm, Thurs. May 28th: after 3pm, and Fri. May 29th: 10-11am or after 4pm – all EST. If you don't mind, please coordinate with related folks on your end, (especially Jon Epstein) and send us an invite. We will accept.
Thanks and look forward to talking with you again!
Jean

From: Ebel,Greg >
Sent: Thursday, May 14, 2020 2:29 PM
To: Patterson, Jean (NIH/NIAID) [E]
Subject: RE: C06 check in

OK thanks a lot, Jean.

Hang in there!

Greg

From: Patterson, Jean (NIH/NIAID) [E]
Sent: Thursday, May 14, 2020 12:24 PM
To: Ebel,Greg >
Subject: RE: C06 check in

Hi Greg,
We are all hanging in here, just working! Hope you are doing well too.
I don't have confirmation yet as to whether the C06 will get picked up. I will say that Mark and I have been thinking of a Plan B just in case and at some point soon plan to set up a call with you all to discuss further.
Sorry I don't have better news, but will explain when we get on a call.
Be in touch!
Jean

From: Ebel,Greg
Sent: Thursday, May 14, 2020 1:25 PM
To: Patterson, Jean (NIH/NIAID) [E] v>
Subject: C06 check in

Hi Jean,

Just wanting to check in on the C06 progress.

Hope things are going well for you and that you're staying safe.

Greg Ebel

From: calisher
Sent: Wednesday, June 17, 2020 2:09 PM EDT
To: Paul Cryan ; Peter Daszak ecohealthalliance.org>; Kevin J. Olival ; Schountz,Tony >; Dick Bowen >
Subject: FW: Rogers 2020 reference from my EndNote library
Attachment(s): "Rogers-2020-6 reasons why bats aren't enemies_.pdf"

From: Robert Tesh <>
Sent: Wednesday, June 17, 2020 12:06 PM
To: Charles H Calisher >
Subject: Fwd: Rogers 2020 reference from my EndNote library

---------- Forwarded message ---------
From: **Ksiazek, Thomas G.**
Date: Tue, Jun 16, 2020, 2:18 PM
Subject: Rogers 2020 reference from my EndNote library
To: Amman, Brian R >, Kemp, Alan >, Nichol, S , Rollin,P (>, Spiropoulou, Christina (CDC/CCID/NCZVED) ( ) >, Swanepoel,R >, Tesh,R(Home) >, Towner, Jonathan S. (CDC/CCID/NCZVED >

There was a program on CNN on Sunday evening which had the usual recent suspects: Daszak and Jon Epstein

Rogers K. (2020, 20200614). **6 reasons why bats aren't enemies: They help make tequila, and other surprising facts you may not know.** CNN Retrieved 0616, 2020,

https://www.cnn.com/2020/06/14/world/bat-facts-cnn-special-coronavirus-scn/index.html

6 reasons why bats aren't enemies: They help make tequila, and other surprising facts you may not know

By Kristen Rogers, CNN

Updated 5:59 AM ET, Sun June 14, 2020

New Zealand says it has zero active cases of Covid-19

Gov. Cuomo: We've been through hell. We'll come out stronger.

Vegas casinos reopen with countdown and virtual fireworks

Trump's CDC director has a controversial past

Tokyo gov warns Oly could be s down in 2(

(CNN) Bats have shouldered much of the blame in the quest for the origins of the novel coronavirus.

In March, researchers published a study that found a 96.2% similarity between the

coronavirus that causes Covid-19 and a virus found in a horseshoe bat from China's Yunnan province.

"Ninety-six percent is a different virus; it's a bit like the difference between us and chimpanzees," Peter Daszak, the president of the non-profit EcoHealth Alliance, explains in CNN Special Report "Bats: The Mystery Behind Covid-19."

"It's a different species of virus. But what it tells us is where the virus probably came from. It means that SARS-CoV-2 probably came from bats and probably in Southern China."

Yunnan province is about a thousand miles from Hubei province, which is where the city of Wuhan saw the early virus outbreaks. A mix of potentially infected wild animals in a wet market could have caused the virus to jump from animals to humans. But zoologists, ecologists and disease experts have said that it's human behaviors — such as destroying natural habitats — that might be to blame for the transfer of the disease.

Overall, bats have caught a bad rap — not only with their connection to Covid-19 and other virus outbreaks but in cultural symbolism as well. Bats have been associated with vampires, darkness, evil, witchcraft and death.

However, as experts tell Anderson Cooper in the CNN special report, these flying mammals have a crucial role in our ecosystem, and there are many unique facts that the average person likely doesn't know about them — including how they help produce tequila.

They save us from mosquitoes

Bats play a large role in the ecosystem by controlling insect populations, said Nancy Simmons, American Museum of Natural History mammalogy curator and coauthor of "Bats:

A World of Science and Mystery."

Newly discovered bats are related to those associated with the pandemic

In an hour, a normal-sized bat can eat up to 500 to 1,000 mosquitoes, which can carry diseases such as the Zika virus, dengue fever or malaria.

Their insect-eating habits also save big money for agriculture. For the US economy, bats are worth over a billion dollars every year "in terms of how many pesticides we don't need to use and how much more food we get," said Dan Riskin, a Canadian evolutionary biologist and television host.

The Mexican free-tailed bat of Texas eats a great number of moths, protecting the corn crops of the region.

They're intrinsically environmentally conscious

Pest control isn't bats' only contribution to our ecosystem. The waste droppings of fruit-eating bats — particularly those in rainforests — disperse seeds, helping to regenerate plants and trees previously damaged or cut down.

Their droppings are also full of nitrogen, which is a vital ingredient for crops since it's a main component of chlorophyll, the compound by which plants use energy from the sun to produce sugars from water and carbon dioxide. This process, called photosynthesis, generates oxygen. Nitrogen is also a crucial element of amino acids, the building blocks of proteins.

And historically, bat caves have been harvested for fertilizer and then explosives during the Civil War. The high nitrate content of their feces provided a key ingredient for the production of gunpowder amid a shortage of supplies.

Cogs in the tequila-making machine

Some bat species serve as the only pollinators of particular types of bananas, mangoes and cacti. The muzzles of long-nosed bats are designed to fit perfectly inside some cactus blossoms, which fittingly only open at night.

This species, whose habitat ranges from the American Southwest to central and southern Mexico, pollinates the blue agave plant — the key ingredient in tequila. They act as surrogates carrying the pollen from one agave plant to another.

"Who doesn't love tequila, right?" Riskin said. "I mean, just right there, that should be reason enough for people to love bats."

They're fighting a disease humans gave them

While we're fighting a virus that potentially came from bats, they're fighting a fungus that might have transferred to them from us.

In North America over the past 15 years, populations of about a dozen bat species have been affected by a disease called "white nose syndrome." In some cases, populations have plummeted by more than 90%.

"It's a cold-loving fungus that grows on the bat when the bats are hibernating in the wintertime," Simmons said. "It's a terrible threat to bats. And ironically, it's a disease that we brought to bats. This disease is identical to fungus that naturally occurs in Europe. And so the thought is that it was simply brought over by people and was accidentally introduced into bat caves."

Lacking disease-related genes

When a virus infects our cells, our immune response will recruit immune cells to the site to

try to clear the infection, said Cara Brook, a postdoctoral Miller Fellow in the department of integrative biology at the University of California-Berkeley, in the CNN special.

The response that signals uninfected cells to turn on their defense system typically results in inflammation — which, in humans, is often in the form of fever or swelling that helps fight infection.

But bats' immune systems don't respond the same way — they're able to withstand strong immune reactions and have an anti-inflammatory response as well.

How vampire bats make friends before sharing meals of blood

Some bat species "are actually missing the genes that we and other animals have that trigger the inflammatory process" in response to pathogens and viruses that can be deadly for people and other animals, said Jonathan Epstein, a veterinarian, disease ecologist and the vice president of science and outreach at EcoHealth Alliance.

Studying bat immunology could help provide insights regarding possible treatments for the current pandemic, as well as any future pandemic of a bat-related virus.

Bats help pave the road to medical discoveries

Bats already contribute to research that could one day be helpful to humans.

In a 2019 study published in the journal Biology Letters, researchers analyzed evolutionary trees reconstructed from the DNA of the majority of known bat species. They found that four species — horseshoe, long-eared, common and mouse-eared — all live at least four times longer than other similarly-sized mammals.

And when adjusted for size, bats exceed the average human lifespan. The study added to previous research that suggested looking further into bats as models for healthy aging, to find traits and mechanisms associated with a long life span.

Vampire bats in particular — a rare species that lives in Central and South America and feeds on the blood of birds, pigs and cattle — have blood-thinning agents in their saliva, which helps them draw free-flowing blood from their prey. Scientists have looked into whether there are insights about their blood that would be helpful for treating humans.

Some studies have also suggested that vampire bats' blood might also lend to treatments for conditions including stroke, hypertension, heart failure and kidney diseases.

And now, studying how bats' immunology enables them to withstand numerous viruses and pathogens could be applied to developing prevention and treatment for humans.

From: zlshi <zlshi
Sent: Monday, April 02, 2018 8:26 PM EDT
To: huben <huben
CC: Christopher Francis Basler < >; Manicassamy, Balaji [MIC] ;
Schountz,Tony
Subject: Fw: Suggested invitees

Dear Ben,

Please add the above three scientists in the list of our invited speakers.

Best regards,

SHI Zhengli, Ph. D
Senior Scientist & Professor
Wuhan Institute of Virology, Chinese Academy of Sciences
44 Xiao Hong Shan
430071 Wuhan, Hubei
China

From: Rong, Lijun
Date: 2018-04-02 20:45
To: zlshi
CC: Christopher Francis Basler; Manicassamy, Balaji [MIC]
Subject: Suggested invitees

Dear Zhengli,

I look forward to attending the October meeting in Wuhan organized by you (even though I have not got the official invitation.

In addition, I would suggest two more speakers for the meeting:
Dr. Chris Basler, Professor and Director of Emerging Viruses Center (?) at Georgia State University. Chris was at Mt Sinai School of Medicine and moved to Georgia. He is a world leader in Ebola virus research.

Dr. Balaji Manicassamy, Assistant Professor at University of Chicago. He attended the meeting two years ago, and his group works on influenza viruses. He has already contributed a lot to the field.

I may suggest one or two more if you like later.

Thank you for your great effort in organizing the meeting! We had a lot of fun last time.

Best regards,
Lijun

Lijun Rong, PhD
Professor of Microbiology and Immunology
College of Medicine
University of Illinois at Chicago

From: Munster, Vincent (NIH/NIAID) [E] <
Sent: Sunday, February 09, 2020 11:38 AM EST
To: Schulz, Jonathan (NIH/NIAID) [F] >; Seifert, Stephanie (NIH/NIAID) [E] ; John Thompson >; Avanzato, Victoria (NIH/NIAID) [F] >; Sterling, Spencer ; Letko, Michael (NIH/NIAID) [F] ; Matson, Jeremiah (NIH/NIAID) [F] >; Fischer, Robert (NIH/NIAID) [F] ; Janine Seetahal >; Vernie Ramkissoon >; Tracey Goldstein ; Anthony, Simon J. ; Jon Epstein ecohealthalliance.org>; Eric Laing ; Broder, Chris (USU-DoD) ; Christine Carrington ; Schountz,Tony

Subject: FW: Your article has been published by Oxford University Press
Attachment(s): "jiz648.pdf"

Dear co-authors,

Please find attached the final published version of our manuscript,

Cheers,

Vincent Munster, PhD
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

From: Oxford University Press
Date: Sunday, February 9, 2020 at 9:33 AM
To: "vincent.munster "
Cc: "jid
Subject: Your article has been published by Oxford University Press

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The Journal of Infectious Diseases

Serological Evidence for Henipa-like and Filo-like Viruses in Trinidad Bats

Jonathan E. Schulz,[1] Stephanie N. Seifert,[1] John T. Thompson,[1] Victoria Avanzato,[1] Spencer L. Sterling,[2] Lianying Yan,[2] Michael C. Letko,[1] M. Jeremiah Matson,[1,7], Robert J. Fischer,[1] Alexandre Tremeau-Bravard,[3] Janine F. R. Seetahal,[4] Vernie Ramkissoon,[4] Jerome Foster,[4] Tracey Goldstein,[3] Simon J. Anthony,[5] Jonathan H. Epstein,[6] Eric D. Laing,[2] Christopher C. Broder,[2] Christine V. F. Carrington,[4] Tony Schountz,[8] and Vincent J. Munster[1,]

[1]Virus Ecology Unit, Rocky Mountain Laboratories, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Hamilton, Montana, USA, [2]Uniformed Services University, Bethesda, Maryland, USA, [3]One Health Institute, School of Veterinary Medicine, University of California, Davis, California, USA, [4]Department of Preclinical Sciences, Faculty of Medical Sciences, The University of the West Indies, St Augustine, Trinidad and Tobago, [5]Center for Infection and Immunity, Mailman School of Public Health, Columbia University, New York, New York, USA, [6]EcoHealth Alliance, New York, New York, USA, [7]Marshall University Joan C Edwards School of Medicine, Huntington West Virginia, USA, [8]Arthropod-borne and Infectious Disease Laboratory, Department of Microbiology, Immunology and Pathology, College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, Colorado, USA

Bat-borne zoonotic pathogens belonging to the family Paramxyoviridae, including Nipah and Hendra viruses, and the family Filoviridae, including Ebola and Marburg viruses, can cause severe disease and high mortality rates on spillover into human populations. Surveillance efforts for henipaviruses and filoviruses have been largely restricted to the Old World; however, recent studies suggest a potentially broader distribution for henipaviruses and filoviruses than previously recognized. In the current study, we screened for henipaviruses and filoviruses in New World bats collected across 4 locations in Trinidad near the coast of Venezuela. Bat tissue samples were screened using previously established reverse-transcription polymerase chain reaction assays. Serum were screened using a multiplex immunoassay to detect antibodies reactive with the envelope glycoprotein of viruses in the genus *Henipavirus* and the family Filoviridae. Serum samples were also screened by means of enzyme-linked immunosorbent assay for antibodies reactive with Nipah G and F glycoproteins. Of 84 serum samples, 28 were reactive with ≥1 henipavirus glycoprotein by ≥1 serological method, and 6 serum samples were reactive against ≥1 filovirus glycoproteins. These data provide evidence of potential circulation of viruses related to the henipaviruses and filoviruses in New World bats.

Keywords. Filovirus; Henipavirus; Trinidad; Bats; Screening; Serology; Luminex; RT-PCR

Since 1994, >350 human fatalities from Hendra (HeV) or Nipah virus (NiV) disease outbreaks have been reported [1–3]. Periodic outbreaks of Ebola and Marburg virus disease caused by members of the family Filoviridae have resulted in approximately 13 700 recorded human fatalities since 1976 [4, 5]. In addition to public health concerns, henipavirus and filovirus spillover events continue to have severe economic and ecological impacts [6–9]. Bats are natural reservoirs for some paramyxoviruses (NiV, Hendra virus, Cedar virus, Menangle virus, and Achimota virus 1 and 2) and some filoviruses (Marburg and Bombali viruses) and are the putative reservoirs for other paramyxovirus and filovirus species [10–21]. In the context of henipaviruses, the geographic distribution outside South and Southeast Asia, Africa, and Australia has yet to be determined [2, 22]. In the context of filoviruses, the broader ecology and circulation within their respective natural reservoirs and the extent of the geographic distribution of filoviruses are still largely unknown [23].

Henipaviruses have only been isolated from pteropid bats in Southeast Asia and Australia [13–15]. However, multiple studies have presented evidence for the presence of henipaviruses in Africa [16, 22, 24–30], with full genome sequences recovered for the bat-borne Ghana henipavirus in Ghana [18]. In addition, recent serological data suggest that African henipaviruses are capable of spillover into human and husbandry animal populations, although this data has not been associated with any recorded morbidity and mortality events [24, 28, 29]. A serological study by de Araujo et al found henipavirus-like antibodies in Brazilian bats. Given the distribution of bat species in Latin America that were serologically positive for the Brazilian henipa-like virus, it is possible that these viruses are circulating in Trinidad and Tobago.

The discovery of filoviruses outside Africa, including Reston virus (RESTV) in the Philippines, Lloviu virus (LLOV) in Spain, and Měnglà, Xīlǎng, and Huángjiāo viruses in China, demonstrates the broad geographic range of filoviruses [31–34]. Serological and polymerase chain reaction (PCR) evidence for filoviruses in China, Singapore, Bangladesh, and Hungary also suggest the possibility that uncharacterized filoviruses may circulate in bat populations beyond the currently described geographic range [35–39]. Han et al [40] used published filovirus surveillance data to predict bat species which may be potential filovirus reservoirs based on behavior, life history, and ecological traits; their study predicted that several New World bats,

Correspondence: Vincent J. Munster, National Institutes of Health, Hamilton, MT (Vincent.Munster@nih.gov).

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DOI: 10.1093/infdis/jiz648

including several bat species with populations in Trinidad and Tobago, may be potential hosts of uncharacterized filoviruses.

In 2012, bats of 6 species were captured from 4 locations in Trinidad. Malmlov et al [41] screened these bat samples and found evidence of the circulation of Tacaribe virus. We describe here the results of surveillance efforts for evidence of henipa-like and filo-like viral infection in the same sample set, because the breadth of the host range and geographic distribution are still largely unknown for these virus families.

METHODS

Ethics Statement

All field work was performed under the approval of the Ethics Committee, Faculty of Medical Sciences, The University of the West Indies (UWI), St Augustine Campus, and under a special game license from the Wildlife Section, Forestry Division, Ministry of Agriculture, Land and Fisheries, Republic of Trinidad and Tobago. All work with infectious henipaviruses and filoviruses was performed under biosafety level 4 conditions at the Rocky Mountain Laboratories, Division of Intramural Research, National Institute of Allergy and Infectious Diseases, National Institutes of Health, according to standard operating protocols approved by the Institutional Biosafety Committee.

Bat Capture

In February 2012, bats were captured with mist nets in Trinidad at 4 locations; Mount Hope (N 10.67120, W 061.28677), Lopinot (N 10.69792, W 061.32243), Santa Cruz (N 10.69596, W 061.44629), and Maracas Valley (N 10.70945, W 061.40177) (Figure 1). Cloth bags were used to individually confine and transport bats to laboratory facilities at the University of the West Indies, St Augustine for processing. Six bat species were obtained: 36 flat-faced fruit bats (*Artibeus planirostris trinitatis*), 31great fruit-eating bats (*Artibeus lituratus*), 3 Pallas's long-tongued bat (*Glossophaga soricina*), 7 greater sac-winged bats (*Sacropteryx bilineata*), 3 little yellow-shouldered bats (*Sturnira lilium*), and 4 Seba's short-tailed bats (*Carollia perspicillata*). Bats were euthanized through inhalation of isoflurane and exsanguination before necropsy. Tissue (lung, liver, kidney, spleen, brain, and blood) and serum samples were stored at −80° C before shipment on dry ice to Rocky Mountain Laboratories for further processing.

Luminex Serology

The presence of immunoglobulins against henipavirus- and filovirus-soluble native-like oligomeric virus envelope glycoproteins was measured using a Luminex xMAP-based multiplex microsphere immunoassay (MIA) [37, 42]. Briefly, soluble tetrameric henipavirus receptor binding proteins (sG_{tet}) (Yan et al in review) and soluble trimeric ectodomains of filovirus envelope glycoproteins were produced, as described elsewhere [37]. Purified $sG_{tet}$and envelope glycoprotein antigens were coupled to Bio-Plex Pro magnetic COOH beads (Bio-Rad). Blood was collected into serum separating tubes by means of cardiac puncture with bats under deep anesthesia, and it was centrifuged at 1000*g* for 10 minutes before serum was collected and frozen at −80°C. We performed the Luminex assay on serial dilutions of negative control serum samples from 14 captive-bred *Rousettus aegyptiacus* bats to determine an appropriate dilution for screening bat serum samples with the Luminex assay. All negative control serum samples were negative at a final dilution of 1:500. Field-collected bat serum samples were heat inactivated at 56°C for 30 minutes and diluted 1:500 before screening, and each sample was run in duplicate.

Enzyme-Linked Immunosorbent Assay

Nunc Maxisorp 96-well flat-bottom Immuno Plates (ThermoFisher) were coated with purified Nipah F and G glycoproteins (50 ng in 100 µL per well, diluted in phosphate-buffered saline [PBS]) overnight at 4°C. Plates were washed 3 times with PBS with 0.1% Tween 20 (PBS-T) and then blocked with 5% nonfat milk in PBS-T (100 µL per well) for 1 hour at room temperature. After being washed 3 times with PBS-T, diluted bat serum samples (1:100, 1:250, or 1:500 in 5% nonfat milk) were added to the wells in duplicate (100 µL) and incubated for 1 hour at room temperature. Plates were washed 5 times with PBS-T. Secondary antibody (goat anti-bat immunoglobulin G [IgG; heavy and light] horseradish peroxidase conjugate; Bethyl; 1:2500) was added to wells (100 µL) and incubated for 1 hour at room temperature. After 5 washes with PBS-T, 100 µL of a 1:1 ratio of 3,3',5,5'-tetramethylbenzidine (TMB) solution and peroxide solution (Pierce TMB Substrate Kit; ThermoFisher) was added to wells. Plates were allowed to develop in the dark. After stopping the reaction with 100 µL of 2 mol/L sulfuric acid, plates were read at 450 nm.

In Vitro Transcription

Bombali virus and LLOV have not been isolated. Therefore, in vitro transcripts were generated as positive controls. RNA-dependent RNA polymerase coding sequence segments of Bombali virus and LLOV were synthesized into pUC57 cloning vectors (Biobasic). Plasmids were transformed into Stellar Competent Cells, following protocol PT5055-2 (Clontech). Plasmids were isolated using a PureLink HiPure Plasmid Midiprep kit (Invitrogen). Linear templates were generated by a single digestion with restriction enzyme EcoR1, according to the manufacturer's protocol (New England Biolabs). Negative-sense RNA was transcribed using the MEGAscript T7 kit.

Nucleic Acid Extraction

RNA and DNA from Trinidad bat tissues were extracted using the Cador Pathogen 96 QIAcube HT Kit and QIAcube robot (Qiagen). The bat tissues were lysed in RLT buffer (Qiagen), followed by incubation in 95%–100% ethanol for 10 minutes before extraction. Extracted RNA from virus stocks of all currently

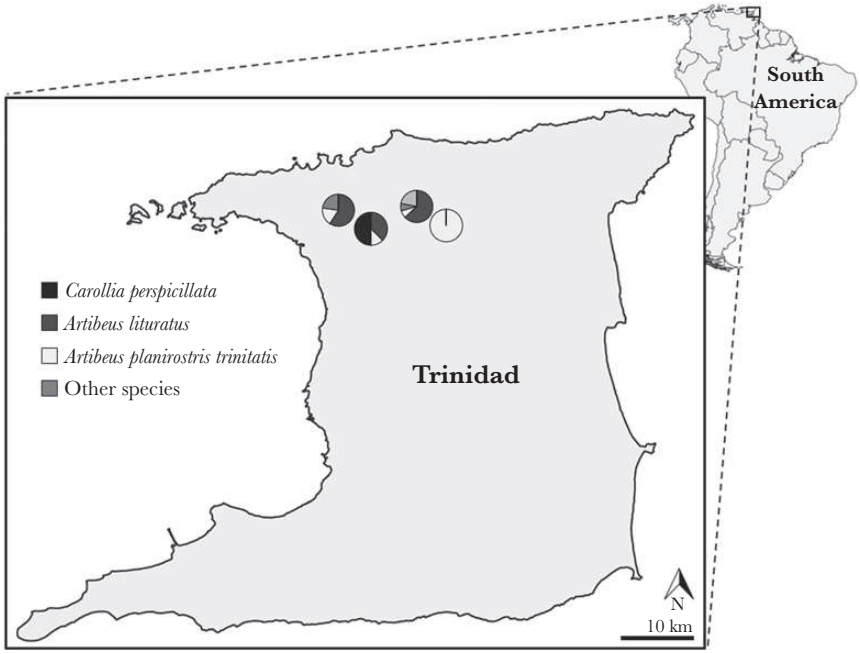

Figure 1. Field sites of bat capture. Collections at Mt Hope were performed during the day at the University of West Indies. Collections at Santa Cruz, Maracas Valley, and Lopinot were performed over 3 nights.

isolated henipavirus and filovirus species were used for assay validation and positive controls. RNA was isolated using the QIAmp Viral RNA Kit (Qiagen) in a biosafety level 4 laboratory, with published modifications appropriate for virus inactivation in biosafety level 4 conditions [43]. Henipaviruses included were NiV, species *Nipah henipavirus*, isolate Malaysia; HeV, species *Hendra henipavirus*, isolate Hendra; and Cedar virus (CedV), species *Cedar henipavirus*, isolate Cedar. Filoviruses included were Ebola virus (EBOV), species *Zaire ebolavirus*, isolate Gabon; Sudan virus (SUDV), species *Sudan ebolavirus*, isolate Boniface; Taï Forest virus (TAFV), species *Taï Forest ebolavirus*, isolate Taï Forest; RESTV, species *Reston ebolavirus*, isolate Pennsylvania; Bundibugyo virus (BDBV), species *Bundibugyo ebolavirus*, isolate Bundibugyo; Marburg virus (MARV), species *Marburg marburgvirus*, isolate Angola; and Ravn virus (RAVV), species *Marburg marburgvirus*, isolate Ravn.

Henipavirus, Morbillivirus, and Respirovirus Assay

Complementary DNA (cDNA) was synthesized from 10 µL of RNA using the SuperScript III or IV First-Strand Synthesis System for reverse-transcription PCR (RT-PCR) (Invitrogen). RT-PCR was performed using TopTaq Master Mix Kit (Qiagen) 50-µL reactions, with 25 µL of TopTaq MasterMix, 5 µL of CoraLoad Dye, 1 µL of 10 µmol/L primers (final concentration 1.0 µmol/L), and 5 µL of cDNA template used for each reaction. Previously designed primers targeting a conserved region of the RNA-dependent RNA polymerase gene for henipaviruses, morbilliviruses, and respiroviruses [44] were used for PCR. Thermal cycling conditions were followed, according to the manufacturer's protocol, with an annealing temperature of 50°C. PCR products were analyzed using a 1% agarose gel and SYBR Safe DNA Gel Stain (Fisher Scientific). The expected fragment size based on the position of the second primer set was approximately 600 base pairs.

Panfilovirus Assay

cDNA was synthesized as described above. Nested RT-PCR was performed using TopTaq Master Mix Kit (Qiagen) 50-µL reactions, including 25 µL of TopTaq MasterMix, 5 µL of CoraLoad Dye, 1 µL of 10 µmol/L primers (final concentration 0.2 µmol/L), and 5 µL of cDNA template for each reaction. Previously designed primers targeting a conserved region of the filovirus RNA-dependent RNA polymerase gene [19] was used for nested PCR, with the addition of a modified forward primer for the second reaction (5'-TYTCHVT/ideoxyI/CAAAA/ideoxyI/CAYTGGGG-3'). Thermal cycling conditions for both rounds were as follows: 94°C for 5 minutes; 15 cycles of 94°C, 60.9°C (−1°C/cycle), and 72°C for 1 minute each; 15 cycles of 94°C, 45.9 °C, and 72°C for 1 minute each; and a final extension at 72 °C for 7 minutes. PCR products were analyzed using a 1% agarose gel and GelRed Nucleic Acid Stain (Phenix Research Products) or SYBR Safe DNA Gel Stain (Fisher Scientific). The expected fragment size based on the position of the second primer set was approximately 680 base pairs.

RT-PCR Limit of Detection

The genome copy number from the respective henipavirus and filovirus controls was determined using a 1-step protocol

for Droplet Digital PCR (ddPCR) and the Automated Droplet Generator (Bio-Rad), according to the manufacturer's instructions. Eight representative filoviruses (Supplementary Figure 1) and 3 representative henipaviruses (NiV, HeV, and CedV) were used to determine the limit of detection (LOD) for the RT-PCR assay with ddPCR before bat screening. Primers and probes used are listed in Supplementary Table 1. The LOD was determined by means of serial 10-fold dilution of viral RNA–positive controls and further refined with serial 2-fold dilution. The LOD was determined based on the highest dilution from which an observable PCR product was obtained.

RESULTS

Serum samples from 84 Trinidad bats were screened with MIA for the presence of antibodies reactive to henipavirus or filovirus envelope glycoproteins. The median fluorescence intensity (MFI) cutoff value was set as 3 times the mean MFIs of a naive serum sample from a captive Egyptian fruit bat (*R. aegyptiacus)*. The percentage of bat serum samples reactive against henipavirus- or filovirus-soluble glycoproteins was 3.57% (3 of 84) and 7.14% (6 of 84), respectively. Six serum samples from *A. lituratus* bats were reactive against the soluble glycoproteins of RAVV, SUDV, RESTVp (pig isolate), RESTVm (primate isolate), EBOV, NiV, GhV, or CedV (Table 1). Serum samples from 1 flat-faced fruit bat (*A. planirostris trinitatis)* and 1 greater sac-winged bat (*S. bilineata*) were reactive against RAVV-soluble glycoprotein (Table 1). The highest MFI value relative to negative control was from an *A. lituratus* bat (bat no. 41) against SUDV-soluble glycoprotein (Table 1). Serological reactivity was observed in sample 41 between SUDV, RESTVp, RESTVm, NiV, and GhV and in sample 64 between SUDV and EBOV (Table 1).

Serum samples were also screened by enzyme-linked immunosorbent assay (ELISA) for the presence of antibodies reactive to Nipah F and G glycoproteins. The MFI cutoff value was set as 3 times the standard deviation of the average MFI of naive bat serum from a captive Egyptian fruit bat. The proportions of bat serum samples reactive against Nipah G and F at 1:100 dilution were 29.76% (25 of 84) and 19.05% (16 of 84), respectively (Table 1). Only 2 samples were reactive against Nipah G and F at dilutions of 1:250 or greater. Twelve samples were reactive against Nipah G, but not Nipah F, and 3 were reactive against Nipah F but not Nipah G. All samples that showed reactivity with MIA were reactive to Nipah G at ELISA. However, only 1 sample (bat 41) was reactive to both Nipah G and F at ELISA and Nipah G at MIA.

Previously established panviral RT-PCR assays for high-throughput screening of biologically derived samples were used to detect respirovirus, morbillivirus, henipaivirus, and filovirus RNA [19]. The panfilovirus assay was modified by incorporating sequence information for recently identified filoviruses and validated for specificity and sensitivity. Eight representative filoviruses (Supplementary Figure 1) and 3 representative henipaviruses were used to determine the LOD for the assays by means of ddPCR before bat screening. The average LOD for the representative henipaviruses and filoviruses was 3.2 and 1.5 copies/μL, respectively (Supplementary Table 2). The L gene segment of LLOV generated product only at starting concentrations >1000 copies/μL and was considered an outlier for the LOD. Tissue samples from 78 Trinidad bats were screened for respiroviruses, morbilliviruses, henipaviruses, and filoviruses by means of RT-PCR. Tissues screened were lung, liver, kidney, spleen, and brain. No henipavirus or filovirus RNA was detected in this sample set.

DISCUSSION

Worldwide virus discovery and surveillance efforts have led to the identification of a variety novel European, African and Chinese henipaviruses and filoviruses [16, 19, 21, 22, 24, 33, 36, 45]. In addition, they have identified potential henipavirus circulation in Latin America [46]. The zoonotic and cross-species spillover potential of these novel viruses is currently unknown. However, these discoveries highlight the importance of virus discovery and surveillance efforts for novel henipavirus and filovirus species given their potential public health, economic, and ecological impacts. Therefore, expanding surveillance efforts beyond the known geographic distributions of henipaviruses and filoviruses may shed further light on the ecology and evolutionary history of these important viruses.

In the current study, we screened phyllostomid and emballonurid bat serum and tissue samples from Trinidad for henipaviruses and filoviruses. Eight of 84 bat serum samples were positive at Luminex serology and reacted to ≥1 of the henipavirus or filovirus glycoproteins. Twenty-eight samples were positive for Nipah G, F, or both at ELISA. Of note, the 3 bat species (*A. lituratus, A. planirostris trinitatis,* and *C. perspicillata*) positive for a henipavirus-like antibodies at MIA or ELISA are 3 of the 6 species that were positive for henipavirus-like antibodies in a Brazilian study [46]. One bat species sampled in this study, *A. lituratus*, which was found to have antibodies reactive against filovirus-soluble glycoproteins, was among those predicted to be potential hosts of novel filoviruses based on a study by Han et al [40]. Several bats from this species showed reactivity to both filovirus and henipavirus antigens (including an individual with antibodies against both), a phenomenon also observed in pteropodid bats [24, 47, 48].

The serological IgG reactivity observed in our study is likely due to the circulation of viruses that have surface glycoproteins antigenically related to henipavirus and filovirus glycoproteins used in our assays. Similar serological cross-reactivity has been observed in a study of *Rousettus* bats experimentally challenged with filoviruses [49]. We found some discordance between the serological results of the ELISA against Nipah G and the multiplex Luminex assay that includes Nipah G, specifically that more

Table 1. Samples Seropositive Against Henipavirus or Filovirus Glycoproteins With Enzyme-Linked Immunosorbent and Multiplex Luminex Serological Assays[a]

			ELISA: NiV		Luminex Multiplex Assay												
Bat No.	Sampling Site	Species	G	F	NiV (G)	HeV (G)	GhV (G)	CeV (G)	TAFV (GP)	SUDV (GP)	RAVV (GP)	EBOV (GP)	MARV (GP)	LLOV (GP)	RESTVp (GP)	RESTVm (GP)	BDBV (GP)
12	UWI Chapel	*Artibeus planirostris trinitatis*	…	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…
14	UWI Chapel	*A. planirostris trinitatis*	1:100	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…
15	UWI Chapel	*A. planirostris trinitatis*	…	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…
17	UWI Chapel	*A. planirostris trinitatis*	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…	…
18	UWI Chapel	*A. planirostris trinitatis*	1:100	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…
20	UWI Chapel	*A. planirostris trinitatis*	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…	…
21	UWI Chapel	*A. planirostris trinitatis*	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…	…
25	UWI Chapel	*A. planirostris trinitatis*	…	…	…	…	…	…	…	…	10.6	…	…	…	…	…	…
30	Lopinot	*A. lituratus*	1:1000	1:500	…	…	…	…	…	…	…	…	…	…	…	…	…
33	Lopinot	*A. lituratus*	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…	…
34	Lopinot	*A. lituratus*	1:100	…	…	…	…	…	…	…	538.1	…	…	…	…	…	…
35	Lopinot	*A. lituratus*	1:100	…	…	…	…	183.6	…	…	…	…	…	…	…	…	…
37	Lopinot	*A. lituratus*	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…	…
38	Lopinot	*A. lituratus*	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…	…
41	Lopinot	*A. lituratus*	1:100	1:100	57.3	…	319.5	…	…	2719.9	…	…	…	…	1305.6	175.0	…
42	Lopinot	*Glossophaga soricina*	1:100	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…
48	Lopinot	*G. soricina*	1:100	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…
53	Lopinot	*A. lituratus*	1:100		…		57.0	…	…	…	…	…	…	…	…	…	…
55	Santa Cruz	*A. lituratus*	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…	…
56	Santa Cruz	*A. lituratus*	1:100	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…
58	Santa Cruz	*Sacropteryx bilineata*	…	…	…	…	…	…	…	…	33.8	…	…	…	…	…	…
59	Santa Cruz	*A. lituratus*	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…	…
63	Santa Cruz	*A. planirostris trinitatis*	1:100	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…
64	Santa Cruz	*A. lituratus*	1:100	1:100	…	…	…	…	…	306.9	…	20.3	…	…	…	…	…
65	Santa Cruz	*A. lituratus*	…	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…
67	Santa Cruz	*S. bilineata*	1:100	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…
75	Santa Cruz	*A. lituratus*	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…	…
77	Maracas Valley	*Carollia perspicillata*	1:100	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…
78	Maracas Valley	*C. perspicillata*	1:100	1:100	…	…	…	…	…	…	…	…	…	…	…	…	…
81	Maracas Valley	*A. lituratus*	1:250	1:250	…	…	…	…	…	…	…	626.3	…	…	…	…	…

Only positive reactivity with the specific assay and glycoprotein is displayed.

Abbreviations: BDBV, Bundibugyo virus; EBOV, Ebola virus; ELISA, enzyme-linked immunosorbent assay; F, fusion glycoprotein; G, attachment glycoprotein; GhV, Ghana henipavirus; G/GP, glycoprotein; HeV, Hendra virus; LLOV, Lloviu virus; MARV, Marburg virus; NiV, Nipah virus; RAVV, Ravn virus; RESTVm, primate isolate; RESTVp, pig isolate; SUDV, Sudan virus; TAFV, Taï Forest virus; UWI, University of West Indies.

[a]ELISA results are reported as the highest dilution for which each sample was seropositive. We report the mean fluorescence intensity (MFI) of the multiplex Luminex assay after subtracting the value of 3 standard deviations plus the mean MFI of the naive serum sample for each antigen.

samples were positive against Nipah G with the ELISA than with the Luminex (Table 1). Most of the samples showing some reactivity against Nipah G with ELISA but not the Luminex assay were not seropositive at dilutions above 1:100, with 2 exceptions in which *A. lituratus* bats (bats 30 and 81 [Table 1]) were seropositive by ELISA for both Nipah G and F at dilutions >1:100.

The multiplex nature of the Luminex assay complicates interpretation of the serological results, because we detected

reactivity against the glycoproteins of unrelated viruses, including filovirus, SUDV, and GhV in serum collected from an *A. lituratus* bat (bat 41 [Table 1]). The specific history of viral exposure is inherently unknown in field-collected samples, and polyclonal serum samples are frequently cross-reactive,; therefore, the conclusions that we can draw from these data are limited. Further efforts to characterize the viral diversity circulating in South American bats are needed to refine these serological assays and allow for the development of specific target antigens.

Although we improved on the sensitivity and specificity of a previously established panfilovirus RT-PCR assay [50–53], we detected no henipavirus or filovirus viral RNA. This is not surprising, given our sample sizes and the comparatively low detection rate of virus shedding compared to that of IgG antibodies against these viruses observed in naturally infected bats in field studies and experimentally infected bats in laboratory studies [54–57]. The geographic distributions of several bat species sampled in our study extend as far as Brazil, where bat serum samples were found to be positive for exposure to henipa-like viruses, with ELISA and immunofluorescence assay [46], suggesting the possibility of widespread circulation of henipa-like viruses in Central and South America. Here we provide evidence for the potential circulation of henipa-like and filo-like viruses in Trinidad. No viral RNA was detected in this set of bat samples using RT-PCR. However, 35.7% of the samples were serologically positive. A primary limitation of our study is the low sample size; prior surveillance studies have found antibody-positive and PCR-positive prevalences for filoviruses as low as 1.7% and 1.9% respectively [11, 58]. Taken together, our findings provide evidence of more widespread geographic distribution of henipaviruses and filoviruses than previously appreciated.

Supplementary Data

Supplementary materials are available at The *Journal of Infectious Diseases* online. Consisting of data provided by the authors to benefit the reader, the posted materials are not copyedited and are the sole responsibility of the authors, so questions or comments should be addressed to the corresponding author.

Notes

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From: Roberto Bruzzone <
Sent: Wednesday, April 03, 2019 1:19 AM EDT
To:

Subject: Fwd: [Call for application] 15th HKU-Pasteur Virology Course: Coronaviruses

Dear All,

I would like to draw your attention on our upcoming Virology course and would be most grateful if you could also circulate this information through your contacts.

Best, Roberto

Date: Wed, 3 Apr 2019 03:36:10 +0800
From: HKU-Pasteur Research Pole of the School of Public Health

Subject: Call for applications 15th HKU-Pasteur Virology Course: Coronaviruses

Message from HKU-Pasteur Research Pole of the School of Public Health

[Call for application] 15th HKU-Pasteur Virology Course: Coronaviruses

Applications are open for the **15th HKU-Pasteur Virology Course** on **Coronaviruses** that will be held from July 7 to 13, 2019 in Hong Kong:

Date: July 7 - 13, 2019

Deadline for application: April 15, 2019

Application form / Tips for application

Most **endemic coronaviruses** (CoV) cause mild respiratory and intestinal infections in animals and humans. The identification of two novel and highly pathogenic coronaviruses as the cause of **SARS** and **MERS** outbreaks has illustrated the risks associated with zoonotic infections from this family of viruses. This course will review our current understanding and knowledge gaps, with special emphasis on the origin, evolution, transmissibility, molecular biology, epidemiological and clinical features of the highly pathogenic SARS-CoV and MERS-CoV. **Practical workshops** will challenge participants to design experimental strategies to mitigate the impact of CoV infections.

Course directors:
Roberto BRUZZONE (Hong Kong); Chris MOK (Hong Kong); Malik PEIRIS (Hong Kong); Noel TORDO (Guinea)

Faculty:
Marcel BOKELMANN (Germany); Roberto BRUZZONE (Hong Kong); Emmie DE WIT (USA); Bart HAAGMANS (Netherlands); Yae-Jean KIM (Korea); Raven KOK (Hong Kong); Mart LAMERS (Netherlands); Eve MIGUEL (France); Jean MILLET (France); Chris MOK (Hong Kong); Malik PEIRIS (Hong Kong); Peter ROTTIER (Netherlands); Zhengli SHI (China); Amy SIMS (USA); Noel TORDO (Guinea); Maria VAN KERKHOVE (Switzerland); Patrick WOO (Hong Kong); Nicholas WU (USA); Jincun ZHAO (USA)

Open to postgraduate students, MD, DVM, postdoctoral fellows and young scientists from Hong Kong and overseas.
Registration fees (HKD 1,500) include accommodation (on sharing twin basis for overseas participants) and food (lunch and coffee breaks). Please return the completed form, including 1-2 letters of recommendation, to hku-pasteur@hku.hk.

The course (MMPH6171) is included in the coursework curriculum for research postgraduate studies of the University of Hong Kong.

[]

Professor Roberto Bruzzone
Co-Director, HKU-Pasteur Research Pole
School of Public Health
The University of Hong Kong
7/F, JCBIR
5 Sassoon Road
Pokfulam, Hong Kong

website: www.hkupasteur.hku.hk
http://www.pasteur.fr/fr/recherche/les-centres-recherche-transversaux/center-global-health-research-and-education
http://isaric.tghn.org/

From: Jon Epstein ecohealthalliance.org>
Sent: Tuesday, September 29, 2020 1:08 PM EDT
To: Schountz,Tony Ebel,Greg >
Subject: Fwd: R24 Discussion

Guys,
This just came through from NIAID.

I suggest that we talk to her first, then we can talk once we have her input. Want to do it on the 7th?

Cheers,
Jon

---------- Forwarded message ---------
From: **Woodson, Sara (NIH/NIAID) [E]**
Date: Tue, Sep 29, 2020 at 12:05 PM
Subject: R24 Discussion
To: epstein ecohealthalliance.org>

Hi Jon,

It's been awhile since we've spoken but I hope you are doing well. Jean forwarded me your question about hypothesis-driven research in an R24. In general, I think we should probably schedule a brief call to discuss some of the specifics of R24s but also to hear about what you're thinking in terms of a hypothesis-driven approach (or aim). I've listed below some times that work for me/Jean/Mark, please let me know if any of those would work for your team as well.

October 5th: 9-9:30a (eastern)

October 7th: 3-3:30pm

October 14th: 10-11am, 1-2pm, or 2:30-3:30p

October 15th: 11a-noon or 3-4pm

In the interim though, here are some additional thoughts:

The R24 FOA indicates that this mechanism should be used to develop, maintain, provide a resource, but it doesn't explicitly state that hypothesis-driven research is not allowed. Our branch currently has one other funded R24 for the World Reference Collection of Emerging Viruses and Arboviruses (WRCEVA) at UTMB. This R24 does include hypothesis-driven research; they conduct small research projects that leverages having full access to the collection and to samples gathered through pursuit of adding new items to the collection. This research is usually a discreet, small project so as not to take up a lot of the budget and makes use of the resource to answer significant research questions that others haven't addressed yet and that may be difficult to work into other separate applications. I will have to search for other R24s across the institute that may have included animal model development as part of their aims, but none are coming to mind at the moment that would serve as a good example.

Sincerely, Sara

Sara E. Woodson, PhD

Program Officer

Virology Branch

Division of Microbiology and Infectious Diseases

National Institute of Allergy and Infectious Dieases, NIH

Getting ready to publish? Share the good news with your program officer asap! NIAID may be able to help publicize your article. And, remember to list your NIAID grant or contract number in the publication.

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

)

web: ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

From: calisher >
Sent: Monday, May 11, 2020 2:50 PM EDT
To: Tom Ksiazek Tom Monath ; Tom Yuill ; Murphy, Frederick A. ; Miller,Charles ; Schountz,Tony >; Dick Bowen ; Paul Cryan < ; Kathryn Holmes V. < ; Kevin Olival ecohealthalliance.org>; Wilusz,Jeffrey >; Suchman,Erica ; Kading,Rebekah ; Doug Watts ; Peter Drotman ; Bill Shachtman >; Sarah Haworth >; Dan Calisher ; Sean ; Evan >
Subject: Good idea

From: Peter Daszak ecohealthalliance.org>
Sent: Monday, February 10, 2020 12:20 AM EST
To: Peter Daszak ecohealthalliance.org>
CC: JMHUGHE ; rcolwell >; Saif, Linda ; William B. Karesh ecohealthalliance.org>; Hume Field ecohealthalliance.org>; Hongying Li ecohealthalliance.org>; Alison Andre ecohealthalliance.org>; Aleksei Chmura ecohealthalliance.org>
Subject: Invitation to act as a signatory on a Statement of Support for Scientists and Health Professionals of China Combatting 2019-nCoV
Attachment(s): "Statement of support 2019nCoV China Final 020920.docx","Signatory list for Statement of support 2019nCoV China 020920.docx"

Dear Fellow Scientists and Colleagues,

Like most of you, I've been following the events around the emergence of 2019-nCoV in China very closely and have been dismayed by the spreading of rumors, misinformation and conspiracy theories on its origins. Some of these are now specifically targeting scientists and health professionals with whom we've all collaborated for many years, and who have been working extremely hard to fight this outbreak and share data with unprecedented speed, openness and transparency. These conspiracy theories threaten to undermine the very global collaborations that we need to deal with a disease that has already spread across continents. They have been condemned by many of you, including today by the WHO DG, Dr. Tedros Adhanom Ghebreyesus.

Drs. Linda Saif, Jim Hughes, Rita Colwell, William Karesh and **Hume Field** have drafted a simple statement of support for scientists, public health and medical professionals of China fighting this outbreak (attached), and we invite you to join us as the first signatories (a full list of invited signatories is also attached). If you agree, we will add your name and affiliation, and make this letter public, with a sign-up webpage for others to show their support. I will also personally present this at my plenary lecture during the International Congress on Infectious Diseases (ICID) conference in Malaysia in just under two weeks, with the goal of sending our message directly to the region under most pressure from this outbreak. We will also circulate a copy of the letter in Mandarin so that our Chinese colleagues are directly communicated with.

I sincerely hope you can join us in this statement. If you agree to add your support, please reply-all to:

a) confirm your support (a simple 'yes' is fine);

b) confirm your full name and affiliation exactly as you would like these to appear on the statement

Thank you for your consideration and support of the scientific and public health community around the world!

Yours sincerely,

Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street – 17th Floor
New York, NY 10001

thalliance.org

EcoHealth Alliance leads cutting-edge scientific research into the critical connections between human and wildlife health and delicate ecosystems. With this science, we develop solutions that prevent pandemics and promote conservation.

Signatories

Dr. James M. Hughes, Professor, Emory University
Dr. Rita Colwell, Distinguished University Professor, University of Maryland College Park
Dr. Linda Saif, Distinguished University Professor, The Ohio State University
Dr. William B. Karesh, Co-Chair, IUCN Species Survival Commission Wildlife Health Specialist Group
Dr. Peter Daszak, President, EcoHealth Alliance
Dr. Hume Field, Honorary Professor, School of Veterinary Science, The University of Queensland

Invited Signatories

Dr. Rob Grenfell, Health Director, Commonwealth Scientific and Industrial Research Organisation (CSIRO)
Dr. W. Ian Lipkin, Professor, Columbia University
Dr. Christian Drosten, Charité - Universitätsmedizin Berlin, Germany
Dr. Juan Lubroth, Chief Veterinary Officer, Food and Agriculture Organization of the United Nations
Dr. Malik Peiris, Professor, The University of Hong Kong
Dr. Leo Poon, Professor, The University of Hong Kong
Dr. Keiji Fukuda, Dean, School of Public Health, The University of Hong Kong
Dr. Jeremy Farrar, Director, The Wellcome Trust
Dr. Richard Hatchett, Chief Executive Officer, Coalition for Epidemic Preparedness Innovations (CEPI)
Dr. Richard Webby, Director, World Health Organization Collaborating Centre for Studies on the Ecology of Influenza in Animals and Birds
Dr. Peter Palese, Professor & Head, Dept Microbiology, Icahn School of Medicine, Mt Sinai Hospital
Dr. John Mackenzie, Professor Emeritus, Curtin University
Dato' Prof. Lam Sai Kit, University of Malaya
Dr. Stanley Perlman, University of Iowa, Carver College of Medicine
Dr. Larry Madoff, Editor, ProMED-mail
Dr. John Brownstein, Harvard University Children's Hospital
Dr. Dennis Carroll, Scowcroft Center, Texas A&M
Dr. Charles Calisher, Colorado State University
Dr. Vincent Munster, NIH Rocky Mountain Laboratories
Dr. Supaporn Wacharapluesadee, Chulalongkorn University
Dr. Bart Haagmans, Erasmus Medical Center, The Netherlands
Dr. Luis Enjuanes, National Center of Biotechnology, Madrid, Spain
Dr. Eric Snijder, Leiden University Medical Center, The Netherlands
Dr. Alexander Gorbalenya, Leiden University Medical Center, The Netherlands
Dr. Mark Denison, Professor, Vanderbilt University
Dr. Yoshihiro Kawaoka, Professor, University of Wisconsin
Dr. Tony Schountz, Professor, Colorado State University
Dr. Jonna Mazet. Professor, University of California, Davis
Dr. Stephen Morse, Professor, Columbia University
Dr. Christopher Broder, Professor, Uniformed Services University of the Health Sciences
Dr. Marion Koopmans, Professor, Erasmus University Medical Ctr, Netherlands
Dr. Ab Osterhaus, Emeritus Professor, Erasmus University Rotterdam
Dr. Susan Lau, Hong Kong University
Dr. Wanda Markotter, Professor, University of Pretoria
Dr. Janusz Paweska, Director, Center for Emerging and Zoonotic Diseases at the National Institute for Communicable Diseases of the National Health Laboratory Service (NICD-NHLS), South Africa

Dr. Bernard Roizman, Joseph Regenstein Distinguished Service Professor Emeritus of Virology, University of Chicago
Dr. Benhur Lee, Icahn School of Medicine at Mt. Sinai

Statement in Support of the Scientists, Public Health, and Medical Professionals of China Combating the Novel Coronavirus Outbreak

We, the undersigned, are public health scientists who have closely followed the emergence of 2019-nCoV, and are deeply concerned about its impact on global health and well-being. We have watched as the scientists, public health and medical professionals of China, in particular, have worked diligently and effectively to rapidly identify the pathogen behind this outbreak, put in place significant measures to reduce its impact, and share their results transparently with the global health community. This effort has been remarkable.

We sign this statement in solidarity with all scientists and health professionals in China who continue to save lives and protect global health during the challenge of this novel coronavirus outbreak. We are all in this together, with our Chinese counterparts in the forefront, against this new viral threat.

The rapid, open and transparent sharing of data on 2019-nCoV is now being threatened by rumors and misinformation around the origins of this outbreak. We stand together to strongly condemn conspiracy theories suggesting that 2019-nCoV does not have a natural origin. Scientists from multiple countries have published and analyzed 2019-nCoV genomes[1], and they overwhelmingly conclude that this virus originated in wildlife[2-9], as have so many other emerging diseases[10,11]. This is further supported by a letter from the Presidents of the US National Academies of Science, Engineering, and Medicine[12], and by the scientific communities they represent. Conspiracy theories do nothing but create fear, rumors, and prejudice that jeopardize our global collaboration in the fight against this virus. We support the call from the Director-General of the World Health Organization to promote scientific evidence and unity over misinformation and conjecture[13]. We want you, the science and health professionals of China, to know that **we stand with you** in your fight against this virus.

We invite others to join us in supporting the scientists, public health, and medical professionals of Wuhan and across China. Stand with our colleagues on the front-line!

Signatories

Dr. James Hughes, Professor Emeritus, Emory University School of Medicine
Dr. Rita Colwell, Distinguished University Professor, University of Maryland College Park
Dr. Linda Saif, Distinguished University Professor, The Ohio State University
Dr. Billy Karesh, Executive Vice President, EcoHealth Alliance
Dr. Peter Daszak, President, EcoHealth Alliance
Dr. Hume Field, Honorary Professor, School of Veterinary Science, The University of Queensland

<<<Further signatories will be added once confirmed>>>

References

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7 Benvenuto, D. *et al.* The 2019-new coronavirus epidemic: Evidence for virus evolution. *J. Med. Virol.* **1-5**, doi:10.1002/jmv.25688 (2020).

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9 Centers for Disease Control and Prevention. *2019 Novel Coronavirus*, <https://www.cdc.gov/coronavirus/2019-nCoV/summary.html> (2020).

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12 NASEM: The National Academies of Science Engineering and Medicine of the USA. NAS, NAE, and NAM Presidents' letter to the White House Office of Science and Technology Policy (OSTP). (2020). <https://www.nationalacademies.org/includes/NASEM%20Response%20to%20OSTP%20re%20Coronavirus_February%206,%202020.pdf>.

13 The World Health Organization. Director-General's remarks at the media briefing on 2019 novel coronavirus on 8 February 2020. *https://www.who.int/dg/speeches/detail/director-general-s-remarks-at-the-media-briefing-on-2019-novel-coronavirus---8-february-2020* (2020).

From: 胡犇 <huben >
Sent: Monday, April 09, 2018 10:06 AM EDT
To: Schountz,Tony
CC: 石正丽 <zlshi ; 周鹏 <peng.zhou
Subject: Invitation to the 8th International Symposium on Emerging Viral Diseases
Attachment(s): "Invitation letter Tony Schountz.pdf"

Dear Dr.Schountz:

The 8th International Symposium on Emerging Viral Diseases will be held in October 20-22, 2018, in Wuhan, China. The biennial symposium is organized by Wuhan Institute of Virology, Chinese Academy of Sciences and has become an important event for leading Chinese and international virologists to discuss cutting-edge science on emerging viruses as well as to foster global collaborations.

Prof Zhengli Shi and Dr.Peng Zhou had a nice experience last year in Colorado when attending the symposium on bat-borne infectious diseases, and we know you have made great contributions to bat virus researches. We sincerely hope that you can attend the symposium. Please find enthe formal invitation letter for the meeting.

If you have any question regarding the conference, please contact me.

Thank you!

Best regards

Ben Hu Ph.D

Research Assistant

Secretary of the 8th International Symposium on Emerging Viral Diseases

Wuhan Institute of Virology, Chinese Academy of Sciences
Wuhan 430071, P.R. China

Tony Schountz, Ph.D
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine, Colorado State University
Fort Collins, CO 80523-1692

Dear Dr. Schountz:

The 8th International Symposium on Emerging Viral Diseases will be held in October 20-22, 2018 in Wuhan, China. The symposium is organized by Wuhan Institute of Virology, Chinese Academy of Sciences, and will cover a variety of topics including pathogen biology of emerging viruses, virus-host interaction, antiviral immunity, etc. This biennial symposium has become an important event for leading Chinese and international virologists to discuss cutting-edge science as well as to foster global collaborations.

It is our great pleasure to invite you to present your work at this symposium. Your accommodation in Wuhan will be covered by the conference. As an invited speaker, your registration fee will be waived. Please note that we are regretfully unable to cover your travel expenses due to budget constrain.

Please submit the abstract of your presentation to the meeting secretary Dr. Ben Hu (huben@wh.iov.cn) by July 31st 2018. We look forward to seeing you in Wuhan.

Sincerely Yours,

Xi Zhou, Ph.D
Senior Scientist & Professor
Wuhan Institute of Virology, CAS
E-mail: zhouxi@wh.iov.cn
Tel: 86-27-87197727

Peng Zhou, Ph.D
Senior Scientist & Professor
Wuhan Institute of Virology, CAS
E-mail: peng.zhou@wh.iov.cn
Tel: 86-27-87197311

From: Kading,Rebekah >
Sent: Monday, June 22, 2020 6:14 PM EDT
To: Joy O'Keefe >; Diana Hews >; Fagre,Anna >; Kevin Castle >; Paul Cryan ; Bowen,Richard Schountz,Tony >; olival ecohealthalliance.org>; epstein ecohealthalliance.org>; Jonathan Towner >; Brian Amman >; raina.plowright ; <martha.m.stokes. >; Robert Kityo ; abelwade >; Tony Goldberg < >; Christine Kreuder Johnson ; dreeder ; Brian H Bird >; Piaggio, Antoinette J - APHIS ; Gilbert, Amy T - APHIS ; David Hayman < >; Grant, Evan H ; Stoner,Kathryn < >; Baric, Ralph S < Bowen,Richard ; Bosco-Lauth,Angela ; Robert Aruho >; Patrick Atimnedi >; Luke Nyakarahuka ; Julian Kerbis >; Margaret Driciru ; Clif McKee spwa ; Charles Calisher ; kosoy >; Franklin, Alan B - APHIS Root, Jeff - APHIS ; Bevins, Sarah N - APHIS >; ksidamonidze ; lelincdc ; c demetria ; wanda.markotter >; Julius Lutwama ; VandeWoude,Susan >; Webb,Colleen >; nisreen.hmoud ; Schuh, Amy (CDC/OID/NCEZID) ; Sealy, Tara K. (CDC/DDID/NCEZID/DHCPP) >
CC: Kingston, Tigga >
Subject: IUCN guidelines
Attachment(s): "IUCN infographic FINAL 062220.pdf"

Dear colleagues,

Hot off the press! The IUCN Species Survival Commission Bat Specialist Group has released guidelines for researchers, to prevent the human-to-bat transmission of SARS-CoV-2. Our infographic is attached, and full guidelines available through either link below. Additional products are to follow shortly, tailored for other stakeholder groups. Please feel free to distribute as you see fit.

Best regards,
Rebekah

https://www.iucnbsg.org/publications.html
https://tinyurl.com/mapforbats

Rebekah C. Kading, PhD
Assistant Professor
Department of Microbiology Immunology and Pathology
Colorado State University

Preventing human-to-bat transmission of SARS-CoV-2

Exposure Risks

Contact exposure
Bats coming into contact with contaminated hands or equipment

Aerosol exposure
Infectious droplets from handlers holding bats in close proximity

Environmental exposure
Sharing enclosed, poorly-ventilated spaces with bats, where virus may persist in the air or on surfaces

MAP your plan to prevent transmission to bats!

Mitigation Strategies

Minimize

Delay, prioritize, or avoid handling bats when possible, i.e. implement acoustic surveys

Assess

Postpone handling bats if there is a probability that you have been exposed to SARS-CoV-2 or if you have symptoms

Protect

Adopt practices that reduce exposure, i.e. face covering, gloves, disinfection procedures

IUCN SSC Bat Specialist Group

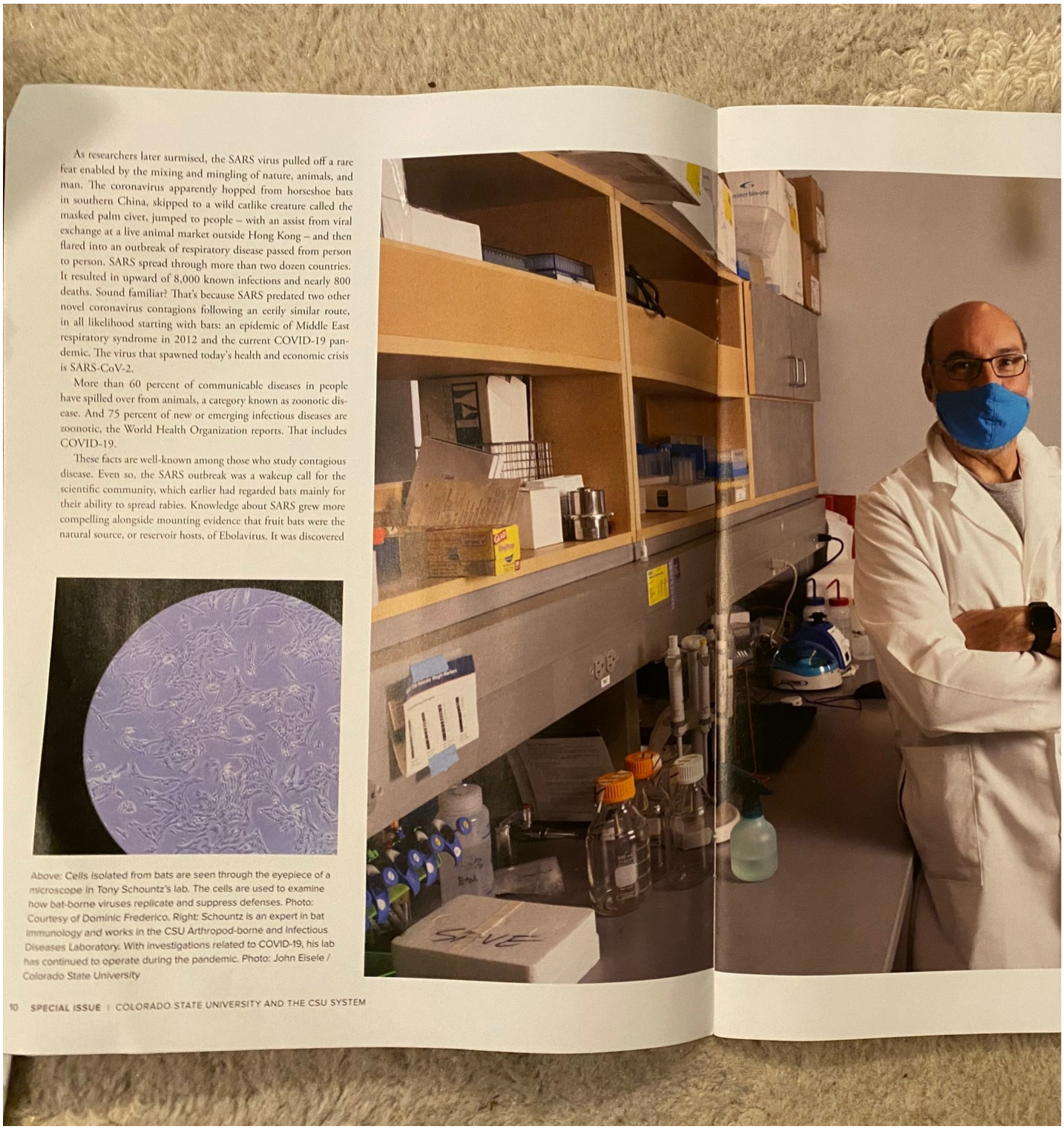
www.iucnbsg.org

Full recommendations @ https://tinyurl.com/mapforbats

From: Kevin Olival ecohealthalliance.org>
Sent: Thursday, July 09, 2020 8:25 AM EDT
To: Schountz,Tony >
CC: epstein ecohealthalliance.org>
Subject: Just opening my CSU alumni mail

Nice one!

Kevin



As researchers later surmised, the SARS virus pulled off a rare feat enabled by the mixing and mingling of nature, animals, and man. The coronavirus apparently hopped from horseshoe bats in southern China, skipped to a wild catlike creature called the masked palm civet, jumped to people – with an assist from viral exchange at a live animal market outside Hong Kong – and then flared into an outbreak of respiratory disease passed from person to person. SARS spread through more than two dozen countries. It resulted in upward of 8,000 known infections and nearly 800 deaths. Sound familiar? That's because SARS predated two other novel coronavirus contagions following an eerily similar route, in all likelihood starting with bats: an epidemic of Middle East respiratory syndrome in 2012 and the current COVID-19 pandemic. The virus that spawned today's health and economic crisis is SARS-CoV-2.

More than 60 percent of communicable diseases in people have spilled over from animals, a category known as zoonotic disease. And 75 percent of new or emerging infectious diseases are zoonotic, the World Health Organization reports. That includes COVID-19.

These facts are well-known among those who study contagious disease. Even so, the SARS outbreak was a wakeup call for the scientific community, which earlier had regarded bats mainly for their ability to spread rabies. Knowledge about SARS grew more compelling alongside mounting evidence that fruit bats were the natural source, or reservoir hosts, of Ebolavirus. It was discovered

Above: Cells isolated from bats are seen through the eyepiece of a microscope in Tony Schountz's lab. The cells are used to examine how bat-borne viruses replicate and suppress defenses. Photo: Courtesy of Dominic Frederico. Right: Schountz is an expert in bat immunology and works in the CSU Arthropod-borne and Infectious Diseases Laboratory. With investigations related to COVID-19, his lab has continued to operate during the pandemic. Photo: John Eisele / Colorado State University

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

From: Kendall,Lon >
Sent: Monday, March 30, 2020 11:31 AM EDT
To: Bowen,Richard >; Bosco-Lauth,Angela >; Schountz,Tony >; epstein ecohealthalliance.org>; Ebel,Greg >; Dean,Gregg ; Szalai,Edit
Subject: Meeting agenda

All,

Here is a proposed agenda for tomorrows meeting. Please edit freely.

Introduction
Lon- why meeting was initially organized, then turf to Jon (I won't be long)
Jon- provide background about program discussions with CSU and NIAID and why we are here (Jon really sparked this discussion, and is probably best to lead)
Jean- Discuss NIAID possibilities and expectations and what's needed from CSU (Thought Jean should go sooner to help frame discussion below. I will send her agenda once we get it finalized)
Ebel- Discuss CVID abilities, and possibilities related to emerging disease, prior C06
Tony- Discuss current research and potential needs
Bowen/Angela- Discuss current research and potential needs
Determine next steps

Lon

Lon V. Kendall, DVM, PhD, DACLAM
Director, Laboratory Animal Resources and
Attending Veterinarian, Colorado State University

From: Jon Epstein ecohealthalliance.org>
Sent: Tuesday, March 27, 2018 12:44 PM EDT
To: Cristina Cassetti Park, Eun-Chung (NIH/NIAID) [E] >; Patricia (NIH/NIAID) Repik [E]
CC: Schountz,Tony >; Linfa Wang
Subject: Nature Lab Animal story on Bat research
Attachment(s): "Bat Research Takes Wing_Lab Animal_Nature 2018.pdf"

Dear Cristina, Eun-Chung and Pat,
Attached is a news piece from Nature: Lab Animal, out yesterday, about the current state of bat research and the need for new lab animal models and reagents. It features a few folks you all may know ;)

Hope you're doing well.

Cheers,
Jon

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

web: ecohealthalliance.org

-

Bat research takes wing

In the field and in the lab, scientists across the globe are working to better understand the biology of the bat

Michael Eisenstein

Bats have a PR problem. In the Western world, at least, they are commonly associated with darkness and filth—and in popular culture, the supernatural forces of evil. But the researchers who actually work with these animals take a different view. "Bats are just such beautiful animals," says Michelle Baker, who studies comparative immunology at the CSIRO Australian Animal Health Laboratory. "They're so gentle."

Unfortunately, their reputation has taken another hit in recent years, with the steady emergence of zoonotic viruses that exploit bats as a Trojan Horse to mount their attack on humanity. These include high-profile threats like Ebola and severe acute respiratory syndrome (SARS) as well as less well-known—but still deadly—viruses like Nipah. "That's a bat virus that is routinely, reliably and predictably spilling over from bats into people," says Jon Epstein, a veterinarian and epidemiologist at the EcoHealth Alliance. "In Bangladesh, it kills about three-quarters of the people that it infects."

The steady emergence of bat-borne viruses has fueled active debate about whether these animals are 'special' in terms of their ability to act as disease hosts. Bats are indeed distinctive in many ways. In addition to being the only mammals capable of powered flight, they are astonishingly diverse and widespread. With over 1,200 species worldwide, bats represent roughly 20% of all mammalian species, with representatives virtually everywhere humans dwell. Bats are also an indisputably rich reservoir for pathogens[1]. "Even if you compensate for research bias in the literature, bats have a disproportionately high number of zoonotic pathogens associated with them compared with other mammals," says Epstein.

Image: Stijn Dijkstra / EyeEm / Getty

Are bats 'special' in their ability to carry disease? Not necessarily, says Tony Schountz. He prefers the word 'different.'

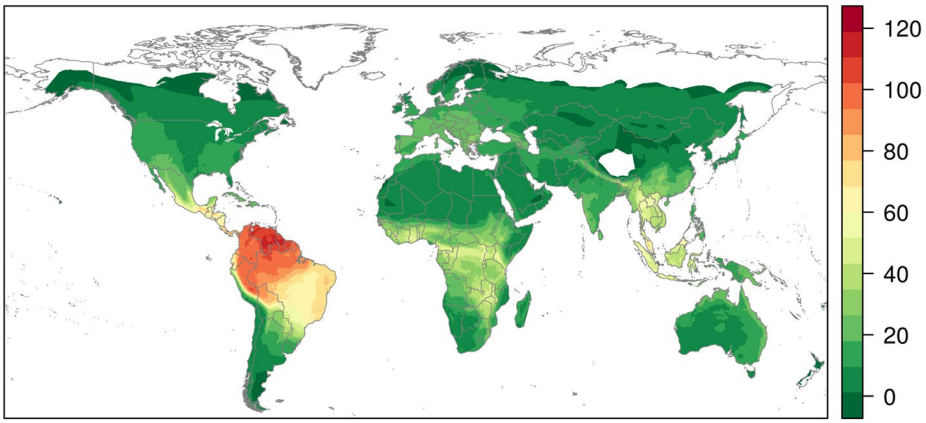
Image: Jackie Strong

However, it remains controversial whether this viral richness arises from unique features of bat immunology and physiology, or merely from bats' capacity to acquire exotic viruses from far and wide and deliver them to human communities. "The word 'special' implies that there's something that makes them better at this, and I don't think that's the case—I prefer the word 'different,'" says Tony Schountz, a microbiologist at Colorado State University. Special or not, researchers are struggling to fill in the blanks about bat biology, and hunting for insights that might clarify why and how bat-borne infections make the leap into humans, and to such deadly effect.

Disease detectives

Historically, bats have mainly been associated with rabies, although they are only seldom responsible for human infection in North America. Bats came back on the radar in the 1990s, with the discovery of the Hendra virus in Australia. "A new virus was isolated from dead horses, and a horse trainer died from the same virus during an outbreak in 1994," says Linfa Wang, director of the Emerging Infectious Diseases Programme at Duke-NUS Medical School. "It took us about a year and a half before we realized that the natural reservoir was bats." In the decade that followed, researchers tied numerous other viral threats to bats, including Nipah, SARS, and Ebola.

It can be difficult to identify the 'spillover' events where these viruses spread to humans. Each outbreak requires careful detective work to identify opportunities for bat-human interaction and obtain molecular confirmation of a shared viral strain between the two species. Most viruses are spread not by bites but through other consequences of close contact that must be pieced together through observation and field work. In Bangladesh, for example, Nipah exposure occurs through the date palm sap that villagers harvest. "Bats visit the pots overnight and lick the sap as it flows down the tree, and sometimes urinate or defecate into the pot," says Epstein, "and a person drinking that sap a few hours later might get infected." In other cases, the route of spillover remains unclear. Baker's



Where to find them: A global map of bat species richness[1]. Copyright 2017 EcoHealth Alliance

lab has studied a wild colony of Australian flying foxes (*Pteropus alecto*) for years, but has yet to learn what causes these bats to 'shed' Hendra virus as a prelude to transmitting infection.

Initial sample collection is often done in a low-tech fashion. "In our studies of paramyxoviruses in sub-Saharan Africa, some of the most important tools we used were plastic sheets," says James Wood, a veterinary epidemiologist at the University of Cambridge. By spreading these under bat roosts, his team could harvest urine and guano for viral profiling. However, evidence of pathogens can often only be detected in blood and saliva—and some bat species live in inaccessible locales or in small numbers rather than large colonies, making it tricky to obtain such samples. Amy Gilbert, a disease ecologist with the US Department of Agriculture, recalls the difficulties she encountered studying Lagos bat virus in African straw-colored fruit bats (*Eidolon helvum*). "They're tree-roosting and migrate really long distances, and the second you get close to the trees they all take off," she says.

Long-term monitoring can reveal patterns of infection and viral transmission over time, but becomes extremely complex for colonies numbering thousands or millions. Epstein's team used RFID tags to 'chip' batches of 100 bats from a large population of Indian flying foxes (*P. giganteus*) in Bangladesh, and only managed 60 recaptures during a six-year-long study[2]. "But that provided tremendous information," he says. "We saw bats that were initially negative for Nipah virus antibodies and were positive at recapture, so we knew they got infected at some point in between."

Safety is also a pressing concern. Most emerging viruses would normally be studied in a tightly-controlled biosafety level (BSL) 4 laboratory, and Epstein notes that field researchers are generally kitted out with full-body protective gear and a respirator, even in the stifling heat of the jungle. Baker likewise notes that personal safety must always be at the front of researchers' minds. "You've just got to be very careful and handle everything as if it's infectious," she says. "'Never get bitten by a bat' is the unspoken rule." Bringing bats 'in-house' to laboratory-based colonies can offer a safer and more controlled research environment than working in the wild, although such efforts are also fraught with challenges (Box 1).

The best defense

Wang recalls stepping into a void when he first began his bat research. "In 1996, if you keyed the words 'bats' and 'immunity' into PubMed, you'd be lucky to get maybe a dozen papers," he says. Fortunately, the ensuing two decades of research have yielded valuable insights.

With some exceptions—most notably, rabies—it seems that the viruses that sicken humans generally do not harm bats. "In all of the experimental viral infections that we've done, our flying foxes just don't

Box 1 | A captive audience

In contrast to the countless rodent vivariums around the world, there are only a handful of such facilities for bats, including colonies at the US Centers for Disease Control and Prevention and the Colorado State University. "We have Jamaican fruit bats in our colony, and so far we've tested six different viruses in our bats," says Schountz, who helped establish the Colorado facility.

Such colonies make long-term studies of viral infection and transmission safer and simpler than working in the field, and eliminate the risk of other infections that could confound the study of a particular pathogen. However, they are also costly and complicated to establish. "In many places, bats are protected and getting permission to catch them is not easy," says Wang, who manages a colony of cave nectar bats (*Eonycteris spelaea*) in Singapore. "Then a young bat takes three years to become sexually mature, and the most active females only have one pregnancy per year with one or two babies per pregnancy." Schountz has had less of a struggle with his colony; Jamaican fruit bats breed every four and a half months, although they still typically only produce one offspring per pregnancy.

Most colonies host fruit-eating bats, which are easy to please from a dietary perspective. Insectivorous bats make far more demanding guests; habituated to hunting flying prey, these bats are reluctant to feed from a dish, and researchers must hand-feed these animals or even put on 'puppet shows'. "We had our BSL4 technicians in full-body spacesuits using forceps with these little worms at the tip, waving them in front of the bats to mimic flying," says Wang.

Far-roaming species may have a hard time coping with captivity, requiring difficult compromises. Wood and his collaborators in Ghana have established a relatively massive *Eidolon helvum* colony. "It's large enough to allow them to fly, and enriched enough that they can roost in relatively normal ways," he says. This requires considerable infrastructure, however, and may not be feasible at many sites. Intermediate-sized pens can be the worst of both worlds. "Some bats will have the wrong perception and think they can fly, and then they'll bump into the cage and get injured," says Wang. His team uses smaller cages to avoid this problem, but this means that the bats are less active than their wild brethren, confounding research into their metabolism and physiology.

Accordingly, every new colony poses a unique challenge, where experience from one species may offer limited insights for another. "We've learned some things from zoos and wildlife parks that do this for a profession," says Wood. "It's something we've put a lot of background work into, and not something I'd undertake lightly."

Bat wrangling: Jon Epstein, pictured in heavy gloves and respirator despite the tropical climate, handles a collared bat in Bangladesh. Image: EcoHealth Alliance 2018

get sick—they don't get a fever, there's just no response at all," says Baker. Epstein has also observed strong indications that many viruses are swiftly defeated by the bat immune system. "They tend to be acute, short-term infections," he says. "For example, we only find about 1–3% of bats in a colony infected with Nipah virus at any given time."

Investigations of bat immunity have uncovered several possible explanations for this apparent tolerance. Baker has found that her bats maintain relatively high levels of interferons, signaling molecules that rouse the initial immune defense against infection and are normally only generated after host immune cells detect a virus. "We think this is giving them a bit of a head start," says Baker. "Then, when they're infected, they can clear the virus much more rapidly." Her bats also seem to mount a different kind of interferon response from humans and rodents, lacking a strong inflammatory component that could otherwise inflict serious tissue damage. Schountz hypothesizes that some viruses survive in bats by churning out interferon-blocking proteins, which could in turn accelerate the evolution of deadlier viruses that can essentially overwhelm the human immune system before it can react. "Human cells may have little chance to combat the virus, which then gets free rein," says Schountz. "That leads to virus replication, and subsequent pathology and cell death."

Wang believes bats may have evolved improved resistance to disease as a consequence of adaptation to the metabolic demands of flight. "During flight, bats' body temperature can go to 38–42 °C, depending on the species, and their heart rate can go up to 1,000 beats per minute," says Wang, who notes that such sustained activity would inflict punishing stress on most organisms, rendering them more vulnerable to disease. "Bats need to have a much more efficient and more finely-tuned defense system," he says.

Starting from scratch

Nevertheless, progress remains slow in untangling the workings of bat immunology due to the limitations of the laboratory toolbox. On one hand, the falling costs and soaring speed and accuracy of DNA sequencing technologies have yielded a steadily growing collection of genome sequences for different bat species. Emma Teeling at University College Dublin is spearheading the ambitious 'Bat 1K Project', which aims to collect genomic data from every bat species on Earth.

However, bat researchers lack many standard reagents that rodent labs take for granted. Cell lines are a powerful resource for gleaning biological insights without the complexity of live animal models, but only a handful are available from bats, and none of these represent the immune cells that respond to viral infection. This has left researchers scrambling for alternatives, such as harvesting and cultivating fresh immune cells from animals for each experiment.

Many experiments rely on antibodies that bind specific proteins, which can be used for applications ranging from imaging to the selective isolation of different cell types. With few bat antibodies commercially available, labs must derive their own. This is time- and labor-intensive, and the result may not be useful across species. "If you were to suggest a researcher should use an antibody developed for a cow in a horse, they'd laugh at you," says Wood. "That's the situation here—these species are very different, and just because we call them all bats doesn't make them close genetically or immunologically."

This highlights another critical challenge. Wang notes that bats diverged evolutionarily from land mammals roughly 100 million years ago, with a second split 30–35 million years later that produced two radically different sub-orders. "The differences between the two can be as big as betweenmice and humans," he says. Most research is focused on known reservoirs of disease, but Baker hopes that heightened interest in bats and the influx of data from projects like Bat 1K will help the community converge on broadly representative 'common denominators'. "We need to get a few model species so we can start sharing reagents and be more productive in what we're doing," says Baker.

Collision course

The extent to which bats are 'unique' as viral reservoirs remains open for debate, but it is indisputable that research into these animals is extremely important from a public health perspective in terms of both known and emerging diseases. "We are discovering loads of new viral sequences, but we don't know about their potential to infect people," says Epstein. And unfortunately, human activity continues to create opportunities for spillover, with ongoing urbanization and agricultural expansion steadily pushing bats and people into closer proximity. Climate change could also increase the risk. For example,

Is a bat a bat? The Jamaican fruit bat (left), cave nectar bat (center), and Indian flying fox (right) are just three of over 1200 different species that can be as varied genetically as mice are to men. Images: Tony Schountz / Linfa Wang / EcoHealth Alliance 2018

Infectious diseases aren't the only reason to study bats. "Modern medicine can learn a lot from bats," says Linfa Wang, in areas like aging and cancer.

Image: Linfa Wang Lab, DukeNUS Medical School

Schountz is monitoring Jamaican fruit bats (*Artibeus jamaicensis*) infected with Tacaribe virus—a pathogen that can sicken and kill these animals. Tacaribe is closely related to numerous dangerous viruses, and although it does not currently infect humans, it could acquire that potential. "The Florida Keys is as far north as they get right now, but climate change seems to be driving this bat species further north," he says. "I get nervous about that."

But some experts also hope the field will move beyond focusing on bats as couriers of disease to explore other unusual characteristics of these animals. For example, Wang notes their exceptional lifespan relative to what scientists would predict based on their body mass and metabolic rate. "A seven-gram bat can live for up to 43 years—that would be roughly equivalent to a human living 1,000 years," he says. He also notes that bats seem to be less prone to cancer, a possible fringe benefit of their finely-tuned 'innate defense system.' "Modern medicine can learn a lot from bats," says Wang.

More generally, Epstein hopes that fears of disease will not cause the public to lose sight of the positive contributions and ecological significance of bats—or the responsibilities humans have towards them. "They're such important animals in terms of pest control and for pollination and seed dispersal," he says. "People are disrupting their environment, and that's causing wildlife pathogens to jump and spill over… it's squarely in our hands to think about that and adjust the way we do things." ❐

Michael Eisenstein

Michael Eisenstein is a freelance science writer in Philadelphia, Philadelphia, USA.
e-mail: michael@eisensteinium.com

Published online: 26 March 2018
https://doi.org/10.1038/s41684-018-0029-4

References

1. Olival, K. J. et al. *Nature* **546**, 646–650 (2017).
2. Epstein, J. H. et al. *PLoS Pathog.* **6**, e1000972 (2010).

From: Jon Epstein ecohealthalliance.org>
Sent: Monday, March 16, 2020 11:26 AM EDT
To: Rudolph,Alan < >
CC: Schountz,Tony >; Ebel,Greg ; Kendall,Lon ; Richard Bowen Foster,Linda
Subject: Re: NIH R24 + C06

Thanks all,
I look forward to the discussion.
Cheers,
Jon

On Mon, Mar 16, 2020 at 11:23 AM Rudolph,Alan > wrote:

> Tony
>
> Copying Linda Foster to help arrange.
>
> Thanks Alan
>
> Sent from my iPad
>
> > On Mar 16, 2020, at 9:22 AM, Schountz,Tony wrote:
> >
> > ï»¿All, just adding Lon Kendall to the email string. He has assured me there is space for the horseshoe bats and probably for the pteropid bats, but he would like to be on the conference call for this discussion.
> >
> > Alan, can you help arrange the call through your office?
> >
> > Thanks,
> >
> > Tony
> > —
> > Tony Schountz, PhD
> > Associate Professor
> > Arthropod-borne and Infectious Disease Laboratory
> > Department of Microbiology, Immunology and Pathology
> > College of Veterinary Medicine
> > Colorado State University
> >
>
> >
> >> On Mar 13, 2020, at 4:58 PM, Schountz,Tony < wrote:
> >>
> >> Alan and Greg, as you know I chatted with Jon Epstein yesterday. He has had discussions with NIH about interest in having a grant submission regarding bats and SARS-CoV-2 and other coronaviruses. I think the four of us ought to have a conference call next week to see if we can make something work.
> >>
> >> Alan, we would need to have access to a room or building large enough to house large flying foxes as well as smaller horseshoe bats. I know the barn at ARBL was once available but I suspect it no longer is?
> >>
> >> Thanks,
> >>
> >> T.
> >> —
> >> Tony Schountz, PhD
> >> Associate Professor
> >> Arthropod-borne and Infectious Disease Laboratory
> >> Department of Microbiology, Immunology and Pathology
> >> College of Veterinary Medicine
> >> Colorado State University
> >>
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Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street, Ste. 1701

New York, NY 10001

)

web: ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

From: calisher <
Sent: Thursday, September 10, 2020 5:18 PM EDT
To: Tom Ksiazek >; Tesh, Robert B. >; Murphy, Frederick A. ; Wilusz,Jeffrey ; David Quammen David Morens >; Beaty,Barry ; Schountz,Tony ; Peter Daszak ecohealthalliance.org>; Raymond tennant ; Nichol Stuart ; Shelley <
Subject: PAPER BY DR. CHAN TOUTED IN BOSTON MAGAZINE

(forwarded to me by a friend)

https://www.biorxiv.org/content/10.1101/2020.05.01.073262v1

Just one sentence acknowledging (barely) the possibility of lab release:

"Even the possibility that a non-genetically-engineered precursor could have adapted to humans while being studied in a laboratory should be considered, regardless of how likely or unlikely"

==========

https://www.bostonmagazine.com/news/2020/09/09/alina-chan-broad-institute-coronavirus/

From: Jon Epstein ecohealthalliance.org>
Sent: Wednesday, June 03, 2020 10:57 AM EDT
To: bpope
CC: Ebel,Greg Schountz,Tony
Subject: Pteropus space requirements

Hi Brian,
I wanted to introduce you to Professor Greg Ebel, who's the Director of the Arthropod-Borne and Infectious Disease Lab at Colorado State and who's recently become a partner in our efforts, with Tony Shountz, to establish a Pteropus breeding colony there. We're trying to get an accurate understanding of the physical space required for the proposed colony, which if you recall we had discussed starting with 40 bats (4 male, 36 female) which would then become about 60-70 bats post breeding.

Could you help give us a sense of what physical space you think would be necessary in terms of a holding / flight cage, plus support rooms like food storage and a handling / exam area? We've got an existing building on campus that's abou 2500 sq ft that could be gutted & equipped as needed, but the concern is that it's just not big enough for the planned number of bats.

Thanks for your help in thinking through this.

Cheers,
Jon

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

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460 West 34th Street, Ste. 1701

New York, NY 10001

web: ecohealthalliance.org

From: Ebel,Greg
Sent: Wednesday, October 07, 2020 5:49 PM EDT
To: Schountz,Tony ; epstein ecohealthalliance.org>
Subject: R24

Hey,

Do you all want me to reach out to Scott W about the WRCEVA R24?

He might say no, but I'm fully OK with asking.

Greg

Gregory D. Ebel
Professor, Department of Microbiology, Immunology and Pathology
Director, Arthropod-Borne and Infectious Diseases Laboratory
College of Veterinary Medicine and Biomedical Sciences
Colorado State University

From: zlshi >
Sent: Tuesday, February 25, 2020 12:38 AM EST
To: Schountz,Tony
Subject: Re: 3rd International Symposium on Infectious Diseases of Bats, 17-19 June 2020, Fort Collins, Colorado, USA

Dear Tony,

I'm sorry to let you know that I'll not be able to particiapte in the ASV meeting and the bat meeting due to the safety issue. I need to calm down myself and get recovered from the rumors of the public.

Best regards,
Zhengli,

SHI Zhengli, Ph. D
Senior Scientist & Professor
Wuhan Institute of Virology, Chinese Academy of Sciences

From: Schountz,Tony
Date: 2020-02-20 07:09
To: Schountz,Tony
Subject: 3rd International Symposium on Infectious Diseases of Bats, 17-19 June 2020, Fort Collins, Colorado, USA

Dear Colleagues,

Registration is now open for the 3rd International Symposium on Infectious Diseases of Bats. With the emergence of yet another pathogenic coronavirus, we are planning to have an extended session to learn from one another about this new virus and I hope some of you can foster collaborative interactions while you are here. The URL for the meeting is:

http://www.batid.org

Please note a few important dates. **Abstract submission closes on April 17, 2020**. The format of the abstract is indicated on the web site and we ask that you follow it for purposes of continuity in the program. In addition, please send MS Word, Apple Pages or Rich Text files so that we can rapidly build the program. Please DO NOT send a PDF because they are much more difficult to integrate into the program. After you submit your abstract, you should receive a confirmation email. If you do not, please let me know and I'll resolve the issue.

Registration will close on May 1, 2020. Registration will be handled by the Colorado State University Conference Services with a direct link on the Bat ID web site. You can select registration only, or registration with dormitory housing on campus near the conference venue (Lory Student Center). Registration included breakfast for the two days, and the dormitory includes breakfast, too. If you prefer to stay in a hotel, the Fort Collins Hilton (on Prospect Avenue) and the Best Western University Inn are walking distance to campus. Links to these hotels are provided on the Registration page.

We also have the pleasure of hosting**This Week in Virology**. Vincent and crew will record an episode from the meeting.

Please let me know if you have questions or comments.

Thanks very much, and we are looking forward to seeing you again in Fort Collins.

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Nov 14, 2019, at 10:52 AM, Schountz,Tony > wrote:

Dear colleagues,

I am pleased to announce the **3rd International Symposium on Infectious Diseases of Bats** that will be held at Colorado State University in Fort Collins, Colorado, 17 June to 19 June, 2020. The previous meetings were quite successful and led to several new collaborations amongst participants. We hope we can continue to foster interactions and additional collaborations between groups. Please forward this email to colleagues and students that may be interested in the symposium.

We are currently finalizing details of the symposium but I wanted to send this email so that you can add the dates to your calendar if you are interested in attending. The American Society for Virology Annual Conference will also be hosted at CSU in 2020 and it ends on Wednesday, June 17 at noon. Thus, the Bat ID Symposium will follow with a reception on the evening of June 17th and two days of talks and posters on the 18th and 19th. As with previous meetings, we will end each day with an open discussion about bats and their infectious agents.

Should you have questions, please do not hesitate to contact me.

We look forward to hosting you next summer.

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Kevin Olival ecohealthalliance.org>
Sent: Thursday, November 14, 2019 1:17 PM EST
To: Schountz,Tony
Subject: Re: 3rd International Symposium on Infectious Diseases of Bats, 17-19 June 2020, Fort Collins, Colorado, USA

Tony, just an FYI, this overlaps (at the tail end) with the World One Health Congress https://onehealthplatform.com/wohc/home. May not be a big deal for most, but I think some of us were going to do the other meeting also. I haven't figured out my travel yet, but nonetheless I'll plan to come to CO so long as I can and really looking forward to this!

Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

www.ecohealthalliance.org

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

> On Nov 14, 2019, at 12:52 PM, Schountz,Tony wrote:
>
> Dear colleagues,
>
> I am pleased to announce the **3rd International Symposium on Infectious Diseases of Bats** that will be held at Colorado State University in Fort Collins, Colorado, 17 June to 19 June, 2020. The previous meetings were quite successful and led to several new collaborations amongst participants. We hope we can continue to foster interactions and additional collaborations between groups. Please forward this email to colleagues and students that may be interested in the symposium.
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>
> Should you have questions, please do not hesitate to contact me.
>
> We look forward to hosting you next summer.
>
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

From: 石正丽 <zlsh
Sent: Thursday, November 14, 2019 8:16 PM EST
To: Schountz,Tony >
Subject: Re: 3rd International Symposium on Infectious Diseases of Bats, 17-19 June 2020, Fort Collins, Colorado, USA

Thanks.

-----原始邮件-----
发件人:"Schountz,Tony"
发送时间:2019-11-15 01:52:06 (星期五)
收件人: "Schountz,Tony" <
抄送:
主题: 3rd International Symposium on Infectious Diseases of Bats, 17-19 June 2020, Fort Collins, Colorado, USA

Dear colleagues,

I am pleased to announce the **3rd International Symposium on Infectious Diseases of Bats** that will be held at Colorado State University in Fort Collins, Colorado, 17 June to 19 June, 2020. The previous meetings were quite successful and led to several new collaborations amongst participants. We hope we can continue to foster interactions and additional collaborations between groups. Please forward this email to colleagues and students that may be interested in the symposium.

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—
Tony Schountz, PhD
Associate Professor
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Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Jon Epstein ecohealthalliance.org>
Sent: Friday, June 23, 2017 11:59 AM EDT
To: Schountz,Tony
CC: Kevin Olival, PhD ecohealthalliance.org>
Subject: Re: Abstracts

Tony,
Is there still time? I'm working on it today.
-Jon

On Wed, Jun 21, 2017 at 10:59 AM, Schountz,Tony > wrote:

> Yup tomorrow's fine. Program gets printed on Friday.
>
> Thanks
>
> Tony
>
> Sent from my iPhone
>
> On Jun 21, 2017, at 7:26 AM, Kevin Olival, PhD ecohealthalliance.org> wrote:
>
>> Pretty sure I never wrote one! Just title. Can get it to you tomorrow if that's ok!
>>
>> On Jun 21, 2017, at 10:24 AM, Schountz,Tony wrote:
>>
>>> Hi Jon and Kevin,
>>>
>>> I don't seem to have abstracts for your bat ID talks. Could you (re)send them directly to me today or tomorrow?
>>>
>>> Thanks
>>>
>>> Tony
>>>
>>> —
>>> Tony Schountz, PhD
>>> Associate Professor
>>> Arthropod-borne and Infectious Disease Laboratory
>>> Department of Microbiology, Immunology and Pathology
>>> College of Veterinary Medicine
>>> Colorado State University

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

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New York, NY 10001

web: ecohealthalliance.org

From: Kevin Olival, PhD ecohealthalliance.org>
Sent: Friday, June 23, 2017 1:26 PM EDT
To: Schountz,Tony
Subject: Re: Abstracts
Attachment(s): "Olival_BatID2017_abstract.docx","ATT00001.htm"

Tony,

Abstract attached! Sorry for the delay.

Estimating viral richness and viral sharing in bats: integrating previously-published and newly-acquired field data

Kevin J. Olival[1], Noam Ross[1], Evan A. Eskew[1], Anna R. Willoughby[1], Carlos Zambrana-Torrelio[1], Peter Daszak[1], and PREDICT Consortium[2]

[1] EcoHealth Alliance, New York, NY 10001, USA
[2] http://www.vetmed.ucdavis.edu/ohi/predict/publications/Authorship.cfm

Objectives: A handful of studies published over the last 8 years have sought to identify the host, ecological, and evolutionary factors that best explain species-level differences in viral richness in bats. Similarly, a few studies have also aimed to answer the golden question: Do bats carry a significantly larger number of total viruses, or a larger number or proportion of zoonotic viruses than other mammals? Our objective is to address these critical questions using statistical models and large datasets collated from the literature and acquired from the field. **Methods:** We collated data from the past 75 years of published for over 2800 mammal-virus associations, representing 754 mammal species and 586 ICTV-named viral species. We fit a series of generalized additive models to these data to identify and examine the functional form of significant predictor variables for total and zoonotic viral richness. Using our best-fit models we also estimate expected viral richness for each host species under a scenario of 'maximum' research effort. We map these viruses in geographic space. We also use species accumulation curves to estimate viral richness from standardized, field-acquired data from the USAID PREDICT project (http://www.healthmap.org/predict/). Network models and statistics were used to compare patterns of viral sharing among bats between the literature and field-acquired datasets. **Results:** For the all mammal analyses: The best-fit model for total viral richness per wild mammal species explained 49.2% of the total deviance, and included a per-species measure of disease-related research effort, phylogenetically corrected body mass, geographic range, mammal sympatry, and taxonomy (order) After controlling for research effort, the proportion of zoonotic viruses per species is predicted by phylogenetic relatedness to humans, host taxonomy and human population within a species range—which may reflect human–wildlife contact. We demonstrate that bats harbor a significantly higher proportion of zoonotic viruses than all other mammalian orders. For the bat field-acquired data we show significant differences in viral richness estimates across bat genera and viral family, as well as differences in the rates of saturation. Clustering in bat host-virus networks follow some predictable patterns and identify additional bat species to target for viruses of interest. **Conclusions:** These host-specific analyses and estimates of viral richness, including the unobserved or 'missing' viruses, allow us to better identify and target which species and regions should be preferentially targeted to characterize the global bat virome.

From: Kevin Olival, PhD ecohealthalliance.org>
Sent: Wednesday, June 21, 2017 10:25 AM EDT
To: Schountz,Tony >
CC: Jon Epstein ecohealthalliance.org>
Subject: Re: Abstracts

Pretty sure I never wrote one! Just title. Can get it to you tomorrow if that's ok!

On Jun 21, 2017, at 10:24 AM, Schountz,Tony wrote:

> Hi Jon and Kevin,
>
> I don't seem to have abstracts for your bat ID talks. Could you (re)send them directly to me today or tomorrow?
>
> Thanks
>
> Tony
>
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

From: Jon Epstein ecohealthalliance.org>
Sent: Friday, June 23, 2017 3:11 PM EDT
To: Schountz,Tony
Subject: Re: Abstracts
Attachment(s): "Bat ID 2017 _ Epstein abstract.docx"

Tony,
Attached is my abstract - it's pretty new stuff, so I've kept the abstract brief. Really just describing the subject of the talk, rather than data. It this OK?

See you next week.

Cheers,
Jon

On Fri, Jun 23, 2017 at 12:07 PM, Schountz,Tony wrote:

> Hi Jon, yes, there's still a bit of time. I'm awaiting a few others, too. Trying to get to the printer this afternoon.
>
> Thanks,
>
> Tony
>
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

From: Jon Epstein ecohealthalliance.org >
Sent: Friday, June 23, 2017 9:59 AM
To: Schountz,Tony
Cc: Kevin Olival, PhD
Subject: Re: Abstracts

Tony,
Is there still time? I'm working on it today.
-Jon

On Wed, Jun 21, 2017 at 10:59 AM, Schountz,Tony > wrote:

> Yup tomorrow's fine. Program gets printed on Friday.
>
> Thanks
>
> Tony
>
> Sent from my iPhone
>
> On Jun 21, 2017, at 7:26 AM, Kevin Olival, PhD ecohealthalliance.org> wrote:
>
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—
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Jonathan H. Epstein DVM, MPH, PhD

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New York, NY 10001

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web: ecohealthalliance.org

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Using serology to understand the dynamics of concurrent viral infections in pteropid bats

Jonathan H. Epstein[1], Noam Ross[1], Ariful Islam[1], Dan Crowley[1,2], Gary Crameri[3], Christopher Broder[4], Linfa Wang[5], and Peter Daszak[1].

1. EcoHealth Alliance, NY USA
2. Columbia University Mailman School of Public Health, NY USA
3. CSIRO Australian Animal Health Laboratory, Geelong, VIC, AUS
4. Uniformed Services University, MD USA
5. Duke-NUS, Singapore

Fruit bats of the genus *Pteropus* are reservoirs for henipaviruses throughout their range. *Pteropus medius* is the natural reservoir for Nipah virus in India and Bangladesh, and mechanisms of spillover to humans primarily involves contamination of date palm sap with excreta. Serological dynamics have provided insight into patterns of Nipah virus infection in this host, but other viruses, including Nipah-like viruses have been identified through pathogen discovery techniques. Little is known about infection patterns of other viruses within this species, or their likelihood of infecting other animals or people. We screened sera from a single population of *P. medius* in Bangladesh collected quarterly over six years for IgG antibodies against henipaviruses (NiV, HeV, CEDV), filoviruses (EBOV, MARV), and Menangle virus, using assays containing virus-specific solubilized glycoproteins or F proteins in a Luminex platform. Here we present preliminary observations of comparative temporal patterns for multiple viral agents that suggest co-circulation in this population. We also discuss challenges in interpretation of serology when studying viral infections in wildlife, particularly when multiple antigenically related viruses may be present.

From: peng.zhou >
Sent: Monday, March 16, 2020 8:07 PM EDT
To: Schountz,Tony >
CC: Wang Linfa ; zlshi >
Subject: Re: Asthma as a comorbidity for COVID-19?

Hi, Tony,

Any respiratory syndrome is suspicious. I suggest you to do a test in your lab, that is what we do here, just to rule out that possibility.

Best wishes,
Peng

peng.zhou

On 03/17/2020 01:40, Schountz,Tony wrote:

Hi Zhengli, Linfa and Peng,

I have a graduate student who is working with SARS-CoV-2 and she informed me she has asthma. Of course, now I am concerned about this. I looked in the literature using various search terms but I could not find an indication whether asthma is a comorbidity associated with severe COVID-19 disease. Have you seen data from China or Singapore (or elsewhere) as to whether it might?

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Wang Linfa >
Sent: Tuesday, March 17, 2020 11:04 AM EDT
To: Schountz,Tony ; 周鹏 <peng.zhou ; zlshi <
Subject: RE: Asthma as a comorbidity for COVID-19?

Hi Tony,

That has not been raised to my attention and I will ask clinicians. IF there is a link, I will let you know.

LF

Linfa (Lin-Fa) WANG, PhD FTSE
Professor & Director
Programme in Emerging Infectious Disease
Duke-NUS Medical School,

-----Original Message-----
From: Schountz,Tony >
Sent: Tuesday, 17 March 2020 1:40 AM
To: Wang Linfa 周鹏 <peng.zhou ; zlshi
Subject: Asthma as a comorbidity for COVID-19?

- External Email -

Hi Zhengli, Linfa and Peng,

I have a graduate student who is working with SARS-CoV-2 and she informed me she has asthma. Of course, now I am concerned about this. I looked in the literature using various search terms but I could not find an indication whether asthma is a comorbidity associated with severe COVID-19 disease. Have you seen data from China or Singapore (or elsewhere) as to whether it might?

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine Colorado State University

From: 石正丽 <zlshi >
Sent: Tuesday, February 05, 2019 1:48 AM EST
To: Schountz,Tony
CC: Christian Drosten >; Wang Linfa ; Michelle Baker >; Susanna Lau ; Patrick Woo >; Martin Schwemmle >; Richard Yanagihara >; Jon Epstein ecohealthalliance.org>
Subject: Re: Bat conference advisory committee

Dear Tony,

Thank you very much for your planning the meeting. I'll be happy to be the committee member and help it out.

Best regards,
Zhengli,

-----原始邮件-----
发件人:"Schountz,Tony" >
发送时间:2019-02-05 04:57:32 (星期二)
收件人: "Christian Drosten" >, "Wang Linfa" >, "Michelle Baker" , "Susanna Lau" >, "Patrick Woo" , "Martin Schwemmle" >, "Richard Yanagihara" >, "Jon Epstein" ecohealthalliance.org>, "石正丽"
抄送:
主题: Bat conference advisory committee

Dear colleagues,

We're planning to host the third international bat infectious disease symposium June 18-20, 2020 here in Fort Collins. This coincides with the end of the 2020 ASV meeting that will also be in Fort Collins and which ends on June 17. I will submit an R13 proposal (Conference Support) to NIH in April to get a few thousand dollars to help with student travel awards for the conference. I hope you don't mind, but I would like to list each of you as members of the advisory committee. Probably not too much for you to do, but it will be helpful for the submission. Is that OK? If you plan to attend the bat symposium, I will waive your registration fee.

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Jon Epstein ecohealthalliance.org>
Sent: Thursday, February 07, 2019 7:42 PM EST
To: Schountz,Tony
Subject: Re: Bat conference advisory committee

Of course!

BTW, I was at NIAID today. Still pushing for a bat model. Eun Chung is really supportive. Just need to find a way to get over the hump!
Does the building at CSU still exist?
-Jon

Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
New York

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On Thu, Feb 7, 2019, 2:04 PM Schountz,Tony wrote:

> Thanks, Jon, I appreciate your support.
>
> I hope all is well, wherever you might be at the moment!
>
> Tony
>
> > On Feb 4, 2019, at 2:00 PM, Jon Epstein ecohealthalliance.org> wrote:
> >
> > Tony,
> > Glad to hear this is happening again. I'm happy to help out.
> > Cheers,
> > Jon
> >
> > On Mon, Feb 4, 2019 at 3:57 PM Schountz,Tony wrote:
> >> Dear colleagues,
> >>
> >> We're planning to host the third international bat infectious disease symposium June 18-20, 2020 here in Fort Collins. This coincides with the end of the 2020 ASV meeting that will also be in Fort Collins and which ends on June 17. I will submit an R13 proposal (Conference Support) to NIH in April to get a few thousand dollars to help with student travel awards for the conference. I hope you don't mind, but I would like to list each of you as members of the advisory committee. Probably not too much for you to do, but it will be helpful for the submission. Is that OK? If you plan to attend the bat symposium, I will waive your registration fee.
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--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

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New York, NY 10001

)

web: ecohealthalliance.org

EcoHealth Alliance leads cutting-edge scientific research into the critical connections between human and wildlife health and delicate ecosystems. With this science, we develop solutions that prevent pandemics and promote conservation.

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Jon Epstein ecohealthalliance.org>
Sent: Monday, February 04, 2019 4:00 PM EST
To: Schountz,Tony
CC: Christian Drosten ; Wang Linfa < ; Michelle Baker ; Susanna Lau ; Patrick Woo ; Martin Schwemmle >; Richard Yanagihara 石正丽 <zlshi
Subject: Re: Bat conference advisory committee

Tony,
Glad to hear this is happening again. I'm happy to help out.
Cheers,
Jon

On Mon, Feb 4, 2019 at 3:57 PM Schountz,Tony > wrote:

> Dear colleagues,
>
> We're planning to host the third international bat infectious disease symposium June 18-20, 2020 here in Fort Collins. This coincides with the end of the 2020 ASV meeting that will also be in Fort Collins and which ends on June 17. I will submit an R13 proposal (Conference Support) to NIH in April to get a few thousand dollars to help with student travel awards for the conference. I hope you don't mind, but I would like to list each of you as members of the advisory committee. Probably not too much for you to do, but it will be helpful for the submission. Is that OK? If you plan to attend the bat symposium, I will waive your registration fee.
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--

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web: ecohealthalliance.org

From: Ebel,Greg >
Sent: Wednesday, April 01, 2020 4:07 PM EDT
To: jean.patterson Kendall,Lon >; Angela Bosco-Lauth >; Bowen,Richard >; Dean,Gregg >; epstein ecohealthalliance.org>; Schountz,Tony ; Szalai,Edit < ; bpope >; Challberg, Mark (NIH/NIAID) [E] >
Subject: RE: Bat Facility meeting

Thanks Jean,

This is extremely helpful and I think the right approach long-term. Many thanks for the update. We will still focus on bats and highlight the current importance of CoVs and bats, as it is timely and reasonable to do so, but will also point out the larger goals of the group and facilities.

Thanks again,

Greg

-----Original Message-----
From: Patterson, Jean (NIH/NIAID) [E]
Sent: Wednesday, April 01, 2020 2:05 PM
To: Kendall,Lon >; Angela Bosco-Lauth >; Bowen,Richard ; Dean,Gregg ; epstein ecohealthalliance.org>; Schountz,Tony >; Szalai,Edit < >; bpope rg, Mark ( ) [E] Ebel >
Subject: RE: Bat Facility meeting

Hi everyone,

We have one update for you. Mark met with Emily and Cristina today and the consensus was that you do not have to focus most of your efforts on coronaviruses research, rather incorporate the idea of this facility to be used as a resource for pandemic preparedness and EIDs. I think you were headed in this direction anyway, but feel free to add additional capacity and thoughts for related research on EIDs. Coronavirus research should be included, but doesn't have to overwhelm the proposal, if you know what I mean.

Great call yesterday!
Jean and Mark

-----Original Appointment-----
From: Kendall,Lon
Sent: Monday, March 30, 2020 10:15 PM
To: Angela Bosco-Lauth; Bowen, Richard; Cassetti, Cristina (NIH/NIAID) [E]; Dean,Gregg; epstein; Schountz, Tony; Szalai,Edit; bpope; Patterson, Jean (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Ebel,Greg
Subject: Bat Facility meeting
When: Tuesday, March 31, 2020 10:00 AM-11:00 AM (UTC-07:00) Mountain Time (US & Canada).
Where: Microsoft Teams Meeting

Here is tomorrow's agenda. Talk to you all tomorrow. You should be able to join by clicking the link below.
Introduction
Lon- why meeting was initially organized, then turf to Jon (I won't be long)
Jon- provide background about program discussions with CSU and NIAID and why we are here (Jon really sparked this discussion, and is probably best to lead)
Jean- Discuss NIAID possibilities and expectations and what's needed from CSU (Thought Jean should go sooner to help frame discussion below. I will send her agenda once we get it finalized)
Ebel- Discuss CVID abilities, and possibilities related to emerging disease, prior C06
Tony- Discuss current research and potential needs
Bowen/Angela- Discuss current research and potential needs Determine next steps _____
Join Microsoft Teams Meeting<https://nam01.safelinks.protection.outlook.com/ap/t-59584e83/?url=https%3A%2F%2Fteams.microsoft.com%2Fl%2Fmeetup-join%2F19%253ameeting_NzEwNWQwYWEtZDA3Yi00OTczLTgzNGMtY2Y4MGU4MWRiNDYw%2540thread.v2%2F0%3Fcontext%3D%257b%2522Tid%2522%253a%2522afb58802-ff7a-4bb1-ab21-367ff2ecfc8b%2522%252c%2522Oid%2522%253a%2522c577d4c0-7b31-47d8-891c-90b281bca62b%2522%257d&data=02%7C01%7CTony.Schountz%40colostate.edu%7Cb3fa0a1f801f4c40668208d7d6785148%7Cafb58802ff7a4bb1ab21367ff2ecfc8b%7C0%7C0%7C637213684564901970
Learn more about Teams<https://nam01.safelinks.protection.outlook.com/?url=https%3A%2F%2Faka.ms%2FJoinTeamsMeeting&data=02%7C01%7CTony.Schountz%40colostate.edu%7Cb3fa0a1f801f4c40668208d7d6785148%7Cafb58802ff7a4bb1ab21367ff2ecfc8b%7C0%7C0 | Meeting options<https://nam01.safelinks.protection.outlook.com/?url=https%3A%2F%2Fteams.microsoft.com%2FmeetingOptions%2F%3ForganizerId%3Dc577d4c0-7b31-47d8-891c-90b281bca62b%26tenantId%3Dafb58802-ff7a-4bb1-ab21-367ff2ecfc8b%26threadId%3D19_meeting_NzEwNWQwYWEtZDA3Yi00OTczLTgzNGMtY2Y4MGU4MWRiNDYw%40thread.v2%26messageId%3D0%26language%3Den-US&data=02%7C01%7CTony.Schountz%40colostate.edu%7Cb3fa0a1f801f4c40668208d7d6785148%7Cafb58802ff7a4bb1ab21367ff2ecfc8b%7C0%7C0%7C637213684564901970&sdata=oG%2B41Iw
_____

From: Jon Epstein ecohealthalliance.org>
Sent: Wednesday, April 01, 2020 4:34 PM EDT
To: jean.patterson
CC: Kendall,Lon ; Angela Bosco-Lauth ; Bowen,Richard ; Dean,Gregg ; Schountz,Tony >; Szalai,Edit >; bpope >; Challberg, Mark (NIH/NIAID) [E] >; Ebel,Greg >
Subject: Re: Bat Facility meeting

Excellent, Jean - thanks.
I'm also glad that the powers that be know that this effort will have much broader application.
Cheers,
Jon

On Wed, Apr 1, 2020 at 4:04 PM Patterson, Jean (NIH/NIAID) [E] > wrote:

> Hi everyone,
>
> We have one update for you. Mark met with Emily and Cristina today and the consensus was that you do not have to focus most of your efforts on coronaviruses research, rather incorporate the idea of this facility to be used as a resource for pandemic preparedness and EIDs. I think you were headed in this direction anyway, but feel free to add additional capacity and thoughts for related research on EIDs. Coronavirus research should be included, but doesn't have to overwhelm the proposal, if you know what I mean.
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> From: Kendall,Lon >
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> To: Angela Bosco-Lauth; Bowen, Richard; Cassetti, Cristina (NIH/NIAID) [E]; Dean,Gregg; epstein; Schountz, Tony; Szalai,Edit; bpope; Patterson, Jean (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Ebel,Greg
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> Learn more about Teams<https://aka.ms/JoinTeamsMeeting> | Meeting options<https://teams.microsoft.com/meetingOptions/?organizerId=c577d4c0-7b31-47d8-891c-90b281bca62b&tenantId=afb58802-ff7a-4bb1-ab21-367ff2ecfc8b&threadId=19_meeting_NzEwNWQwYWEtZDA3Yi00OTczLTgzNGMtY2Y4MGU4MWRiNDYw@thread.v2&messageId=0&language=en-US>
> ___

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Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
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New York, NY 10001

web: ecohealthalliance.org

From: Patterson, Jean (NIH/NIAID) [E]
Sent: Wednesday, April 01, 2020 4:04 PM EDT
To: Kendall,Lon >; Angela Bosco-Lauth Bowen,Richard ; Dean,Gregg ; epstein ecohealthalliance.org>; Schountz,Tony >; Szalai,Edit >; bpope ; Challberg, Mark (NIH/NIAID) [E] >; Ebel,Greg
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Great call yesterday!
Jean and Mark

From: Jon Epstein ecohealthalliance.org>
Sent: Tuesday, March 17, 2020 1:32 PM EDT
To: Kendall,Lon >
CC: Richard Bowen >; Ebel,Greg >; Schountz,Tony

Subject: Re: Bat housing

I'd like to loop in Brian Pope, Director of Lubee Bat Conservancy. He has deep knowledge of husbandry.

He's been part of this team since inception.
Ok with everyone?
-Jon

Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
New York

(

On Tue, Mar 17, 2020, 1:25 PM Kendall,Lon wrote:

> All,
>
> Alan asked me to follow up on the renovations of the bull barn for bat holding. I did a quick space assessment of the building. It is approximately 2500 sf, including a 100 sf storage area. I am assuming of the 2500 sf we'll need about 500 sf for storage, feed prep and procedure space. The AZA recommendations for Pteropus giganteus is 15'x30' per 6 bats. With 2000 sf, that leave us holding for 24-29 bats. If there are some other housing guidelines someone has, please let me know.
>
> On the call we discussed 40-60 bats. I'm looking for advice on how to proceed. We can look at extending the footprint to accommodate 40-60, but I'm not sure what the program needs will be.
>
> Thanks,
>
> Lon
>
> Lon V. Kendall, DVM, PhD, DACLAM
>
> Director, Laboratory Animal Resources and
>
> Attending Veterinarian, Colorado State University

From: Kendall,Lon >
Sent: Tuesday, March 17, 2020 1:32 PM EDT
To: Jon Epstein ecohealthalliance.org>
CC: Richard Bowen >; Ebel,Greg >; Schountz,Tony >
Subject: RE: Bat housing

Yes. I meant to ask for that.

Lon V. Kendall, DVM, PhD, DACLAM
Director, Laboratory Animal Resources and
Attending Veterinarian, Colorado State University

From: Jon Epstein ecohealthalliance.org>
Sent: Tuesday, March 17, 2020 11:32 AM
To: Kendall,Lon
Cc: Richard Bowen Ebel,Greg >; Schountz,Tony >
Subject: Re: Bat housing

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> Thanks,
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> Lon
>
> Lon V. Kendall, DVM, PhD, DACLAM
> Director, Laboratory Animal Resources and
> Attending Veterinarian, Colorado State University

From: Schountz,Tony >
Sent: Saturday, February 01, 2020 1:04 PM EST
To: zlshi >; 周鹏 <peng.zhou
CC: Schountz,Tony
Subject: Re: Bat ID conference

Dear Zhengli,

If there is anything I can do to help you with your travels, please let me know. I can prepare a letter of invitation for you if you need it.

Peng, I'm sorry you cannot make it. I was looking forward to visiting with you about bat immunology. We have tried many ways of making bone marrow dendritic cells and macrophages but with little success. We have tried adapting mouse protocols with artibeus bat cytokine orthologs but the do not work as well with the bats as they do with mice. I am beginning to think the developmental pathways of bats and mice are substantially different.

I am sure all of you are overwhelmed with the coronavirus outbreak. I really hope it subsides soon because it has been really terrible for China.

Be safe.

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Jan 30, 2020, at 9:24 PM, zlshi wrote:

Dear Tony,

I plan to participate in the ASV meeting and the Bat meeting. In view the current situation, I'm not sure if I can get permission to travel and the Visa as well.

Best regards,
Zhengli,

SHI Zhengli, Ph. D
Senior Scientist & Professor
Wuhan Institute of Virology, Chinese Academy of Sciences
44 Xiao Hong Shan
430071 Wuhan, Hubei
China

From: Schountz,Tony
Date: 2020-01-31 04:46
To: 周鹏; 石正丽
Subject: Bat ID conference

Dear Zhengli and Peng,

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Thank you,

Tony

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: peng.zhou >
Sent: Monday, February 03, 2020 3:57 AM EST
To: Schountz,Tony
CC: zlshi
Subject: Re: Bat ID conference

Hi, Tony, we have used bat CSF1 proteins for the differentiation. You may consider this.

peng.zhou

On 02/02/2020 02:04, Schountz,Tony wrote:

Dear Zhengli,

If there is anything I can do to help you with your travels, please let me know. I can prepare a letter of invitation for you if you need it.

Peng, I'm sorry you cannot make it. I was looking forward to visiting with you about bat immunology. We have tried many ways of making bone marrow dendritic cells and macrophages but with little success. We have tried adapting mouse protocols with artibeus bat cytokine orthologs but the do not work as well with the bats as they do with mice. I am beginning to think the developmental pathways of bats and mice are substantially different.

I am sure all of you are overwhelmed with the coronavirus outbreak. I really hope it subsides soon because it has been really terrible for China.

Be safe.

Tony
—
Tony Schountz, PhD
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From: Schountz,Tony
Sent: Thursday, January 30, 2020 4:25 PM EST
To: Kevin Olival ecohealthalliance.org>
CC: Schountz,Tony ; Peter Daszak ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>
Subject: Re: Bat ID meeting

Right, Edinburgh. Somehow, I had in my mind it was the EEID meeting in Paris.

We will be sorry to miss your group here, it's always brought good science and information to the symposium.

Let me know if things change and we'll get you in.

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
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> On Jan 30, 2020, at 2:03 PM, Kevin Olival ecohealthalliance.org> wrote:
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> Cheers,
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Jonathan H. Epstein DVM, MPH, PhD

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New York, NY 10001

web: ecohealthalliance.org

EcoHealth Alliance leads cutting-edge scientific research into the critical connections between human and wildlife health and delicate ecosystems. With this science, we develop solutions that prevent pandemics and promote conservation.

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web: ecohealthalliance.org

From: Schountz,Tony >
Sent: Wednesday, June 14, 2017 2:06 PM EDT
To: Jon Epstein ecohealthalliance.org>
Subject: Re: bat meeting

Hi Jon

The Hilton on Prospect is only half a mile from the meeting. Theres also the University Inn Best Western on College Ave that is about a quarter of a mile.

See you in a couple of weeks.

Tony

Sent from my iPhone

On Jun 14, 2017, at 10:35 AM, Jon Epstein ecohealthalliance.org> wrote:

> Tony,
> Should I book in at the Hilton for the bat meeting? Or is there a more convenient hotel?
> -Jon
>
> --
>
> **Jonathan H. Epstein DVM, MPH, PhD**
>
> *Vice President for Science and Outreach*
>
> EcoHealth Alliance
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> -
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From: Munster, Vincent (NIH/NIAID) [E] <
Sent: Friday, December 07, 2018 7:43 AM EST
To: Schountz,Tony < ; Kevin Olival < ecohealthalliance.org>
CC: Laing, Eric ; Broder, Chris (USU-DoD) ; Luke Hamel ecohealthalliance.org>
Subject: Re: Bat MERS-CoV sera for S protein luminex-based assay R&D

Hey Kevin, indeed the seroconversion is very minimal so I don't know if they would be of any use. I'll check once I get back, but you can include that line anyway

Already sharing hamster, camel, mice and NHP sera with Eric and Chris for validation and sensitivity,

Would be good to add an alternate target to the assay as well (like N),

Cheers,

Vincent

From: Tony Schountz >
Date: Tuesday, December 4, 2018 at 8:54 PM
To: "Kevin Olival," ecohealthalliance.org>
Cc: Tony Schountz >, "vincent.munster " >, "Laing, Eric" >, "Broder, Chris (USU-DoD)" < , Luke Hamel ecohealthalliance.org>
Subject: Re: Bat MERS-CoV sera for S protein luminex-based assay R&D

Hi Kevin,

How much serum (volume) do you need? We have just finished an infection experiment with our Aj bats but we have not done the serology, yet.

Tony

> On Dec 4, 2018, at 12:25 PM, Kevin Olival ecohealthalliance.org> wrote:
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Thanks Vincent. I'll add a line about sharing the sera from bats and others with Eric and Chris.

Will let Eric and Chris comment on the N gene target.

Kevin

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Sent: Tuesday, December 04, 2018 3:04 PM EST
To: Schountz,Tony
CC: Munster, Vincent (NIH/NIAID) [E] >; Laing, Eric >; Chris Broder ; Luke Hamel ecohealthalliance.org>
Subject: Re: Bat MERS-CoV sera for S protein luminex-based assay R&D

Thanks for the quick reply Tony. Good to hear the work is going on.

I'll let Eric answer the volume issue, I know it's 2uL per run, but not sure how much would be needed in total for the validation process.

Also, I think Eric has already reached out to Vincent about MERS+ bat sera in a separate request. My email falls under the same overall scope of work, and so just letting everyone know this isn't duplicative and keeping everyone in the loop here. Just hopeful we can find some additional $ support for this. Appreciate everyone's collaborative spirit!

Cheers,
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From: Ebel,Greg >
Sent: Tuesday, June 02, 2020 6:52 PM EDT
To: epstein ecohealthalliance.org>
CC: Schountz,Tony
Subject: RE: Bat space at CSU

They were from Lon. He would be the person who would ultimately decide requirements, and he knows that space better than anyone.

I'd like to hear what Brian has to say but don't know him so please reach out if you can.

It seems like we need ~4x the space that we have so even if there was a 100% overestimate on the space needs for Pteropus we'd still be 25K ft2 short.

Greg

From: Jon Epstein ecohealthalliance.org>
Sent: Tuesday, June 02, 2020 4:48 PM
To: Ebel,Greg
Cc: Schountz,Tony >
Subject: Re: Bat space at CSU

Greg,
That's really disappointing. Can I ask where the space estimates came from? Just wondering if we could get Brian Pope to weigh in on this, as an expert on Pteropus husbandry.
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On Tue, Jun 2, 2020 at 6:44 PM Ebel,Greg > wrote:

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> If it is the Pteropus, a renovated barn could hold approximately 25 bats. Maybe good for some short term studies, but insufficient for a breeding colony.
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> Sorry not to have better news.
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> Greg
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> Gregory D. Ebel
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Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance

From: Munster, Vincent (NIH/NIAID) [E]
Sent: Friday, May 19, 2017 10:12 AM EDT
To: Schountz,Tony Jon Epstein ecohealthalliance.org>
Subject: Re: Bat tissue

If we get it, I would still give it a try for celllines

From: Tony Schountz >
Date: Friday, May 19, 2017 at 8:08 AM
To: Jon Epstein ecohealthalliance.org>
Cc: "Munster, Vincent (NIH/NIAID) [E]"
Subject: Re: Bat tissue

No, I didn't get anything, Jon. Frozen tissues? Too bad we couldn't get live bone marrow and spleen.

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Jon Epstein < ecohealthalliance.org>
Sent: Friday, May 19, 2017 7:48 AM
To: Schountz,Tony
Cc: Munster, Vincent
Subject: Bat tissue

Tony,
I just heard that Lubee's P. giganteus recently died and I think they've harvested tissue. Were you aware? Did you get any samples?
-Jon

From: Patterson, Jean (NIH/NIAID) [E]
Sent: Thursday, April 02, 2020 4:09 PM EDT
To: Ebel,Greg >; Challberg, Mark (NIH/NIAID) [E] >
CC: epstein ecohealthalliance.org>; Schountz,Tony ; Dean,Gregg ; Kendall,Lon >; Szalai,Edit
Subject: RE: C06 update documents

Will let you know, Greg after I hear back from Malgorzata. She will probably want 100% confirmation from NIAID first, but we are getting close!

From: Ebel,Greg
Sent: Thursday, April 2, 2020 4:05 PM
To: Patterson, Jean (NIH/NIAID) [E] ; Challberg, Mark (NIH/NIAID) [E]
Cc: epstein ecohealthalliance.org>; Schountz, Tony >; Dean,Gregg ; Kendall,Lon >; Szalai,Edit
Subject: RE: C06 update documents

Dear Jean,

Thank you! I can make time for a call with ORIP pretty much anytime. Will you set up the call or shall I attempt to do so?

Greg

From: Patterson, Jean (NIH/NIAID) [E]
Sent: Thursday, April 02, 2020 1:44 PM
To: Ebel,Greg >; Challberg, Mark (NIH/NIAID) [E]
Cc: epstein ecohealthalliance.org>; Schountz,Tony < ; Dean,Gregg Kendall,Lon >; Szalai,Edit >
Subject: RE: C06 update documents

Dear Greg,

Mark and I concur that this updated plan looks terrific! Our next step would be to get on a call with ORIP. I will let Malgorzata Klosek (ORIP) know that this is ready for them. See below her contact info. When you are ready, we (CSU, EcoHealth Alliance, ORIP and NIAID) can discuss with her and her team.

No need for additional letters, I think this team (including Jon of course) speaks for itself.
And I was the one who needed the letter from Vincent as I have to send it forward to our OD office, so you don't have to do anything.

Thanks again and will chat soon,
Jean

Dr. Malgorzata Klosek (Gosha is her nickname)
Director, Division of Construction and Instrumentation, ORIP, OD

From: Ebel,Greg >
Sent: Thursday, April 2, 2020 12:12 PM
To: Patterson, Jean (NIH/NIAID) [E] ; Challberg, Mark (NIH/NIAID) [E]
Cc: epstein ecohealthalliance.org>; Schountz, Tony >; Dean,Gregg >; Kendall,Lon ; Szalai,Edit
Subject: C06 update documents

Dear Jean and Mark,

As promised, I'm attaching a two page update on the C06.

It highlights (a) the overall rationale for the project, (b) our vision for how it would be used, and (c) a summary of current bat-focused experimental research that it would support.

The overall picture that I would like to convey is that CSU is an ideal environment for locating a bat facility due to our longstanding interest in emerging zoonotic and vector-borne infections and our commitment to developing infrastructure to support research in this area. I very much hope that this comes through. If you think that there are points that are being missed, please let me know and I can edit further.

I'm also attaching a letter of support from Dr. Vincent Munster at RML. If you think it would be helpful in moving this forward, we can also obtain a letter from EcoHealth alliance supporting the project.

Thanks so much for your attention and do let me know how I can further help move this project forward.

Best regards,

Greg

From: Patterson, Jean (NIH/NIAID) [E]
Sent: Thursday, April 02, 2020 3:44 PM EDT
To: Ebel,Greg >; Challberg, Mark (NIH/NIAID) [E]
CC: epstein ecohealthalliance.org>; Schountz,Tony Dean,Gregg >; Kendall,Lon >; Szalai,Edit
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Best regards,

Greg

From: Kevin Olival ecohealthalliance.org>
Sent: Wednesday, March 18, 2020 8:56 AM EDT
To: Schountz,Tony
Subject: Re: Cancelation of the 3rd International Symposium on Infectious Diseases of Bats

Damn emerging bat CoV messing everything up!

-Kevin

On Mar 17, 2020, at 3:44 PM, Schountz,Tony > wrote:

Dear Colleagues,

As you may have expected, due to the COVID-19 outbreak, the*3rd International Symposium on Infectious Diseases of Bats* has been canceled. We are considering hosting the meeting in the summer of 2021 if the resources are available to do so. If so, I will send another email this fall altering you.

For those of you who have already paid your registration, you will receive a full refund from the Colorado State University Conference Services. I have been told this can take about a month, so if you have not received a refund by April 20, please email me and I will contact Conference Services.

Thank you for your understanding.

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Feb 19, 2020, at 4:09 PM, Schountz,Tony > wrote:

Dear Colleagues,

Registration is now open for the 3rd International Symposium on Infectious Diseases of Bats. With the emergence of yet another pathogenic coronavirus, we are planning to have an extended session to learn from one another about this new virus and I hope some of you can foster collaborative interactions while you are here. The URL for the meeting is:

http://www.batid.org

Please note a few important dates. **Abstract submission closes on April 17, 2020**. The format of the abstract is indicated on the web site and we ask that you follow it for purposes of continuity in the program. In addition, please send MS Word, Apple Pages or Rich Text files so that we can rapidly build the program. Please DO NOT send a PDF because they are much more difficult to integrate into the program. After you submit your abstract, you should receive a confirmation email. If you do not, please let me know and I'll resolve the issue.

Registration will close on May 1, 2020. Registration will be handled by the Colorado State University Conference Services with a direct link on the Bat ID web site. You can select registration only, or registration with dormitory housing on campus near the conference venue (Lory Student Center). Registration included breakfast for the two days, and the dormitory includes breakfast, too. If you prefer to stay in a hotel, the Fort Collins Hilton (on Prospect Avenue) and the Best Western University Inn are walking distance to campus. Links to these hotels are provided on the Registration page.

We also have the pleasure of hosting**This Week in Virology**. Vincent and crew will record an episode from the meeting.

Please let me know if you have questions or comments.

Thanks very much, and we are looking forward to seeing you again in Fort Collins.

Tony

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Patterson, Jean (NIH/NIAID) [E] >
Sent: Friday, April 10, 2020 12:27 PM EDT
To: Ebel,Greg Kendall,Lon ; epstein ecohealthalliance.org>
CC: Schountz,Tony
Subject: RE: CO6 follow up

Yes, Greg and Lon, thanks for circling back on this. Mark and I are waiting on final word from NIAID OD before we can trigger this with ORIP. We are close however! Hopefully in the next week we will have the email we need.

From: Ebel,Greg
Sent: Friday, April 10, 2020 12:15 PM
To: Kendall,Lon ; epstein ecohealthalliance.org>; Patterson, Jean (NIH/NIAID) [E]

Cc: Schountz, Tony >
Subject: RE: CO6 follow up

Hi all,

Yes, I was wondering about this the other day. Last I remember the ball was in the NIAID court and we were waiting to hear from Gosha before proceeding.

Thanks for any new information!

Greg

From: Kendall,Lon
Sent: Friday, April 10, 2020 10:07 AM
To: epstein ecohealthalliance.org>; jean.patterson <
Cc: Ebel,Greg >; Schountz,Tony
Subject: CO6 follow up

Jean and Jon,

I can't recall, what are the next steps with the C06?

I know Greg is really busy, and just wanted to keep this momentum.

Lon

Lon V. Kendall, DVM, PhD, DACLAM
Director, Laboratory Animal Resources and
Attending Veterinarian, Colorado State University

Colorado State University
Fort Collins, CO 80523

From: Patterson, Jean (NIH/NIAID) [E] >
Sent: Monday, April 20, 2020 10:02 AM EDT
To: Ebel,Greg ; Kendall,Lon ; epstein ecohealthalliance.org>
CC: Schountz,Tony
Subject: RE: CO6 follow up

Hi all,
A quick update – we have hit a small snag in the process and trying to get unstuck. Without giving any details, think we might have a solution, so hang in there.
Jean

From: Ebel,Greg
Sent: Friday, April 10, 2020 1:05 PM
To: Patterson, Jean (NIH/NIAID) [E] >; Kendall,Lon >; epstein ecohealthalliance.org>
Cc: Schountz, Tony
Subject: RE: CO6 follow up

Thanks a lot Jean!
Greg

From: Patterson, Jean (NIH/NIAID) [E] >
Sent: Friday, April 10, 2020 10:28 AM
To: Ebel,Greg Kendall,Lon >; epstein ecohealthalliance.org>
Cc: Schountz,Tony >
Subject: RE: CO6 follow up

Yes, Greg and Lon, thanks for circling back on this. Mark and I are waiting on final word from NIAID OD before we can trigger this with ORIP. We are close however! Hopefully in the next week we will have the email we need.

From: Ebel,Greg >
Sent: Friday, April 10, 2020 12:15 PM
To: Kendall,Lon ; epstein ecohealthalliance.org>; Patterson, Jean (NIH/NIAID) [E] >
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Thanks for any new information!

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To: epstein ecohealthalliance.org>; jean.patterson <
Cc: Ebel,Greg >; Schountz,Tony
Subject: CO6 follow up

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Lon

Lon V. Kendall, DVM, PhD, DACLAM
Director, Laboratory Animal Resources and
Attending Veterinarian, Colorado State University
2007 Painter Center
Colorado State University
Fort Collins, CO 80523

From: Patterson, Jean (NIH/NIAID) [E]
Sent: Tuesday, May 05, 2020 10:37 AM EDT
To: Ebel,Greg < Kendall,Lon >; epstein ecohealthalliance.org>
CC: Schountz,Tony >; Challberg, Mark (NIH/NIAID) [E]
Subject: RE: CO6 follow up

Hi Greg, Lon, and Jon,
We are still waiting to hear on our end as to the status of the C06. Sorry this is taking so long. There is still high level scientific interest and support, so that is not the problem. If we don't have confirmation in the next few weeks, we will circle back with you all. Mark and I have a "Plan B" to propose, just in case.
Talk soon,
Jean

From: Ebel,Greg >
Sent: Monday, April 20, 2020 11:36 AM
To: Patterson, Jean (NIH/NIAID) [E] >; Kendall,Lon >; epstein ecohealthalliance.org>
Cc: Schountz, Tony
Subject: RE: CO6 follow up

Thanks, Jean.

Hanging in there!

Let me know whether there's anything I can do to help.

Greg

From: Patterson, Jean (NIH/NIAID) [E]
Sent: Monday, April 20, 2020 8:03 AM
To: Ebel,Greg ; Kendall,Lon ; epstein ecohealthalliance.org>
Cc: Schountz,Tony
Subject: RE: CO6 follow up

Hi all,
A quick update – we have hit a small snag in the process and trying to get unstuck. Without giving any details, think we might have a solution, so hang in there.
Jean

From: Ebel,Greg >
Sent: Friday, April 10, 2020 1:05 PM
To: Patterson, Jean (NIH/NIAID) [E] Kendall,Lon >; epstein ecohealthalliance.org>
Cc: Schountz, Tony >
Subject: RE: CO6 follow up

Thanks a lot Jean!
Greg

From: Patterson, Jean (NIH/NIAID) [E] >
Sent: Friday, April 10, 2020 10:28 AM
To: Ebel,Greg < ; Kendall,Lon >; epstein ecohealthalliance.org>
Cc: Schountz,Tony >
Subject: RE: CO6 follow up

Yes, Greg and Lon, thanks for circling back on this. Mark and I are waiting on final word from NIAID OD before we can trigger this with ORIP. We are close however! Hopefully in the next week we will have the email we need.

From: Ebel,Greg
Sent: Friday, April 10, 2020 12:15 PM
To: Kendall,Lon ; epstein @ecohealthalliance.org>; Patterson, Jean (NIH/NIAID) [E]

Cc: Schountz, Tony
Subject: RE: CO6 follow up

Hi all,

Yes, I was wondering about this the other day. Last I remember the ball was in the NIAID court and we were waiting to hear from Gosha before proceeding.

Thanks for any new information!

Greg

From: Kendall,Lon >
Sent: Friday, April 10, 2020 10:07 AM
To: epstein ecohealthalliance.org>; jean.patterson
Cc: Ebel,Greg >; Schountz,Tony
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Lon

Lon V. Kendall, DVM, PhD, DACLAM
Director, Laboratory Animal Resources and
Attending Veterinarian, Colorado State University

From: Ebel,Greg
Sent: Friday, April 10, 2020 12:14 PM EDT
To: Kendall,Lon ; epstein < ecohealthalliance.org>; jean.patterson

CC: Schountz,Tony
Subject: RE: CO6 follow up

Hi all,

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Thanks for any new information!

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To: epstein ecohealthalliance.org>; jean.patterson >
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Attending Veterinarian, Colorado State University

From: Ebel,Greg >
Sent: Friday, March 20, 2020 5:53 PM EDT
To: epstein ecohealthalliance.org>
CC: Schountz,Tony
Subject: RE: CSU Bat Facility

Jon,

Here's a link to the narrative portion of our proposal. Let me know if it meets your needs.

https://www.sugarsync.com/pf/D965006_09546385_650221

Greg

From: Jon Epstein ecohealthalliance.org>
Sent: Friday, March 20, 2020 3:11 PM
To: Kendall,Lon
Cc: Bowen,Richard ; Angela Bosco-Lauth >; Schountz,Tony Ebel,Greg Brian Pope ; Patterson, Jean (NIH/NIAID) [E]
Subject: Re: CSU Bat Facility

Lon,
Looping in Brian Pope, Director of the Lubee Bat Conservancy and Jean Patterson, program officer from NIAID with whom I've been working on developing bat models and the C06 /R24 plans.

Brian and Jean, this call is with the CSU team who will be building out the Pteropus facility & also housing Rhinolophus.

It's time to bring everyone together.

Cheers,
Jon

Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
New York

On Fri, Mar 20, 2020, 3:59 PM Kendall,Lon wrote:

> All,
>
> Just following up to schedule a meeting to start discussions on the bat facility. Please respond to the doodle poll and I'll let everyone know the date. I've also added everyone to the MS Team VPR Bat Facility
>
> Jon- I don't have Brian's contact information. Can you please forward this to him and provide me his email so I can add him to the team.
>
> https://doodle.com/poll/tgswptaa4295tae5
>
> Thanks,
>
> Lon
>
> Lon V. Kendall, DVM, PhD, DACLAM
> Director, Laboratory Animal Resources and
> Attending Veterinarian, Colorado State University
> 2007 Painter Center
> Colorado State University
> Fort Collins, CO 80523

From: Jon Epstein ecohealthalliance.org>
Sent: Friday, March 20, 2020 5:10 PM EDT
To: Kendall,Lon >
CC: Bowen,Richard Angela Bosco-Lauth
Schountz,Tony >; Ebel,Greg Brian Pope
; Patterson, Jean (NIH/NIAID) [E] >
Subject: Re: CSU Bat Facility

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> Thanks,
>
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> Lon V. Kendall, DVM, PhD, DACLAM
>
> Director, Laboratory Animal Resources and
>
> Attending Veterinarian, Colorado State University

From: Ebel,Greg >
Sent: Tuesday, August 18, 2020 12:37 AM EDT
To: jean.patterson >
CC: epstein ecohealthalliance.org>; Schountz,Tony Challberg, Mark (NIH/NIAID) [E]
Subject: RE: CSU Bat space

Hi Jean,

Thanks a lot. We've started our attempts to gauge the actual (as opposed to theoretical) interest at CSU in committing funds to renovate the space we have identified as a candidate for the bat facility. We should have a renovation estimate in fairly short order and then can approach our VPR with some harder numbers. He might then (a) say "go for it!!" or (b) gag and tell us to take a hike.

Let's let this process play out before we all get together on the phone again.

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Sent: Thursday, August 13, 2020 12:28 PM
To: Ebel,Greg
Cc: epstein ecohealthalliance.org>; Schountz,Tony ; Challberg, Mark (NIH/NIAID) [E]

Subject: RE: CSU Bat space

Hi Greg,
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Thank you!
Jean

From: Ebel,Greg >
Sent: Thursday, August 13, 2020 1:21 PM
To: Patterson, Jean (NIH/NIAID) [E] >
Cc: epstein ecohealthalliance.org>; Schountz, Tony >
Subject: CSU Bat space

Dear Jean,

I'm writing to let you know that as of this AM, we are seeing some traction toward renovation funds for a bat facility at CSU. I think it makes sense to discuss next steps as long as interest remains at NIAID in moving forward with this effort.

Thank you,

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Gregory D. Ebel
Professor, Department of Microbiology, Immunology and Pathology
Director, Arthropod-Borne and Infectious Diseases Laboratory
College of Veterinary Medicine and Biomedical Sciences
Colorado State University

Ft. Collins CO 80526

From: Patterson, Jean (NIH/NIAID) [E]
Sent: Thursday, August 13, 2020 2:27 PM EDT
To: Ebel,Greg
CC: epstein ecohealthalliance.org>; Schountz,Tony >; Challberg, Mark (NIH/NIAID) [E]
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Professor, Department of Microbiology, Immunology and Pathology
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College of Veterinary Medicine and Biomedical Sciences
Colorado State University

Ft. Collins CO 80526

From: Patterson, Jean (NIH/NIAID) [E]
Sent: Tuesday, August 18, 2020 8:29 AM EDT
To: Ebel,Greg
CC: epstein ecohealthalliance.org>; Schountz,Tony ; Challberg, Mark (NIH/NIAID) [E]
Subject: RE: CSU Bat space

Sounds like a plan, Greg. Good luck! Just curious, but if everything lines up, are you shooting for an R24 submission date of Sept. 25? Or Jan. 25, 2021?

From: Ebel,Greg >
Sent: Tuesday, August 18, 2020 12:37 AM
To: Patterson, Jean (NIH/NIAID) [E] >
Cc: epstein ecohealthalliance.org>; Schountz, Tony >; Challberg, Mark (NIH/NIAID) [E]

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Gregory D. Ebel
Professor, Department of Microbiology, Immunology and Pathology
Director, Arthropod-Borne and Infectious Diseases Laboratory
College of Veterinary Medicine and Biomedical Sciences
Colorado State University

Ft. Collins CO 80526

From: Schountz,Tony
Sent: Thursday, December 07, 2017 1:59 PM EST
To: Mattina Alonge >
CC: Munster, Vincent (NIH/NIAID) [E] < >; Olson, Sarah ; Schountz,Tony ; Theresa Laverty >; Nate Fuller ; Raina Plowright ; Liam Mcguire >; Kevin Olival ecohealthalliance.org>; Lausen, Cori <c
Subject: Re: E-introduction

Hi Mattina,

I'm not sure who all needs to be on this reply so I cc'd everyone.

We can get these tissues for you from Jamaican fruit bats in our colony; however, they will have to be collected opportunistically. It may not be until January before we could collect them for you.

Regards,

Tony

> On Dec 7, 2017, at 11:33 AM, Mattina Alonge > wrote:
>
> Thanks a ton Vincent. I appreciate your help in spreading the word!
>
> Mattina
>
> On Thu, Dec 7, 2017 at 9:50 AM, Munster, Vincent (NIH/NIAID) [E]< wrote:
>
> > Hi Mattina,
> >
> > I'm looping in my friends Tony Schountz and Dick Bowen from CSU, Tony might have access to tissues from Carollia and Artibeus bats. And Dick my know people who once in a while get bats submitted for rabies testing.
> >
> > Cheers,
> >
> > Vincent Munster
> >
> > ---
> >
> > **From:** Mattina Alonge
> > **Date:** Tuesday, December 5, 2017 at 8:35 PM
> > **To:** Sarah Olson
> > **Cc:** Theresa Laverty >, Nate Fuller , Raina Plowright >, "vincent.munster >, Liam Mcguire , "Kevin Olival," <oliva , "Lausen, Cori"
> > **Subject:** Re: E-introduction
> >
> > Hi Sarah, Thanks! As for gaining field experience within the next year I think I am limited to North America purely to minimize cost of gaining a foundation of skills/training...but for research questions I am able to develop and field studies I may want to propose for funding, a wider (global) range of locations can certainly be relevant and beneficial!
> >
> > For all that are curious or may be interested, here's a nutshell explanation of what my science interests are:
> >
> > Right now I'd like to characterize the localization and expression of gonadotropin inhibitory hormone (GnIH) in bats; it's a neuropeptide that inhibits the downstream signals involved in the hypothalamic-pituitary-gonadal

axis in vertebrates, but has yet to be described in any bat species. This fits into my broad interest of how environmental and social cues modulate reproductive physiology at a molecular level. For this basic early work, I'm looking to find people who are willing to donate existing, or collect, some tissue samples for me to work on in the lab (IHC, qPCR, westerns...). I'm looking for brains and gonads from any species of bat (male and female) either isolated and flash frozen, or fixed in formaldehyde of some kind. If any of you have insight into this that'd be awesome!

After this initial step, I'd also like to do my own field studies (shooting for 2018-2019) to wild-catch some bats across seasons within a region where species exhibit hibernation or torpor, and examine how GnIH and GnRH fluctuate seasonally across reproductive life history stages and suppression. This connects to ideas within the context of energy partitioning and tradeoff, within which I think those of you working in disease dynamics and immunology could be cool collaborators if interested. If I am able to terminally collect samples for myself perhaps others can collect data on immune aspects of the individuals across seasons as well. Just some early thoughts.

Looking forward to any feedback, potential field work training I can get, and maybe even ideas about where I can get tissues to start.

Mattina

On Tue, Dec 5, 2017 at 10:26 AM, Olson, Sarah > wrote:

> Hi Mattina!
>
> I'm at a remote field camp so I'll cut to the chase. I'm copying in a few folks and members of my WNS team to see if something might work or if someone might be interested in collaborating. I'm not sure if your project is limited to NA so I've also looped in some additional friends.
>
> Hopefully something works out,
>
> Sarah
>
> ---------- Forwarded message ----------
> From: **Mattina Alonge**
> Date: Mon, Dec 4, 2017 at 10:59 AM
> Subject: [wbwg] Berkeley PhD Student - Looking to help you with field work / Bat Tissues
> To: wbwglist
>
> Hello all!
>
> My name is Mattina and I'm a first year PhD student at UC Berkeley within the Integrative Biology Dept. I'm working under the supervision of Dr. George Bentley, developing projects that broadly encompass the ways animals translate environmental cues via neuroendocrinology to support (or inhibit) reproductive physiology. I have a few different project ideas surrounding bat reproductive neuroendocrine regulation that I'd be happy to chat about if anyone is interested, but I'm reaching out to this group to also offer my help, and ask for some help.
>
> - **I'm really interested in gaining some bat field experience and training in wild-capture (handling, mist netting, harp traps, etc.)** as this is something I'd like to do as part of my dissertation but have no experience. If you are planning to do field work of any capacity over the upcoming Spring/Summer and

would like a responsible set of eyes and hands to help, please let me know!

- I'm attempting to get some preliminary data this year regarding localization and expression of a neurohormone that inhibits the HPG axis in vertebrates. I'd like to characterize it in bats as a starting point and build funding proposals off of that for future field studies. This is where I need help - I am hoping to get some donated **brain, ovary, and testes** tissues from a few different bat species for me to do some IHC/gene expression work on. **If anyone has bat tissues of this type that they do not need for their own research programs, I'd love to talk further!** Flash frozen is ideal, and RNAlater or PFA fixed is also okay.

Thanks so much!

Mattina

--

Mattina Alonge

PhD Student, University of California, Berkeley

Bentley Lab (Reproductive Neuroendocrinology)

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Mattina Alonge

PhD Student, University of California, Berkeley

Bentley Lab (Reproductive Neuroendocrinology)

--
Mattina Alonge
PhD Student, University of California, Berkeley
Bentley Lab (Reproductive Neuroendocrinology)

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Munster, Vincent (NIH/NIAID) [E] >
Sent: Thursday, December 07, 2017 12:50 PM EST
To: Mattina Alonge ; Olson, Sarah >; Schountz,Tony >
CC: Theresa Laverty ; Nate Fuller ; Raina Plowright ; Liam Mcguire >; Kevin Olival ecohealthalliance.org>; Lausen, Cori >
Subject: Re: E-introduction

Hi Mattina,

I'm looping in my friends Tony Schountz and Dick Bowen from CSU, Tony might have access to tissues from Carollia and Artibeus bats. And Dick my know people who once in a while get bats submitted for rabies testing.

Cheers,

Vincent Munster

From: Mattina Alonge
Date: Tuesday, December 5, 2017 at 8:35 PM
To: Sarah Olson >
Cc: Theresa Laverty >, Nate Fuller >, Raina Plowright >, "vincent.munster , Liam Mcguire "Kevin Olival," ecohealthalliance.org>, "Lausen, Cori"
Subject: Re: E-introduction

Hi Sarah, Thanks! As for gaining field experience within the next year I think I am limited to North America purely to minimize cost of gaining a foundation of skills/training...but for research questions I am able to develop and field studies I may want to propose for funding, a wider (global) range of locations can certainly be relevant and beneficial!

For all that are curious or may be interested, here's a nutshell explanation of what my science interests are:

Right now I'd like to characterize the localization and expression of gonadotropin inhibitory hormone (GnIH) in bats; it's a neuropeptide that inhibits the downstream signals involved in the hypothalamic-pituitary-gonadal axis in vertebrates, but has yet to be described in any bat species. This fits into my broad interest of how environmental and social cues modulate reproductive physiology at a molecular level. For this basic early work, I'm looking to find people who are willing to donate existing, or collect, some tissue samples for me to work on in the lab (IHC, qPCR, westerns...). I'm looking for brains and gonads from any species of bat (male and female) either isolated and flash frozen, or fixed in formaldehyde of some kind. If any of you have insight into this that'd be awesome!

After this initial step, I'd also like to do my own field studies (shooting for 2018-2019) to wild-catch some bats across seasons within a region where species exhibit hibernation or torpor, and examine how GnIH and GnRH fluctuate seasonally across reproductive life history stages and suppression. This connects to ideas within the context of energy partitioning and tradeoff, within which I think those of you working in disease dynamics and immunology could be cool collaborators if interested. If I am able to terminally collect samples for myself perhaps others can collect data on immune aspects of the individuals across seasons as well. Just some early thoughts.

Looking forward to any feedback, potential field work training I can get, and maybe even ideas about where I can get tissues to start.

Mattina

On Tue, Dec 5, 2017 at 10:26 AM, Olson, Sarah wrote:

> Hi Mattina!
>
> I'm at a remote field camp so I'll cut to the chase. I'm copying in a few folks and members of my WNS team to see if something might work or if someone might be interested in collaborating. I'm not sure if your project is limited to NA so I've also looped in some additional friends.
>
> Hopefully something works out,
> Sarah
>
> ---------- Forwarded message ----------
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> Date: Mon, Dec 4, 2017 at 10:59 AM
> Subject: [wbwg] Berkeley PhD Student - Looking to help you with field work / Bat Tissues
> To: wbwglist

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Thanks so much!

Mattina

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Mattina Alonge
PhD Student, University of California, Berkeley
Bentley Lab (Reproductive Neuroendocrinology)

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Mattina Alonge
PhD Student, University of California, Berkeley
Bentley Lab (Reproductive Neuroendocrinology)

From: Nate Fuller
Sent: Friday, December 08, 2017 12:57 PM EST
To: Schountz,Tony <
CC: Mattina Alonge >; Munster, Vincent (NIH/NIAID) [E] ; Olson, Sarah < ; Theresa Laverty >; Raina Plowright ; Liam Mcguire ; Kevin Olival ecohealthalliance.org>; Lausen, Cori >
Subject: Re: E-introduction

Hi Mattina,

As for gaining relevant field experience, I would keep your eyes on the Eco-Log and/or TAMU job boards for volunteer bat handling gigs. The type of experience you're after will vary by species, habitat, region, etc., so think broadly.

As a side note, you will want to start reaching out to permitting agencies early on, especially if you're planning to sacrifice North American hibernating bats. Many folks are sensitive to the steep population declines caused by WNS and thus may be wary of such studies. In that context, it might be easier to gain experience and develop your project in a tropical system where bats are less threatened (but not by much....)

Nate Fuller, Ph.D.
TTU Biology

On Thu, Dec 7, 2017 at 12:59 PM, Schountz,Tony wrote:

> Hi Mattina,
>
> I'm not sure who all needs to be on this reply so I cc'd everyone.
>
> We can get these tissues for you from Jamaican fruit bats in our colony; however, they will have to be collected opportunistically. It may not be until January before we could collect them for you.
>
> Regards,
>
> Tony
>
> > On Dec 7, 2017, at 11:33 AM, Mattina Alonge > wrote:
> >
> > Thanks a ton Vincent. I appreciate your help in spreading the word!
> >
> > Mattina
> >
> > On Thu, Dec 7, 2017 at 9:50 AM, Munster, Vincent (NIH/NIAID) [E]< wrote:
> >
> > > Hi Mattina,
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> > > **To:** Sarah Olson >
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PhD Student, University of California, Berkeley

Bentley Lab (Reproductive Neuroendocrinology)

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Mattina Alonge

PhD Student, University of California, Berkeley

Bentley Lab (Reproductive Neuroendocrinology)

From: Jon Epstein ecohealthalliance.org>
Sent: Thursday, August 13, 2020 1:30 AM EDT
To: Schountz,Tony >
Subject: Re: Email

Tony,
any progress?

On Mon, Aug 3, 2020 at 10:03 AM Schountz,Tony wrote:

> Jon, I think thinks are moving forward with Alan Rudolf. I'm getting on a conference call right now but hope to hear more from him later today.
>
> Good news, for sure.
>
> T.
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

On Jul 30, 2020, at 3:48 PM, Jon Epstein ecohealthalliance.org> wrote:

That's great news. Please let me know if you need any info before then.
Fingers crossed....
-Jon

On Thu, Jul 30, 2020 at 5:44 PM Schountz,Tony > wrote:

> Jon, I have been told to contact Alan Rudolph, so I just sent him an email to see if he will be interested in providing funds to renovate the bull barn. I'll let you know as soon as I hear anything.
>
> T.
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> Tony Schountz, PhD
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> Colorado State University

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

web: ecohealthalliance.org

From: Schountz,Tony >
Sent: Monday, August 03, 2020 12:29 PM EDT
To: epstein ecohealthalliance.org>
CC: Schountz,Tony < >
Subject: Re: Email

Jon, any chance you could get *Rousettus leschenaultii* bats? The Ace2 receptor of this species has 16 of the 20 critical spike protein binding residues.

—

Tony Schountz, PhD
Associate Professor
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--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

web: ecohealthalliance.org

From: Jon Epstein ecohealthalliance.org>
Sent: Wednesday, August 05, 2020 11:30 AM EDT
To: Schountz,Tony >
Subject: Re: Email

Yes - these are common in Bangladesh and we could negotiate to include this species for our Nipah work as well.
-Jon

On Mon, Aug 3, 2020 at 12:29 PM Schountz,Tony wrote:

> Jon, any chance you could get *Rousettus leschenaultii* bats? The Ace2 receptor of this species has 16 of the 20 critical spike protein binding residues.
> —
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Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

web: ecohealthalliance.org

From: Schountz,Tony <
Sent: Sunday, October 21, 2018 11:44 PM EDT
To: 胡犇 <huben
Subject: Re: Final Program of the 8th International Symposium on Emerging Viral Diseases

Hi Ben

Do I need to schedule a ride to the airport tomorrow? Also do you know if I can print my boarding passes here at the hotel?

Thanks

Tony

Sent from my iPhone

On Oct 18, 2018, at 10:16 PM, 胡犇 <huben > wrote:

> Dear Dr.Schountz:
>
> I have an app via which I can follow the status of any flight.
>
> So I can arrange with flexibility.
>
> But hope everything will be fine.
>
> Sincerely
>
> Ben

> -----原始邮件-----
> **发件人:**"Schountz,Tony" <
> **发送时间:**2018-10-18 21:59:58 (星期四)
> **收件人:** "胡犇" <huben >
> **抄送:**
> **主题:** Re: Re:Re: Final Program of the 8th International Symposium on Emerging Viral Diseases
>
> Hi Ben,
>
> It looks like heavy thunderstorms for my arrival in Tokyo. Hopefully, they will not delay my connection to Wuhan. If I miss the flight to Wuhan, I will email you so that you can let the driver know. Otherwise, I should see him/her in about 24 hours!
>
> Thanks,
>
> Tony
>
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University
>
> ---
>
> **From:** 胡犇 <huben
> **Sent:** Wednesday, October 17, 2018 9:54 AM
> **To:** Schountz,Tony
> **Subject:** Re:Re: Final Program of the 8th International Symposium on Emerging Viral Diseases
>
> Yes Dr.Schountz.

The pick-up from the airport to the hotel will be arranged.

Safe journey and see you soon.

Best

Ben

在 2018-10-17 23:41:10，"Schountz,Tony" 写道：

>Hi Ben,
>
>
>I just want to verify a driver will pick me up at the airport upon my arrival and take me to the hotel.
>
>
>Thank you,
>
>
>Tony

From: Jon Epstein ecohealthalliance.org>
Sent: Monday, February 10, 2020 11:57 AM EST
To: Munster, Vincent (NIH/NIAID) [E] >
CC: Schulz, Jonathan (NIH/NIAID) [F] Seifert, Stephanie (NIH/NIAID) [E] ; John Thompson Avanzato, Victoria (NIH/NIAID) [F] ; Sterling, Spencer >; Letko, Michael (NIH/NIAID) [F] >; Matson, Jeremiah (NIH/NIAID) [F] >; Fischer, Robert (NIH/NIAID) [F] ; Janine Seetahal >; Vernie Ramkissoon ; Tracey Goldstein ; Anthony, Simon J. >; Eric Laing >; Broder, Chris (USU-DoD) ; Christine Carrington >; Schountz,Tony >
Subject: Re: FW: Your article has been published by Oxford University Press

Excellent - congratulations Vincent and all!
-Jon

On Sun, Feb 9, 2020 at 11:38 AM Munster, Vincent (NIH/NIAID) [E] > wrote:

> Dear co-authors,
>
> Please find attached the final published version of our manuscript,
>
> Cheers,
>
> Vincent Munster, PhD
>
> Chief, Virus Ecology Section
>
> Laboratory of Virology
>
> Rocky Mountain Laboratories
>
> NIAID/NIH
>
> ---
>
> **From:** Oxford University Press >
> **Date:** Sunday, February 9, 2020 at 9:33 AM
> **To:** "vincent.munster " >
> **Cc:** "jid
> **Subject:** Your article has been published by Oxford University Press
>
> Dear Author,
>
> I am pleased to inform you that Oxford University Press has published your article in The Journal of Infectious Diseases.
>
> Here are the links to your online article:
>
> - Abstract: https://academic.oup.com/jid/advance-article-abstract/doi/10.1093/infdis/jiz648/5731483
> - Article (free access): https://academic.oup.com/jid/advance-article/doi/10.1093/infdis/jiz648/5731483?guestAccessKey=9bcac963-434c-4c19-9a74-e1d7c153984d
>
> These are persistent links that will always take you to your article, even if it is first published as an advance article ahead of being assigned to an issue.
>
> Please see below for additional information and the conditions of use for links.
>
> I trust that you have been perfectly satisfied with the service you have received. So that we can continue to improve, I should be very grateful if you would complete our questionnaire. There are only 6 short sections and it should take no

more than 10 minutes to complete. Please click the following link or paste it into your web browser to access the questionnaire: http://www.surveymonkey.com/s/VBN7YSP

Thank you for publishing with Oxford University Press, and I hope to be of service to you again soon.

Best wishes,

Author Support Team
Oxford University Press

Additional information (please read)

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There are several advantages to providing you with a free-access link to your article instead of a PDF file, including:

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- We guarantee that you (and your co-authors) will have continued access to your article without the responsibility of maintaining and updating these files.
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- The link may be posted to your personal/institutional website. However, the article should only be viewed from the Oxford Academic website and not posted to your own personal/institutional web site or that of other third parties.
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- The link must not be shared via social media.
- The link must not be shared through subject-based repositories.

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--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street, Ste. 1701

New York, NY 10001

web: ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

From: Jon Epstein ecohealthalliance.org>
Sent: Wednesday, October 21, 2020 4:05 PM EDT
To: Schountz,Tony >
Subject: Re: Genome paper

Yes! I agree.

Should we schedule a time to talk? So we can start to organize for writing this thing?

On Wed, Oct 21, 2020 at 3:33 PM Schountz,Tony > wrote:

> Jon, I suspect you've seen this?
>
> https://www.frontiersin.org/articles/10.3389/fmicb.2020.01807/full
>
> Should be quite helpful for the grant.
>
> T.
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520 Eighth Avenue, Ste. 1200

New York, NY 10018

)

web: ecohealthalliance.org

From: Miller,Charles
Sent: Monday, May 11, 2020 8:15 PM EDT
To: calisher >; Tom Ksiazek ; Tom Monath >; Tom Yuill ; Murphy, Frederick A. ; Schountz,Tony < >; Dick Bowen >; Paul Cryan ; Kathryn Holmes V. ; Kevin Olival ecohealthalliance.org>; Wilusz,Jeffrey ; Suchman,Erica < >; Kading,Rebekah >; Doug Watts >; Peter Drotman < >; Bill Shachtman >; Sarah Haworth ; Dan Calisher < ; Sean Evan >
Subject: Re: Good idea
Attachment(s): "bat.anus.jpg"

Hi Charlie, That billboard was great. One of my kids asked yesterday what I thought about a link on the coronavirus by Mercola so I read it--I have clipped part of it. The tissue from the "anus of a bat." Give me a break. This author on the fringe and others who are putting this stuff out for the most part know how to tweak the interest of the general public--pangolins for example seems to be an interesting model animal. CW ps Hi Tom Monath--I remember working with you many decades ago--simpler times and enjoyable times. After the vaccination against yellow fever my arm pit swelled up and when I asked you about it, you said, "better see your doctor." "Dr. Monath you are my doctor" I replied. I recovered to be able to fly fish the next day and haven't gotten YF yet!!!

From: calisher
Sent: Monday, May 11, 2020 12:50 PM
To: Tom Ksiazek Tom Monath ; Tom Yuill >; 'Murphy, Frederick A.' Miller,Charles Schountz,Tony >; Dick Bowen 'Paul Cryan' Kathryn Holmes V. < >; 'Kevin Olival' ecohealthalliance.org>; Wilusz,Jeffrey ; Suchman,Erica ; Kading,Rebekah ; Doug Watts >; Peter Drotman >; Bill Shachtman >; 'Sarah Haworth' >; 'Dan Calisher' ; Sean ; Evan
Subject: Good idea

How to Accelerate the Evolution of a Virus

As explained by Kennedy, the way they accelerate evolution is by taking the coronavirus from the anus of the bat and replicate it in animal tissue such as pangolin kidney tissue. Next, the grown viruses are placed on feral monkey kidney cells, followed by mouse brain tissue.

Each time you transfer the virus to another animal tissue, you increase the risk of zoonotic animal virus contamination in addition to mutations.

From: Tom Monath <
Sent: Tuesday, May 12, 2020 5:38 AM EDT
To: calisher >; Miller,Charles >; Tom Ksiazek ; Tom Yuill Murphy, Frederick A. Schountz,Tony ; Dick Bowen Paul Cryan ; Kathryn Holmes V. Kevin Olival ecohealthalliance.org>; Wilusz,Jeffrey >; Suchman,Erica >; Kading,Rebekah >; Doug Watts >; Peter Drotman ; Bill Shachtman ; Sarah Haworth ; Dan Calisher ; Sean Evan
Subject: RE: Good idea

I had forgotten this—you mean the USN let you work in Peru first w/out YF vaccine? I guess this was ok in Lima but ….

Thomas P Monath MD FASTMH
Principal Investigator, CEPI Nipah vaccine program
Managing Director & CSO
Crozet BioPharma LLC

From: calisher
Sent: Monday, May 11, 2020 8:28 PM
To: 'Miller,Charles' ; 'Tom Ksiazek' ; Tom Monath < 'Tom Yuill' >; 'Murphy, Frederick A.' < 'Schountz,Tony' ; 'Dick Bowen' 'Paul Cryan' ; 'Kathryn Holmes V.' ; 'Kevin Olival' ecohealthalliance.org>; 'Wilusz,Jeffrey' ; 'Suchman,Erica' ; 'Kading,Rebekah' < 'Doug Watts' < 'Peter Drotman' Bill Shachtman' ; 'Sarah Haworth' ; 'Dan Calisher' ; 'Sean' ; 'Evan' >
Subject: RE: Good idea

Sounds like you dodged the yellow fever virus but not the vaccine.

Charlie

From: Miller,Charles <
Sent: Monday, May 11, 2020 6:16 PM
To: calisher Tom Ksiazek >; Tom Monath Tom Yuill 'Murphy, Frederick A.' ; Schountz,Tony >; Dick Bowen ; 'Paul Cryan' ; Kathryn Holmes V. ; 'Kevin Olival' ecohealthalliance.org>; Wilusz,Jeffrey ; Suchman,Erica ; Kading,Rebekah Doug Watts ; Peter Drotman ; Bill Shachtman Sarah Haworth' ; 'Dan Calisher' ; Sean Evan <
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>;

From: Schountz,Tony
Sent: Friday, May 11, 2018 12:01 PM EDT
To: 胡犇 <huben >
CC: Schountz,Tony ; 石正丽 <zlshi 周鹏 <peng.zhou
Subject: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Hi Ben,

I have my flight booked and will arrive in Wuhan at 10:00 PM on October 19 (All Nippon Airways **NH 937**). Can you tell me the name and address of the hotel? I will need it for my visa and for my university administrators.

Thank you,

Tony

> On Apr 9, 2018, at 8:06 AM, 胡犇 <huben > wrote:
>
> Dear Dr.Schountz:
>
> The 8th International Symposium on Emerging Viral Diseases will be held in October 20-22, 2018, in Wuhan, China. The biennial symposium is organized by Wuhan Institute of Virology, Chinese Academy of Sciences and has become an important event for leading Chinese and international virologists to discuss cutting-edge science on emerging viruses as well as to foster global collaborations.
>
> Prof Zhengli Shi and Dr.Peng Zhou had a nice experience last year in Colorado when attending the symposium on bat-borne infectious diseases, and we know you have made great contributions to bat virus researches. We sincerely hope that you can attend the symposium. Please find enthe formal invitation letter for the meeting.
>
> If you have any question regarding the conference, please contact me.
>
> Thank you!
>
> Best regards
>
> Ben Hu Ph.D
>
> Research Assistant
>
> Secretary of the 8th International Symposium on Emerging Viral Diseases
>
> Wuhan Institute of Virology, Chinese Academy of Sciences
> Wuhan 430071, P.R. China
>
> <Invitation letter Tony Schountz.pdf>

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Kevin Olival, PhD ecohealthalliance.org>
Sent: Monday, April 10, 2017 10:08 AM EDT
To: Schountz,Tony
CC: Jon Epstein ecohealthalliance.org>
Subject: Re: Invited talks

Hi Tony,

Just wondering if you need a full abstract submitted by the end of this week for my talk?

Cheers,
Kevin

On Mar 29, 2017, at 4:48 PM, Kevin Olival, PhD ecohealthalliance.org> wrote:

Tony, gave a thought to what I'd like to present, and we've done a bunch of new stuff to build models to estimate viral richness in bats and further examine patterns in viral sharing. Thoughts this would be of general interest to the group. This builds on analyses using previously published data (literature reviews) from our own group and others (e.g. Luis et al.); but will also include some analysis of recent field data from PREDICT and other EHA projects.

Title: "Estimating viral richness and viral sharing in bats: integrating previously-published and newly-aquired field data".

Cheers,
Kevin

Kevin J. Olival, PhD

Associate Vice President for Research

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

On Mar 27, 2017, at 5:28 PM, Schountz,Tony > wrote:

It would be great if I could have titles by Wednesday. I want to get the web page updated with the invited speaker list.

Thanks,

Tony

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we've done with global data on bat virus associations; network models; etc; some of it still in the works - but will be done by June!

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www.ecohealthalliance.org

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I hope you're still planning to attend the symposium. I am just now getting around to sending out emails to invited speakers and would like to invite each of you to give talks. If so, could you email me your provisional titles?

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From: Schountz,Tony >
Sent: Monday, March 27, 2017 5:28 PM EDT
To: Kevin Olival, PhD ecohealthalliance.org>
CC: Schountz,Tony ; Jon Epstein ecohealthalliance.org>
Subject: Re: Invited talks

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> > College of Veterinary Medicine
> > Colorado State University

From: Jon Epstein ecohealthalliance.org>
Sent: Wednesday, March 29, 2017 4:42 PM EDT
To: Schountz,Tony
CC: Kevin Olival, PhD ecohealthalliance.org>
Subject: Re: Invited talks

Tony,
My talk: "Using serology to understand the dynamics of concurrent viral infections in pteropid bats"

Cheers,
Jon

On Mon, Mar 27, 2017 at 5:28 PM, Schountz,Tony > wrote:

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Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

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460 West 34th Street – 17th floor
New York, NY 10001

web: ecohealthalliance.org

-

From: Jon Epstein ecohealthalliance.org>
Sent: Monday, March 27, 2017 5:30 PM EDT
To: Schountz,Tony
CC: Kevin Olival, PhD ecohealthalliance.org>
Subject: Re: Invited talks

Thanks Tony.
I'm planning to come as well. I'll send something by Wednesday.
-Jon

On Mon, Mar 27, 2017 at 5:28 PM, Schountz,Tony > wrote:

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From: Kevin Olival, PhD ecohealthalliance.org>
Sent: Monday, April 10, 2017 12:01 PM EDT
To: Schountz,Tony
Subject: Re: Invited talks

Ok, thanks Tony. Looking forward to it!

Kevin J. Olival, PhD

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On Apr 10, 2017, at 11:16 AM, Schountz,Tony > wrote:

No, just the title for now. I'll need an abstract in a few weeks for the program. I already have you listed on the web site with your title.

I've received quite a few abstracts - more than the last time, it seems, so I think it will shape up to be another good meeting.

Thanks,

T.

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> Colorado State University

From: Ebel,Greg >
Sent: Monday, March 30, 2020 11:39 AM EDT
To: Kendall,Lon >; Bowen,Richard >; Bosco-Lauth,Angela Schountz,Tony epstein ecohealthalliance.org>; Dean,Gregg >; Szalai,Edit
Subject: RE: Meeting agenda

Hi Lon,

Thanks for doing this. I think the agenda looks good.

Greg

From: Kendall,Lon >
Sent: Monday, March 30, 2020 9:32 AM
To: Bowen,Richard < ; Bosco-Lauth,Angela >; Schountz,Tony ; epstein ecohealthalliance.org>; Ebel,Greg >; Dean,Gregg >; Szalai,Edit >
Subject: Meeting agenda

All,

Here is a proposed agenda for tomorrows meeting. Please edit freely.

Introduction
Lon- why meeting was initially organized, then turf to Jon (I won't be long)
Jon- provide background about program discussions with CSU and NIAID and why we are here (Jon really sparked this discussion, and is probably best to lead)
Jean- Discuss NIAID possibilities and expectations and what's needed from CSU (Thought Jean should go sooner to help frame discussion below. I will send her agenda once we get it finalized)
Ebel- Discuss CVID abilities, and possibilities related to emerging disease, prior C06
Tony- Discuss current research and potential needs
Bowen/Angela- Discuss current research and potential needs
Determine next steps

Lon

Lon V. Kendall, DVM, PhD, DACLAM
Director, Laboratory Animal Resources and
Attending Veterinarian, Colorado State University

From: Jon Epstein ecohealthalliance.org>
Sent: Monday, March 30, 2020 12:05 PM EDT
To: Kendall,Lon
CC: Bowen,Richard >; Bosco-Lauth,Angela
Schountz,Tony ; Ebel,Greg >; Dean,Gregg
Szalai,Edit >; jean.patterson >
Subject: Re: Meeting agenda

Hi,
Looks good. I noticed Jean wasn't copied on the email and added her in.

Cheers,
Jon

On Mon, Mar 30, 2020 at 11:31 AM Kendall,Lon wrote:

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Jonathan H. Epstein DVM, MPH, PhD

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web: ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

From: Angela Bosco-Lauth
Sent: Monday, March 30, 2020 4:25 PM EDT
To: epstein ecohealthalliance.org>
CC: Kendall,Lon >; Bowen,Richard >; Bosco-Lauth,Angela >; Schountz,Tony ; Ebel,Greg >; Dean,Gregg >; Szalai,Edit jean.patterson
Subject: Re: Meeting agenda

Agenda looks good, thanks Lon!
Angela

Angela Bosco-Lauth
Department of Biomedical Sciences
Colorado State University

On Mon, Mar 30, 2020 at 10:06 AM Jon Epstein ecohealthalliance.org> wrote:

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CC: Bowen,Richard >; Bosco-Lauth,Angela >; Schountz,Tony < >; epstein ecohealthalliance.org>; Ebel,Greg >; Dean,Gregg >; Szalai,Edit < >
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> Jon- provide background about program discussions with CSU and NIAID and why we are here (Jon really sparked this discussion, and is probably best to lead)
> Jean- Discuss NIAID possibilities and expectations and what's needed from CSU (Thought Jean should go sooner to help frame discussion below. I will send her agenda once we get it finalized)
> Ebel- Discuss CVID abilities, and possibilities related to emerging disease, prior C06
> Tony- Discuss current research and potential needs
> Bowen/Angela- Discuss current research and potential needs
> Determine next steps
>
> Lon
>
> Lon V. Kendall, DVM, PhD, DACLAM
> Director, Laboratory Animal Resources and
> Attending Veterinarian, Colorado State University
>
> Colorado State University
> Fort Collins, CO 80523

From: Jon Epstein ecohealthalliance.org>
Sent: Monday, October 19, 2020 4:38 PM EDT
To: Schountz,Tony
Subject: Re: Monoclonal antibodies

Awesome - and agree.
I would like to brainstorm together for the letters before we approach anyone. I'll start a google doc and we can live edit it.
Let's think about who the 'dream team' will be for this.
It also occurred to me - what do you think about building in a facility in Bangladesh where we keep a captive breeding colony, that would serve as a feeder if we need more bats along the way? We could develop and fund a closed colony there, like what Cambridge did in Ghana, and we'd know the status of each bat. Brian Pope would be great at helping set this up. And it would allow the colony at CSU to fluctuate a bit in size, and we could pull in new bats as needed. I think it's a nice insurance policy to support the colony in CO as we develop it. This could be something I would manage - but I think we could convince the govt and if we provide all the funding for construction and upkeep, it could really happen.

Thoughts?

On Mon, Oct 19, 2020 at 4:27 PM Schountz,Tony > wrote:

> Jon, I think a really important part of the grant will be to make monoclonal antibodies to various proteins (e.g., CD antigens, cytokines) and cytokines as reagents. If you agree, I'd like to approach a colleague of my, Brian Geiss, to see if he is willing to be on the grant. Recombinant protein expression is his "thing" and he would be a great asset for the grant.
>
> I also think we should get as many letters of support that we can get. I can probably get at least 10 from people we've helped over the years (provided tissues and cells, conducted experimental infections, etc.).
>
> Let me know what you think.
>
> Just moved into our new building. It is really sweet. :)
>
> Thanks,
>
> T.
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

web: ecohealthalliance.org

From: Jon Epstein ecohealthalliance.org>
Sent: Wednesday, April 01, 2020 1:00 AM EDT
To: Schountz,Tony >
Subject: Re: Multimammate rats

Tony,
I wasn't able to work on this tonight - I'm going to have to pick it up tomorrow afternoon.
I got a letter of support from Vincent.
-Jon

On Tue, Mar 31, 2020 at 5:35 PM Schountz,Tony > wrote:

> Jon, I've gotten tied up with some unanticipated things so I probably can't get you anything before you start working on it. Please send to me and I'll get on it tonight and have it to you tomorrow morning.
>
> Thanks,
>
> T.
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

> On Mar 31, 2020, at 11:57 AM, Jon Epstein ecohealthalliance.org> wrote:
>
> Wow. You're doing some great stuff. I'm always amazing at how quickly you can spin up these experimental infections. I think we should include a US species in our proposal so we can help address questions of US relevance in terms of spillback. I can find out which ones NWHC is using.
> -Jon
>
> On Tue, Mar 31, 2020 at 1:24 PM Schountz,Tony > wrote:
>
> > We might know that soon. One of the bats we euthanized yesterday was pregnant.
> >
> > —
> > Tony Schountz, PhD
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> > Colorado State University
>
> > On Mar 31, 2020, at 11:22 AM, Jon Epstein ecohealthalliance.org> wrote:
> >
> > I don't know either. We could try to catch them while pregnant. I also don't know if there's vertical transmission. This will be challenging, but I'm confident we can get to a point where we can safely ship. Maybe if they go straight into a BL3 facility, CDC will have less concern.
> > -Jon
> >
> > On Tue, Mar 31, 2020 at 12:50 PM Schountz,Tony > wrote:
> >
> > > RML imported the Lassa virus reservoir by having them born in captivity in Africa, then the offspring were imported directly to RML. Don't know if horseshoe bats can be born in captivity, but that could be an avenue to alleviate CDC concerns.
> > > —
> > > Tony Schountz, PhD
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> > > Department of Microbiology, Immunology and Pathology
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Sent: Tuesday, March 31, 2020 1:22 PM EDT
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Subject: Re: Multimammate rats

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Jonathan H. Epstein DVM, MPH, PhD

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New York, NY 10001

)

web: ecohealthalliance.org

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Sent: Tuesday, March 31, 2020 1:57 PM EDT
To: Schountz,Tony
Subject: Re: Multimammate rats

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New York, NY 10001

web: ecohealthalliance.org

From: Park, Eun-Chung (NIH/NIAID) [E]
Sent: Thursday, March 29, 2018 4:59 AM EDT
To: Jon Epstein ecohealthalliance.org>; Cassetti, Cristina (NIH/NIAID) [E] ; Repik, Patricia (NIH/NIAID) [E] >
CC: Schountz,Tony ; Linfa Wang >
Subject: RE: Nature Lab Animal story on Bat research

Thank you—all-star cast!

Sincerely,
Eunchung

From: Jon Epstein [mailto ecohealthalliance.org]
Sent: Tuesday, March 27, 2018 12:45 PM
To: Cassetti, Cristina (NIH/NIAID) [E] ; Park, Eun-Chung (NIH/NIAID) [E] >; Repik, Patricia (NIH/NIAID) [E] <
Cc: Schountz, Tony >; Linfa Wang >
Subject: Nature Lab Animal story on Bat research

Dear Cristina, Eun-Chung and Pat,
Attached is a news piece from Nature: Lab Animal, out yesterday, about the current state of bat research and the need for new lab animal models and reagents. It features a few folks you all may know ;)

Hope you're doing well.

Cheers,
Jon

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

web: ecohealthalliance.org

-

From: Jon Epstein ecohealthalliance.org>
Sent: Thursday, March 19, 2020 6:01 PM EDT
To: Rudolph,Alan
CC: VPR Bridge Line 2 Kendall,Lon
Bowen,Richard < Angela Bosco-Lauth ; Schountz,Tony
; Ebel,Greg <
Subject: Re: NIH R24 + C06 (update w/ Jon Epste

hi 1 minute....

On Thu, Mar 19, 2020 at 5:25 PM Rudolph,Alan wrote:

> Dial (no passcode required)
> Background e-mail attached.
>
> Thanks!
> Linda
>
> Linda M. Foster, Executive Assistant to the Vice President and Sr. Associate VP for Research
> Colorado State University – Office of the Vice President for Research

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street, Ste. 1701

New York, NY 10001

web: ecohealthalliance.org

From: Richard Bowen
Sent: Wednesday, March 18, 2020 1:18 AM EDT
To: Foster,Linda
CC: Ebel,Greg ; Jon Epstein ecohealthalliance.org>; Kendall,Lon ; Rudolph,Alan >; Schountz,Tony

Subject: Re: NIH R24 + C06

Sorry I missed the call, let me know if I can help in any way

On Mon, Mar 16, 2020 at 10:16 Foster,Linda > wrote:

> This call is set for today at 11 am MT (1 pm ET).
>
> Thanks!
>
> Linda
>
> Linda M. Foster, Executive Assistant to the Vice President and Sr. Associate VP for Research
>
> Colorado State University – Office of the Vice President for Research
>
> **From:** Jon Epstein ecohealthalliance.org>
> **Sent:** Monday, March 16, 2020 9:27 AM
> **To:** Rudolph,Alan
> **Cc:** Schountz,Tony >; Ebel,Greg >; Kendall,Lon ; Richard Bowen >; Foster,Linda
>
> **Subject:** Re: NIH R24 + C06
>
> Thanks all,
>
> I look forward to the discussion.
>
> Cheers,
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> Jon
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> On Mon, Mar 16, 2020 at 11:23 AM Rudolph,Alan > wrote:
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>> Alan, we would need to have access to a room or building large enough to house large flying foxes as well as smaller horseshoe bats. I know the barn at ARBL was once available but I suspect it no longer is?
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--
R. A. Bowen Colorado State University

From: Schountz,Tony
Sent: Monday, March 16, 2020 11:22 AM EDT
To: Schountz,Tony <
CC: Jon Epstein ecohealthalliance.org>; Ebel,Greg ; Rudolph,Alan Kendall,Lon >; Richard Bowen
Subject: Re: NIH R24 + C06

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Alan, can you help arrange the call through your office?

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From: Jon Epstein ecohealthalliance.org>
Sent: Monday, March 16, 2020 12:08 PM EDT
To: Foster,Linda >
CC: Kendall,Lon >; Richard Bowen ; Ebel,Greg >; Schountz,Tony >; Rudolph,Alan

Subject: Re: NIH R24 + C06

Sorry, Is this CST?
I'm in NY and just confirming the time.
I could do a call at 1pm ET or 2pm ET
-Jon

On Mon, Mar 16, 2020 at 12:00 PM Foster,Linda > wrote:

> Is everyone on board with a call today at 11 am?

From: Kendall,Lon >
Sent: Monday, March 16, 2020 9:56 AM
To: Foster,Linda >; Jon Epstein ; Richard Bowen ; Ebel,Greg >; Schountz,Tony

Cc: Rudolph,Alan
Subject: RE: NIH R24 + C06

These are best for me.

3/16 11-12 and 1-2

3/17 8-9 and 4-5

Lon V. Kendall, DVM, PhD, DACLAM

Director, Laboratory Animal Resources and

Attending Veterinarian, Colorado State University

From: Foster,Linda
Sent: Monday, March 16, 2020 9:38 AM
To: Jon Epstein ecohealthalliance.org>; Richard Bowen <r ; Kendall,Lon ; Ebel,Greg >; Schountz,Tony >
Cc: Rudolph,Alan >; Foster,Linda
Subject: RE: NIH R24 + C06

Alan is currently available to connect by phone, MT:

- Monday, 3/16 – 11-12; 12-1; 1-2;
- Tuesday, 3/17 – 8-9; 4-5.

Please let me know your availability and I'll confirm via Outlook with a conference line

Thanks,

Linda

Linda M. Foster, Executive Assistant to the Vice President and Sr. Associate VP for Research

Colorado State University – Office of the Vice President for Research

From: Jon Epstein ecohealthalliance.org>
Sent: Monday, March 16, 2020 9:27 AM
To: Rudolph,Alan >
Cc: Schountz,Tony >; Ebel,Greg >; Kendall,Lon >; Richard Bowen >; Foster,Linda

Subject: Re: NIH R24 + C06

Thanks all,

I look forward to the discussion.

Cheers,

Jon

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EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

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From: Jon Epstein ecohealthalliance.org>
Sent: Thursday, March 19, 2020 4:09 PM EDT
To: Foster,Linda
CC: Rudolph,Alan ; Schountz,Tony ; Kendall,Lon ; Richard Bowen >; Ebel,Greg
Subject: Re: NIH R24 + C06

Hi Linda and all,
Is there any way for this team to jump on a 10 minute call this afternoon or tomorrow morning?
I have news from NIAID to share.
Ideally, 6pm ET

-Jon

On Mon, Mar 16, 2020 at 12:16 PM Foster,Linda wrote:

> This call is set for today at 11 am MT (1 pm ET).
>
> Thanks!
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> Linda M. Foster, Executive Assistant to the Vice President and Sr. Associate VP for Research
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Colorado State University – Office of the Vice President for Research

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From: Jon Epstein ecohealthalliance.org>
Sent: Monday, March 16, 2020 11:26 AM EDT
To: Rudolph,Alan >
CC: Schountz,Tony >; Ebel,Greg ; Kendall,Lon ; Richard Bowen Foster,Linda >
Subject: Re: NIH R24 + C06

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From: Foster,Linda >
Sent: Monday, March 16, 2020 12:12 PM EDT
To: Jon Epstein ecohealthalliance.org>
CC: Kendall,Lon ; Richard Bowen >; Ebel,Greg >; Schountz,Tony ; Rudolph,Alan >
Subject: RE: NIH R24 + C06

It is Mountain Time so I'll go ahead and set it for 11 am (1 pm ET). Hopefully it fits for all? Please call to connect (no passcode required). Thanks! Linda

From: Jon Epstein ecohealthalliance.org>
Sent: Monday, March 16, 2020 10:08 AM
To: Foster,Linda >
Cc: Kendall,Lon >; Richard Bowen >; Ebel,Greg >; Schountz,Tony < >; Rudolph,Alan
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-Jon

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> **Cc:** Rudolph,Alan <
> **Subject:** RE: NIH R24 + C06
>
> These are best for me.
>
> 3/16 11-12 and 1-2
> 3/17 8-9 and 4-5
>
> Lon V. Kendall, DVM, PhD, DACLAM
> Director, Laboratory Animal Resources and
> Attending Veterinarian, Colorado State University
>
> Colorado State University
> Fort Collins, CO 80523
>
> **From:** Foster,Linda >
> **Sent:** Monday, March 16, 2020 9:38 AM
> **To:** Jon Epstein ecohealthalliance.org>; Richard Bowen < ; Kendall,Lon ; Ebel,Greg < Schountz,Tony >
> **Cc:** Rudolph,Alan >; Foster,Linda >
> **Subject:** RE: NIH R24 + C06
>
> Alan is currently available to connect by phone, MT:
>
> - Monday, 3/16 – 11-12; 12-1; 1-2;
> - Tuesday, 3/17 – 8-9; 4-5.
>
> Please let me know your availability and I'll confirm via Outlook with a conference line
>
> Thanks,
> Linda
>
> Linda M. Foster, Executive Assistant to the Vice President and Sr. Associate VP for Research
> Colorado State University – Office of the Vice President for Research

From: Jon Epstein ecohealthalliance.org>
Sent: Monday, March 16, 2020 9:27 AM
To: Rudolph,Alan >
Cc: Schountz,Tony ; Ebel,Greg >; Kendall,Lon ; Richard Bowen ; Foster,Linda >
Subject: Re: NIH R24 + C06

Thanks all,
I look forward to the discussion.
Cheers,
Jon

On Mon, Mar 16, 2020 at 11:23 AM Rudolph,Alan wrote:

> Tony
>
> Copying Linda Foster to help arrange.
>
> Thanks Alan
>
> Sent from my iPad
>
> > On Mar 16, 2020, at 9:22 AM, Schountz,Tony wrote:
> >
> > All, just adding Lon Kendall to the email string. He has assured me there is space for the horseshoe bats and probably for the pteropid bats, but he would like to be on the conference call for this discussion.
> >
> > Alan, can you help arrange the call through your office?
> >
> > Thanks,
> >
> > Tony
> > —
> > Tony Schountz, PhD
> > Associate Professor
> > Arthropod-borne and Infectious Disease Laboratory
> > Department of Microbiology, Immunology and Pathology
> > College of Veterinary Medicine
> > Colorado State University
> >
>
> >
> >> On Mar 13, 2020, at 4:58 PM, Schountz,Tony > wrote:
> >>
> >> Alan and Greg, as you know I chatted with Jon Epstein yesterday. He has had discussions with NIH about interest in having a grant submission regarding bats and SARS-CoV-2 and other coronaviruses. I think the four of us ought to have a conference call next week to see if we can make something work.
> >>
> >> Alan, we would need to have access to a room or building large enough to house large flying foxes as well as smaller horseshoe bats. I know the barn at ARBL was once available but I suspect it no longer is?
> >>
> >> Thanks,
> >>
> >> T.
> >> —
> >> Tony Schountz, PhD
> >> Associate Professor
> >> Arthropod-borne and Infectious Disease Laboratory
> >> Department of Microbiology, Immunology and Pathology
> >> College of Veterinary Medicine
> >> Colorado State University
> >>
>
> >>
> >

--

From: Ebel,Greg >
Sent: Saturday, March 14, 2020 12:14 PM EDT
To: Schountz,Tony ; Jon Epstein ecohealthalliance.org>; Rudolph,Alan

Subject: Re: NIH R24 + C06

Hi all,
Absolutely. With spring break and school closures I expect that my life will be a bit bananas but let's set up a zoom to discuss. I'll make it work!
Greg

Get Outlook for iOS

From: Schountz,Tony
Sent: Friday, March 13, 2020 4:58:39 PM
To: Jon Epstein ecohealthalliance.org>; Ebel,Greg < ; Rudolph,Alan

Subject: NIH R24 + C06

Alan and Greg, as you know I chatted with Jon Epstein yesterday. He has had discussions with NIH about interest in having a grant submission regarding bats and SARS-CoV-2 and other coronaviruses. I think the four of us ought to have a conference call next week to see if we can make something work.

Alan, we would need to have access to a room or building large enough to house large flying foxes as well as smaller horseshoe bats. I know the barn at ARBL was once available but I suspect it no longer is?

Thanks,

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine

From: Jon Epstein ecohealthalliance.org>
Sent: Wednesday, April 15, 2020 9:37 AM EDT
To: Schountz,Tony
Subject: Re: NSF bat immunology interest

Nice.

Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
New York

On Wed, Apr 15, 2020, 9:13 AM Schountz,Tony > wrote:

> Yes, we're going to target T cells and the innate response in Jamaican fruit bats to see how it impacts viral shedding, tissue tropism and disease (if any).
>
> T.
>
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

From: Jon Epstein ecohealthalliance.org>
Sent: Wednesday, April 15, 2020 12:06 AM
To: Schountz,Tony
Subject: Re: NSF bat immunology interest

Tony,
Are you planning to apply?
-Jon

On Tue, Apr 14, 2020 at 6:48 PM Schountz,Tony wrote:

> Hi everyone,
>
> I hope you are all safe.
>
> I wanted to let you know about two NSF programs that have urgent deadlines (first week of May) that has bat immunology as its principal interest. The first is a RAPID for 12 months/$200k (including direct costs) and EAGER for 2 years/$300k (including direct costs). The NSF contact is Dr. Joanna Shisler . My understanding is they are interested in the biology of bat immune systems relevant to coronaviruses, but because of the potential spill back issues they will also consider nonviral diseases, including white nose syndrome. I don't have other information but I'm sure Dr. Shisler will be happy to chat with you if you are interested.
>
> If you know of others who are interested in the biology of bat immunity, please pass this email along to them.
>
> Thanks,
>
> Tony
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory

From: Jon Epstein ecohealthalliance.org>
Sent: Wednesday, April 15, 2020 2:06 AM EDT
To: Schountz,Tony >
Subject: Re: NSF bat immunology interest

Tony,
Are you planning to apply?
-Jon

On Tue, Apr 14, 2020 at 6:48 PM Schountz,Tony > wrote:

> Hi everyone,
>
> I hope you are all safe.
>
> I wanted to let you know about two NSF programs that have urgent deadlines (first week of May) that has bat immunology as its principal interest. The first is a RAPID for 12 months/$200k (including direct costs) and EAGER for 2 years/$300k (including direct costs). The NSF contact is Dr. Joanna Shisler My understanding is they are interested in the biology of bat immune systems relevant to coronaviruses, but because of the potential spill back issues they will also consider nonviral diseases, including white nose syndrome. I don't have other information but I'm sure Dr. Shisler will be happy to chat with you if you are interested.
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> Tony Schountz, PhD
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> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street, Ste. 1701

New York, NY 10001

web: ecohealthalliance.org

From: Jon Epstein ecohealthalliance.org>
Sent: Tuesday, June 23, 2020 3:45 PM EDT
To: Schountz,Tony >
CC: bpope ; Ebel,Greg >
Subject: Re: Pteropus space requirements

Good, Tony. We do have a real opportunity here. I spoke with Jean again, and I think if we can find a way to make this work, we'll be in a strong position to get substantial research support from NIH. My gut says that longer-term, if we're successful with the startup, we could find ways to bring in money to expand the infrastructure.

Good luck with these conversations. Please let me know if there's anything you need from me that could help.

Cheers,
Jon

On Tue, Jun 23, 2020 at 3:36 PM Schountz,Tony wrote:

> Hi Jon,
>
> We'd like to move this forward, but we will have to get support from a few levels above us. Give us a week or so to see what progress we can make.
>
> Thanks,
>
> Tony
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

> On Jun 18, 2020, at 8:40 AM, Jon Epstein ecohealthalliance.org> wrote:
>
> Thanks so much Brian.
> It sounds like the space might be too small for the size colony we were thinking of founding (as you noted, Greg). We should discuss whether a smaller founder colony might still make sense given the opportunity we have. I think the consideration is whether the colony could produce a sufficient birth cohort each year to allow for meaningful research. For example, if we reduced the planned size from 40 to 20, with 3 males and 17 females, with 15 expected to produce pups each year, we'd have 35 bats in Y1 - still within capacity. And we could plan to use most if not all of F1. Long term, we would just have to manage the colony to keep it within size. We could selectively breed a subgroup of females in alternate years, as well.
>
> Just brainstorming here. Tony and Greg, please weigh in. Meanwhile, I'm also going to speak with Jean to push back on the need for construction money to build a bigger facility.
>
> Cheers,
> Jon

> On Mon, Jun 8, 2020 at 2:57 PM Brian Pope wrote:
>
>> Jon,
>>
>> Based on Association of Zoos and Aquariums Bat Taxon Advisory Group space requirements, you can fit approximately 38 bats in a 2500 sq. ft. building. Keep in mind these are AZA requirements and wouldn't affect your holding or operation. That being said, you want the bats to be in an environment that limits stress, provides for natural behaviors, and is ultimately conducive to proper research. Please provide specifics on the building - images, dimensions (including ceiling height), existing facilities, etc?
>>
>> Food storage wouldn't take up much (ours is 160 sq. ft. and that holds diet for 200 bats with plenty of room to spare). Where would the diet be prepared?

An appropriate exam room should be sufficient to not only perform procedures but also hold bats that may be injured. 300-400 sq. ft. should suffice.

Brian Pope

Director

Lubee Bat Conservancy

http://www.lubee.org

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GIANT FLYING FOX CAM

MIXED SPECIES FLYING FOX CAM

From: Jon Epstein [mailto ecohealthalliance.org]
Sent: Wednesday, June 3, 2020 10:57 AM
To: Brian Pope
Cc: Ebel,Greg ; Tony Schountz
Subject: Pteropus space requirements

Hi Brian,

I wanted to introduce you to Professor Greg Ebel, who's the Director of the Arthropod-Borne and Infectious Disease Lab at Colorado State and who's recently become a partner in our efforts, with Tony Shountz, to establish a Pteropus breeding colony there. We're trying to get an accurate understanding of the physical space required for the proposed colony, which if you recall we had discussed starting with 40 bats (4 male, 36 female) which would then become about 60-70 bats post breeding.

Could you help give us a sense of what physical space you think would be necessary in terms of a holding / flight cage, plus support rooms like food storage and a handling / exam area? We've got an existing building on campus that's abou 2500 sq ft that could be gutted & equipped as needed, but the concern is that it's just not big enough for the planned number of bats.

Thanks for your help in thinking through this.

Cheers,

Jon

--

From: Schountz,Tony
Sent: Tuesday, June 23, 2020 3:36 PM EDT
To: epstein ecohealthalliance.org>
CC: bpope ; Ebel,Greg ; Schountz,Tony

Subject: Re: Pteropus space requirements

Hi Jon,

We'd like to move this forward, but we will have to get support from a few levels above us. Give us a week or so to see what progress we can make.

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Jun 18, 2020, at 8:40 AM, Jon Epstein ecohealthalliance.org> wrote:

Thanks so much Brian.
It sounds like the space might be too small for the size colony we were thinking of founding (as you noted, Greg). We should discuss whether a smaller founder colony might still make sense given the opportunity we have. I think the consideration is whether the colony could produce a sufficient birth cohort each year to allow for meaningful research. For example, if we reduced the planned size from 40 to 20, with 3 males and 17 females, with 15 expected to produce pups each year, we'd have 35 bats in Y1 - still within capacity. And we could plan to use most if not all of F1. Long term, we would just have to manage the colony to keep it within size. We could selectively breed a subgroup of females in alternate years, as well.

Just brainstorming here. Tony and Greg, please weigh in. Meanwhile, I'm also going to speak with Jean to push back on the need for construction money to build a bigger facility.

Cheers,
Jon

On Mon, Jun 8, 2020 at 2:57 PM Brian Pope > wrote:

> Jon,
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> Food storage wouldn't take up much (ours is 160 sq. ft. and that holds diet for 200 bats with plenty of room to spare). Where would the diet be prepared?
>
> An appropriate exam room should be sufficient to not only perform procedures but also hold bats that may be injured. 300-400 sq. ft. should suffice.
>
> Brian Pope
>
> Director
>
> Lubee Bat Conservancy

http://www.lubee.org

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GIANT FLYING FOX CAM

MIXED SPECIES FLYING FOX CAM

From: Jon Epstein [mailto ecohealthalliance.org]
Sent: Wednesday, June 3, 2020 10:57 AM
To: Brian Pope < >
Cc: Ebel,Greg >; Tony Schountz
Subject: Pteropus space requirements

Hi Brian,

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Thanks for your help in thinking through this.

Cheers,

Jon

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street, Ste. 1701

New York, NY 10001

From: Brian Pope
Sent: Monday, June 08, 2020 2:57 PM EDT
To: epstein ecohealthalliance.org>
CC: Ebel,Greg Schountz,Tony <
Subject: RE: Pteropus space requirements

Jon,

Based on Association of Zoos and Aquariums Bat Taxon Advisory Group space requirements, you can fit approximately 38 bats in a 2500 sq. ft. building. Keep in mind these are AZA requirements and wouldn't affect your holding or operation. That being said, you want the bats to be in an environment that limits stress, provides for natural behaviors, and is ultimately conducive to proper research. Please provide specifics on the building - images, dimensions (including ceiling height), existing facilities, etc?

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Brian Pope
Director
Lubee Bat Conservancy

http://www.lubee.org
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From: Jon Epstein ecohealthalliance.org]
Sent: Wednesday, June 3, 2020 10:57 AM
To: Brian Pope
Cc: Ebel,Greg ; Tony Schountz
Subject: Pteropus space requirements

Hi Brian,
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Cheers,
Jon

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Jonathan H. Epstein DVM, MPH, PhD
Vice President for Science and Outreach
EcoHealth Alliance
460 West 34th Street, Ste. 1701
New York, NY 10001

web: ecohealthalliance.org

From: Jon Epstein ecohealthalliance.org>
Sent: Thursday, June 18, 2020 10:40 AM EDT
To: bpope
CC: Ebel,Greg Schountz,Tony >
Subject: Re: Pteropus space requirements

Thanks so much Brian.
It sounds like the space might be too small for the size colony we were thinking of founding (as you noted, Greg). We should discuss whether a smaller founder colony might still make sense given the opportunity we have. I think the consideration is whether the colony could produce a sufficient birth cohort each year to allow for meaningful research. For example, if we reduced the planned size from 40 to 20, with 3 males and 17 females, with 15 expected to produce pups each year, we'd have 35 bats in Y1 - still within capacity. And we could plan to use most if not all of F1. Long term, we would just have to manage the colony to keep it within size. We could selectively breed a subgroup of females in alternate years, as well.

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Cheers,
Jon

On Mon, Jun 8, 2020 at 2:57 PM Brian Pope wrote:

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Sent: Wednesday, June 3, 2020 10:57 AM
To: Brian Pope
Cc: Ebel,Greg ; Tony Schountz
Subject: Pteropus space requirements

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Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street, Ste. 1701

New York, NY 10001

web: ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street, Ste. 1701

New York, NY 10001

From: Jon Epstein ecohealthalliance.org>
Sent: Thursday, July 23, 2020 5:33 PM EDT
To: Schountz,Tony ; Ebel,Greg >
Subject: Re: Pteropus space requirements

Greg and Tony,
I'm just checking in to see if you've had further discussion and would like to move forward with this effort. I was contacted again by Jean. She's *very* supportive of us moving on an R24 application. Let me know if you'd like to talk.

Cheers,
Jon

On Tue, Jun 23, 2020 at 3:45 PM Jon Epstein ecohealthalliance.org> wrote:

> Good, Tony. We do have a real opportunity here. I spoke with Jean again, and I think if we can find a way to make this work, we'll be in a strong position to get substantial research support from NIH. My gut says that longer-term, if we're successful with the startup, we could find ways to bring in money to expand the infrastructure.
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> Tony
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> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
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> Colorado State University

On Jun 18, 2020, at 8:40 AM, Jon Epstein ecohealthalliance.org> wrote:

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Brian Pope

Director

Lubee Bat Conservancy

http://www.lubee.org

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GIANT FLYING FOX CAM

MIXED SPECIES FLYING FOX CAM

From: Jon Epstein ecohealthalliance.org]
Sent: Wednesday, June 3, 2020 10:57 AM
To: Brian Pope
Cc: Ebel,Greg >; Tony Schountz
Subject: Pteropus space requirements

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Thanks for your help in thinking through this.

Cheers,

From: Ebel,Greg <
Sent: Tuesday, September 29, 2020 1:10 PM EDT
To: epstein ecohealthalliance.org>; Schountz,Tony >
Subject: RE: R24 Discussion

Works for me. Sarah is my PO for at least one of my grants.
Greg

From: Jon Epstein ecohealthalliance.org>
Sent: Tuesday, September 29, 2020 11:08 AM
To: Schountz,Tony >; Ebel,Greg
Subject: Fwd: R24 Discussion

Guys,
This just came through from NIAID.

I suggest that we talk to her first, then we can talk once we have her input. Want to do it on the 7th?

Cheers,
Jon

---------- Forwarded message ---------
From: **Woodson, Sara (NIH/NIAID) [E]**
Date: Tue, Sep 29, 2020 at 12:05 PM
Subject: R24 Discussion
To: epstein ecohealthalliance.org>

Hi Jon,
It's been awhile since we've spoken but I hope you are doing well. Jean forwarded me your question about hypothesis-driven research in an R24. In general, I think we should probably schedule a brief call to discuss some of the specifics of R24s but also to hear about what you're thinking in terms of a hypothesis-driven approach (or aim). I've listed below some times that work for me/Jean/Mark, please let me know if any of those would work for your team as well.
October 5th: 9-9:30a (eastern)
October 7th: 3-3:30pm
October 14th: 10-11am, 1-2pm, or 2:30-3:30p
October 15th: 11a-noon or 3-4pm

In the interim though, here are some additional thoughts:
The R24 FOA indicates that this mechanism should be used to develop, maintain, provide a resource, but it doesn't explicitly state that hypothesis-driven research is not allowed. Our branch currently has one other funded R24 for the World Reference Collection of Emerging Viruses and Arboviruses (WRCEVA) at UTMB. This R24 does include hypothesis-driven research; they conduct small research projects that leverages having full access to the collection and to samples gathered through pursuit of adding new items to the collection. This research is usually a discreet, small project so as not to take up a lot of the budget and makes use of the resource to answer significant research questions that others haven't addressed yet and that may be difficult to work into other separate applications. I will have to search for other R24s across the institute that may have included animal model development as part of their aims, but none are coming to mind at the moment that would serve as a good example.

Sincerely, Sara

Sara E. Woodson, PhD
Program Officer
Virology Branch
Division of Microbiology and Infectious Diseases
National Institute of Allergy and Infectious Dieases, NIH

From: Ebel,Greg
Sent: Wednesday, October 07, 2020 4:01 PM EDT
To: Woodson, Sara (NIH/NIAID) [E] >; epstein ecohealthalliance.org>; Schountz,Tony

CC: jean.patterson ; Challberg, Mark (NIH/NIAID) [E]
Subject: RE: R24 Discussion

Thanks a lot, Sara, Jean and Mark,

This is really helpful I know Scott quite well and have no problem reaching out to him about the WRCEVA application.

Have a great rest of your week.

Greg

From: Woodson, Sara (NIH/NIAID) [E]
Sent: Wednesday, October 07, 2020 1:51 PM
To: epstein ecohealthalliance.org>; Schountz,Tony ; Ebel,Greg
>
Cc: jean.patterson Challberg, Mark (NIH/NIAID) [E] >
Subject: RE: R24 Discussion

Hi Tony, Jon, and Greg;
Here are the example R24's you may want to look up in NIH Reporter:

R24AI059830 PI: Jacques Robert (University of Rochester, animal model containing)
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As Mark mentioned on the phone, NIAID doesn't allow a lot of R24 grants and thus not many are funded, so there aren't many relevant examples to what you would be putting forth in your R24. Please let me know if you have other questions or concerns!
Happy writing 😊
Sincerely, Sara

-----Original Appointment-----
From: Woodson, Sara (NIH/NIAID) [E]
Sent: Wednesday, September 30, 2020 1:22 PM
To: Woodson, Sara (NIH/NIAID) [E]; ecohealthalliance.org; Schountz, Tony; Ebel,Greg; Patterson, Jean (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Beaubien, Candice (NIH/NIAID) [E]
Subject: R24 Discussion
When: Wednesday, October 7, 2020 3:00 PM-3:30 PM (UTC-05:00) Eastern Time (US & Canada).
Where: Skype Meeting

Please use this Zoom link for our meeting this afternoon instead…..

https://www.zoomgov.com/j/1614258516?pwd=bGVHUDFrbHVxWm91M2ZGUEdWcXF4QT09

Sincerely, Sara

From: Schountz,Tony >
Sent: Wednesday, October 07, 2020 3:58 PM EDT
To: Woodson, Sara (NIH/NIAID) [E] >
CC: epstein ecohealthalliance.org>; Schountz,Tony >; Ebel,Greg ; jean.patterson ; Challberg, Mark (NIH/NIAID) [E]

Subject: Re: R24 Discussion

Yes, thanks much, Sara. I appreciate that you, Jean and Mark chatted with us today.

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Oct 7, 2020, at 1:51 PM, Woodson, Sara (NIH/NIAID) [E] > wrote:

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Sincerely, Sara

From: Jon Epstein ecohealthalliance.org>
Sent: Tuesday, September 29, 2020 4:26 PM EDT
To: Ebel,Greg < >
CC: Schountz,Tony >
Subject: Re: R24 Discussion

Tony?

On Tue, Sep 29, 2020 at 1:10 PM Ebel,Greg > wrote:

> Works for me. Sarah is my PO for at least one of my grants.
>
> Greg
>
> **From:** Jon Epstein ecohealthalliance.org>
> **Sent:** Tuesday, September 29, 2020 11:08 AM
> **To:** Schountz,Tony ; Ebel,Greg >
> **Subject:** Fwd: R24 Discussion
>
> Guys,
>
> This just came through from NIAID.
>
> I suggest that we talk to her first, then we can talk once we have her input. Want to do it on the 7th?
>
> Cheers,
>
> Jon
>
> ---------- Forwarded message ---------
> From: **Woodson, Sara (NIH/NIAID) [E]**
> Date: Tue, Sep 29, 2020 at 12:05 PM
> Subject: R24 Discussion
> To: epstein ecohealthalliance.org>
>
> Hi Jon,
>
> It's been awhile since we've spoken but I hope you are doing well. Jean forwarded me your question about hypothesis-driven research in an R24. In general, I think we should probably schedule a brief call to discuss some of the specifics of R24s but also to hear about what you're thinking in terms of a hypothesis-driven approach (or aim). I've listed below some times that work for me/Jean/Mark, please let me know if any of those would work for your team as well.
>
> October 5th: 9-9:30a (eastern)
>
> October 7th: 3-3:30pm
>
> October 14th: 10-11am, 1-2pm, or 2:30-3:30p
>
> October 15th: 11a-noon or 3-4pm
>
> In the interim though, here are some additional thoughts:
>
> The R24 FOA indicates that this mechanism should be used to develop, maintain, provide a resource, but it doesn't explicitly state that hypothesis-driven research is not allowed. Our branch currently has one other funded R24 for the World Reference Collection of Emerging Viruses and Arboviruses (WRCEVA) at UTMB. This R24 does include hypothesis-driven research; they conduct small research projects that leverages having full access to the collection and to

samples gathered through pursuit of adding new items to the collection. This research is usually a discreet, small project so as not to take up a lot of the budget and makes use of the resource to answer significant research questions that others haven't addressed yet and that may be difficult to work into other separate applications. I will have to search for other R24s across the institute that may have included animal model development as part of their aims, but none are coming to mind at the moment that would serve as a good example.

Sincerely, Sara

Sara E. Woodson, PhD

Program Officer

Virology Branch

Division of Microbiology and Infectious Diseases

National Institute of Allergy and Infectious Dieases, NIH

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

)

web: ecohealthalliance.org

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To: epstein ecohealthalliance.org>; Schountz,Tony < >; Ebel,Greg

CC: jean.patterson Challberg, Mark (NIH/NIAID) [E]
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Sent: Wednesday, September 30, 2020 11:05 AM EDT
To: Woodson, Sara (NIH/NIAID) [E] >
CC: Schountz,Tony Ebel,Greg >
Subject: Re: R24 Discussion

Sara,
Thank you - it would be great to talk. Let's plan for Oct 7th at 3 pm EDT. I'm copying my colleagues Tony Schountz and Greg Ebel at CSU, who will join us.
Cheers,
Jon

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> **Sara E. Woodson, PhD**
>
> Program Officer
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> Virology Branch
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> Division of Microbiology and Infectious Diseases
>
> National Institute of Allergy and Infectious Dieases, NIH
>
>

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To: Ebel,Greg
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Me, too.
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-Jon

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> Greg

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Cc: Schountz,Tony ; Ebel,Greg >
Subject: Re: R24

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On Sep 14, 2020, at 11:25 AM, Jon Epstein ecohealthalliance.org> wrote:

Tony and Greg,

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Otherwise, suggest some times this week when you're free.

-Jon

On Mon, Sep 14, 2020 at 12:12 PM Schountz,Tony > wrote:

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On Sep 14, 2020, at 9:57 AM, Schountz,Tony > wrote:

Here's a Zoom link in case we need it. I'm limited to 30 minutes.

Topic: R24 Zoom Meeting

Time: Sep 14, 2020 10:00 AM Mountain Time (US and Canada)

Join Zoom Meeting

https://us02web.zoom.us/j/5861713088?pwd=RVJmb2VsenlWR1U3TkdiVGp4WUc2QT09

Meeting ID: 586 171 3088

Passcode: 4e5ZJe

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On Aug 31, 2020, at 7:19 AM, Jon Epstein
ecohealthalliance.org> wrote:

Sorry, I have a meeting at that time. I'm free either the hour before or after that.

Could we do 10AM MST?

On Fri, Aug 28, 2020 at 2:00 PM Schountz,Tony
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> How about September 14 at 9:00 AM MST?
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> **From:** Ebel,Greg >
> **Sent:** Friday, August 28, 2020 11:57 AM
> **To:** epstein ecohealthalliance.org>; Schountz,Tony
>
> **Subject:** RE: R24
>
> The morning of the 14th is OK for me.
>
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>
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On Fri, Aug 28, 2020 at 1:54 PM Schountz,Tony
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Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

From: Schountz,Tony >
Sent: Thursday, September 24, 2020 11:37 AM EDT
To: Schountz,Tony >
CC: epstein ecohealthalliance.org>; Ebel,Greg >
Subject: Re: R24

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

ACE2 Residues Involved in Spike Interactic

Suscept
Not susc
Unknow

Twenty Ace2 Residues Involved in SARS-CoV-2 Receptor Binding

	ACE2	AA position																		
Common Name	**Species name**	24	27	28	30	31	34	35	37	38	41	42	45	82	83	330	353	354	355	357
Human	*Homo sapiens*	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R
Syrian hamster	*Mesocricetus auratus*	Q	T	F	D	K	Q	E	E	D	Y	Q	L	N	Y	N	K	G	D	R
Leschenault's rousette	*Rousettus leschenaultii*	L	T	F	E	K	T	E	E	D	Y	Q	L	T	Y	K	K	G	D	R
Domestic cat	*Felis catus*	L	T	F	E	K	H	E	E	E	Y	Q	L	T	Y	N	K	G	D	R
Pearson's horseshoe bat	*Rhinolophus pearsonii*	R	T	F	D	K	H	E	E	D	H	E	L	D	Y	N	K	D	D	R
Least horseshoe bat	*Rhinolophus pusillus*	L	K	F	N	D	S	E	E	D	Y	1	L	N	Y	N	K	G	D	R
Ferret	*Mustela putorius*	L	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	K	R	D	R
Big-eared horseshoe bat	*Rhinolophus macrotis*	E	K	F	D	K	S	K	E	D	Y	E	L	N	Y	K	K	G	D	R
Chinese rufous horseshoe bat	*Rhinolophus sinicus*	E	I	F	D	K	T	K	E	D	H	Q	L	N	Y	N	K	G	D	R
Lander's horseshoe bat	*Rhinolophus landeri*	L	T	F	D	D	S	A	E	N	Y	Q	L	N	F	N	K	G	D	R
Jamaican fruit bat	*Artibeus jamaicensis*	D	T	F	E	K	T	E	E	E	Y	E	L	A	Y	N	K	N	D	R
Norway rat	*Rattus norvegicus*	K	S	F	N	K	Q	E	E	D	Y	Q	L	N	F	N	H	G	D	R
House mouse	*Mus musculus*	N	T	F	N	N	Q	E	E	D	Y	Q	L	S	F	N	H	G	D	R
Greater horseshoe bat	*Rhinolophus ferrumequinum*	L	K	F	D	D	S	E	E	N	H	Q	L	N	F	N	K	G	D	R
Vampire bat	*Desmodus rotundus*	E	T	F	E	N	T	E	E	E	Y	Q	L	T	Y	N	N	K	D	R
Halcyon horseshoe bat	*Rhinolophus alcyone*	L	I	F	D	N	S	E	E	N	H	Q	L	K	F	N	K	N	D	R
Brandt's bat	*Myotis brandii*	K	I	F	E	N	S	K	E	D	H	E	L	T	Y	N	K	G	D	R
Little brown bat	*Myotis lucifugus*	K	I	F	E	N	S	A	E	D	H	E	L	T	Y	N	K	G	D	R
Japanese house bat	*Pipistrellus abramus*	E	R	F	V	K	H	E	E	N	H	E	L	G	F	D	K	N	D	R

20 Residues (white/blue) fro
5 Residues (blue) fr

On Sep 24, 2020, at 8:54 AM, Schountz,Tony > wrote:

Here's the zoom info:

Topic: Tony Schountz's Zoom Meeting
Time: Sep 24, 2020 09:00 AM Mountain Time (US and Canada)

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Passcode: 4e5ZJe

—
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Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Sep 16, 2020, at 5:41 PM, Jon Epstein ecohealthalliance.org> wrote:

Shall we say 9 MST /11 EDT ?

Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
New York

On Wed, Sep 16, 2020, 7:09 PM Schountz,Tony > wrote:

> Yes, MST. Sorry.
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> Tony Schountz, PhD
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> On Sep 16, 2020, at 4:43 PM, Jon Epsteir ecohealthalliance.org> wrote:
>
> Is that mountain time?
>
> Jonathan Epstein DVM, MPH, PhD
>
> Vice President for Science and Outreach
>
> EcoHealth Alliance
> New York
>
> On Wed, Sep 16, 2020, 6:27 PM Ebel,Greg > wrote:
>
> > I could do those times on Thursday.
> >
> > Greg
> >
> > ---
> >
> > **From:** Schountz,Tony >
> > **Sent:** Wednesday, September 16, 2020 3:59 PM
> > **To:** epstein ecohealthalliance.org>
> > **Cc:** Ebel,Greg >; Schountz,Tony >
> > **Subject:** Re: R24
> >
> > Jon and Greg, do Tu or Th mornings, say 9 or 10, look good for you?
> >
> > —
> > Tony Schountz, PhD
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> Time: Sep 14, 2020 10:00 AM Mountain Time (US and Canada)
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> Join Zoom Meeting
>
> https://us02web.zoom.us/j/5861713088?pwd=RVJmb2VsenlWR1U3TkdiVGp4WUc2QT09
>
> Meeting ID: 586 171 3088
>
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>
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> Tony Schountz, PhD
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From: Jon Epstein ecohealthalliance.org>
Sent: Thursday, September 24, 2020 12:03 PM EDT
To: Schountz,Tony
Subject: Re: R24

I had seen this list, too. I think we could get these tissues but export is always tricky.
We should definitely include it in our proposal.

-Jon

On Thu, Sep 24, 2020 at 12:00 PM Schountz,Tony wrote:

> Jon, attached is the paper with the ACE2 sequences that led us down the deer mouse path for SARS2 susceptibility. I've highlighted the 7 Rhinolophus species on page 2 as well as the table with the 20 critical amino acids. (Deer mice have 17 of these 20.) So, R. pearsonii is the closest, but I suspect there may be other Rhinolophus species that have not had ACE2 sequences determined that may be closer to the 20 found in humans, and which may be more likely to be susceptible. It would be helpful if we could get as many ACE2 sequences as possible but we'd need access to lung RNA from each of them to do the PCR and sequencing. I'm suspect someone at Wuhan or elsewhere in China are already doing this. Identifying which facilitate virus entry (e.g., transfection experiments) would point to the best candidates for susceptibility and which we would want to import for one-off susceptibility experiments.
>
> T.
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> <Screen Shot 2020-09-24 at 9.36.55 AM.png>
>
> On Sep 24, 2020, at 8:54 AM, Schountz,Tony > wrote:
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Sent: Wednesday, September 16, 2020 3:59 PM
To: epstein ecohealthalliance.org>
Cc: Ebel,Greg ; Schountz,Tony

Subject: Re: R24

Jon and Greg, do Tu or Th mornings, say 9 or 10, look good for you?

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> On Sep 16, 2020, at 3:22 PM, Jon Epstein ecohealthalliance.org> wrote:
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> Me, too.
>
> Tuesday and thursday are fairly open if you want to suggest some times that work for you.
>
> -Jon
>
> On Wed, Sep 16, 2020 at 5:01 PM Ebel,Greg > wrote:
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> > For me next week is a lot better.
> >
> > Greg
> >
> > ---
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> > **To:** epstein ecohealthalliance.org>
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> > Ebel,Greg <
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I asked Jean about research and for an example R24. She said she'd send one and get back to us regarding the limitations of an R24.
Cheers,
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> **To:** epstein ecohealthalliance.org>
> **Cc:** Ebel,Greg >; Schountz,Tony
>
> **Subject:** Re: R24
>
> Jon and Greg, do Tu or Th mornings, say 9 or 10, look good for you?
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> Tony Schountz, PhD
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Cc: Schountz,Tony >; Ebel,Greg

Subject: Re: R24

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> Topic: R24 Zoom Meeting
>
> Time: Sep 14, 2020 10:00 AM Mountain Time (US and Canada)
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> Join Zoom Meeting
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> https://us02web.zoom.us/j/5861713088?pwd=RVJmb2VsenlWR1U3TkdiVGp4WUc2QT09
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>
> Passcode: 4e5ZJe
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> > Arthropod-borne and Infectious
> > Disease Laboratory
> > Department of Microbiology, Immunology and Pathology
> > College of Veterinary Medicine

Colorado State University

From: Ebel,Greg

Sent: Friday, August 28, 2020 11:57 AM
To: epstein ecohealthalliance.org>; Schountz,Tony >
Subject: RE: R24

The morning of the 14th is OK for me.

Greg

From: Jon Epstein ecohealthalliance.org>
Sent: Friday, August 28, 2020 11:56 AM
To: Schountz,Tony >
Cc: Ebel,Greg

Subject: Re: R24

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-Jon

On Fri, Aug 28, 2020 at 1:54 PM Schountz,Tony

wrote:

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> Tony Schountz, PhD
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> Department of Microbiology, Immunology and Pathology

College of Veterinary Medicine
Colorado State University

From: Jon Epstein ecohealthalliance.org>
Sent: Friday, August 28, 2020 11:52 AM
To: Schountz,Tony

Cc: Ebel,Greg

Subject: Re: R24

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Thanks,

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--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

web: ecohealthalliance.org

From: Schountz,Tony
Sent: Thursday, September 24, 2020 12:00 PM EDT
To: epstein ecohealthalliance.org>
CC: Schountz,Tony
Subject: Re: R24
Attachment(s): "jmv.25817.pdf"

Jon, attached is the paper with the ACE2 sequences that led us down the deer mouse path for SARS2 susceptibility. I've highlighted the 7 Rhinolophus species on page 2 as well as the table with the 20 critical amino acids. (Deer mice have 17 of these 20.) So, R. pearsonii is the closest, but I suspect there may be other Rhinolophus species that have not had ACE2 sequences determined that may be closer to the 20 found in humans, and which may be more likely to be susceptible. It would be helpful if we could get as many ACE2 sequences as possible but we'd need access to lung RNA from each of them to do the PCR and sequencing. I'm suspect someone at Wuhan or elsewhere in China are already doing this. Identifying which facilitate virus entry (e.g., transfection experiments) would point to the best candidates for susceptibility and which we would want to import for one-off susceptibility experiments.

T.
—
Tony Schountz, PhD
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Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Sep 24, 2020, at 9:37 AM, Schountz,Tony wrote:

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

<Screen Shot 2020-09-24 at 9.36.55 AM.png>

On Sep 24, 2020, at 8:54 AM, Schountz,Tony > wrote:

Here's the zoom info:

Topic: Tony Schountz's Zoom Meeting
Time: Sep 24, 2020 09:00 AM Mountain Time (US and Canada)

Join Zoom Meeting
https://us02web.zoom.us/j/5861713088?pwd=RVJmb2VsenlWR1U3TkdiVGp4WUc2QT09

Meeting ID: 586 171 3088
Passcode: 4e5ZJe

—
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Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

970-491-7350

On Sep 16, 2020, at 5:41 PM, Jon Epstein ecohealthalliance.org> wrote:

Shall we say 9 MST /11 EDT ?

Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
New York

(

On Wed, Sep 16, 2020, 7:09 PM Schountz,Tony wrote:

> Yes, MST. Sorry.
> —
> Tony Schountz, PhD
> Associate Professor
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> On Sep 16, 2020, at 4:43 PM, Jon Epstein ecohealthalliance.org> wrote:
>
> Is that mountain time?
>
> Jonathan Epstein DVM, MPH, PhD
>
> Vice President for Science and Outreach
>
> EcoHealth Alliance
> New York
>
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Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance

Received: 5 March 2020 | Accepted: 30 March 2020

DOI: 10.1002/jmv.25817

SHORT COMMUNICATION

JOURNAL OF MEDICAL VIROLOGY WILEY

SARS-CoV-2 spike protein favors ACE2 from *Bovidae* and *Cricetidae*

Junwen Luan[1] | Xiaolu Jin[1,2] | Yue Lu[1,2] | Leiliang Zhang[1]

[1]Institute of Basic Medicine, Shandong Provincial Hospital Affiliated to Shandong First Medical University, Jinan, Shandong, China

[2]School of Medicine and Life Sciences, Shandong Academy of Medical Sciences, University of Jinan, Jinan, Shandong, China

Correspondence
Leiliang Zhang, PhD, Institute of Basic Medicine, Shandong Provincial Hospital Affiliated to Shandong First Medical University, Jinan, 250062 Shandong, China.
Email: armzhang@hotmail.com

Funding information
National Key Plan for Research and Development of China, Grant/Award Number: 2016YFD0500300; Shandong Academy of Medical Sciences Grant, Grant/Award Number: 2017-52; Innovation Project of Shandong Academy of Medical Sciences; Academic promotion programme of Shandong First Medical University, Grant/Award Number: 2019LJ001

Abstract

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) causes the recent COVID-19 public health crisis. Bat is the widely believed original host of SARS-CoV-2. However, its intermediate host before transmitting to humans is not clear. Some studies proposed pangolin, snake, or turtle as the intermediate hosts. Angiotensin-converting enzyme 2 (ACE2) is the receptor for SARS-CoV-2, which determines the potential host range for SARS-CoV-2. On the basis of structural information of the complex of human ACE2 and SARS-CoV-2 receptor-binding domain (RBD), we analyzed the affinity to S protein of the 20 key residues in ACE2 from mammal, bird, turtle, and snake. Several ACE2 proteins from *Primates*, *Bovidae*, *Cricetidae*, and *Cetacea* maintained the majority of key residues in ACE2 for associating with SARS-CoV-2 RBD. The simulated structures indicated that ACE2 proteins from *Bovidae* and *Cricetidae* were able to associate with SARS-CoV-2 RBD. We found that nearly half of the key residues in turtle, snake, and bird were changed. The simulated structures showed several key contacts with SARS-CoV-2 RBD in turtle and snake ACE2 were abolished. This study demonstrated that neither snake nor turtle was the intermediate hosts for SARS-CoV-2, which further reinforced the concept that the reptiles are resistant against infection of coronavirus. This study suggested that *Bovidae* and *Cricetidae* should be included in the screening of intermediate hosts for SARS-CoV-2.

KEYWORDS

ACE2, *Bovidae*, *Cricetidae*, intermediate host, SARS-CoV-2

1 | INTRODUCTION

Coronavirus disease 2019 (COVID-19), which was first reported in Wuhan, Hubei province, China, has caused over 80 422 human infections and more than 2984 deaths (as of 4 March 2020) in China.[1,2] The confirmed cases outside China are increasing, which raised major global concern. Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was identified to be the pathogen of COVID-19. SARS-CoV-2 has joined SARS-CoV and Middle East respiratory syndrome-related coronavirus (MERS-CoV) as another coronavirus that causes severe respiratory disease and human death.[3,4]

The specificity of the interaction between virus and receptor determines its host range for the virus. Spike protein (S) of SARS-CoV-2 has attracted great attention because of its role in receptor binding. Angiotensin-converting enzyme 2 (ACE2) binds to the receptor-binding domain (RBD) of SARS-CoV-2 S protein and functions as a receptor for SARS-CoV-2.[5,6] The origin of SARS-CoV-2 is considered as bat.[6] However, the intermediate host is unknown. Some studies suggest that pangolin is involved in the evolution of SARS-CoV-2.[7,8] Others suggested that snake and turtles are potential intermediate hosts for SARS-CoV-2.[9,10] In this study, we compared the key amino acids (AAs) in ACE2 from different species for the binding ability to RBD. On the basis of

potential interaction between S protein and ACE2, it was speculated that SARS-CoV-2 preserved the ability to infect *Bovidae* and *Cricetidae* but not snake or turtle.

2 | METHODS

2.1 | Sequence analysis of ACE2

A total of 93 ACE2 protein sequences were selected from 85 mammals, 4 birds, 3 turtles, and 1 snake. These ACEs with their corresponding species are listed as follows: hACE2: *Homo sapiens* (BAB40370.1), RhiACE2: *Rhinopithecus roxellana* (XP_010364367.2), MacmACE2: *Macaca mulatta* (NP_001129168.1), MuseACE2: *Mustela erminea* (XP_032187679.1), CamdACE2: *Camelus dromedarius* (XP_031301717.1), PlACE2: *Procyon lotor* (XP_031301717.1), PcACE2: *Paguma larvata* (AAX63775.1), RmACE2: *Rhinolophus macrotis* (ADN93471.1), RfACE2: *Rhinolophus ferrumequinum* (BAH02663.1), RsACE2: *Rhinolophus sinicus* (ADN93472.1), RlACE2: *Rousettus leschenaultii* (BAF50705.1), SsACE2: *Sus scrofa* (NP_001116542.1), MpfACE2: *Mustela putorius furo* (BAE53380.1), RatACE2: *Rattus norvegicus* (Q5EGZ1), MmACE2: *Mus musculus* (Q3URC9), ClfACE2: *Canis lupus familiaris* (J9P7Y2), FcACE2: *Felis catus* (A0A384DV19), MjACE2: *Manis javanica* (XP_017505752.1), RpACE2: *Rhinolophus pearsonii* (ABU54053.1), PvACE2: *Pteropus vampyrus* (XP_011361275.1), PoaACE2: *Pongo abelii* (NP_001124604.1), EcACE2: *Equus caballus* (F6V9L3), BtACE2: *Bos taurus* (Q58DD0), PtACE2: *Pan troglodytes* (A0A2J8KU96), OraACE2: *Ornithorhynchus anatinus* (F7FDA2), OvaACE2: *Ovis aries* (W5PSB6), PanACE2: *Papio Anubis* (A0A096N4X9), LaACE2: *Loxodonta africana* (G3T6Q2), SsdACE2: *Sus scrofa domesticus* (A0A220QT48), EeACE2: *Erinaceus europaeus* (A0A1S3APE5), OcACE2: *Oryctolagus cuniculus* (G1TEF4), NpACE2: *Nyctereutes procyonoides* (B4XEP4), VvACE2: *Vulpes vulpes* (A0A3Q7-RAT9), PhcACE2: *Phodopus campbelli* (C7ECU7), MaACE2: *Mesocricetus auratus* (C7ECV1), CjACE2: *Callithrix jacchus* (F7CNJ6), SusACE2: *Suricata suricatta* (XP_029786256.1), HgACE2: *Heterocephalus glaber* (A0A0N8EUX7), DoACE2: *Dipodomys ordii* (A0A1S3GHT7), ItACE2: *Ictidomys tridecemlineatus* (XP_005316051.3), CpACE2: *Cavia porcellus* (XP_023417808.1), CgACE2: *Cricetulus griseus* (A0A061HZ66), ChACE2: *Capra hircus*(A0A452EVJ5); BibtACE2: *Bos indicus x Bos taurus* (A0A4W2H3A1), BmACE2: *Bos mutus* (L8I4I4), NlACE2: *Nomascus leucogenys* (G1RE79); CsACE2: *Chlorocebus sabaeus* (A0A0D9RQZ0); MfACE2: *Macaca fascicularis* (A0A2K5X283); PpACE2: *Pan paniscus* (A0A2R9BKD8); CaACE2: *Cercocebus atys* (A0A2K5KSD8); MnACE2: *Macaca nemestrina* (A0A2K6D1N8); MalACE2: *Mandrillus leucophaeus* (A0A2K5ZV99); TsACE2: *Tarsius syrichta* (A0A1U7TY97); PrcACE2: *Propithecus coquereli* (A0A2K6GHW5); UmACE2: *Ursus maritimus* (A0A452TT30); OgACE2: *Otolemur garnettii* (H0WMI5); SbbACE2: *Saimiri boliviensis boliviensis* (A0A2K6SBD4); CciACE2: *Cebus capucinus imitator* (A0A2K5PYM0); GggACE2: *Gorilla gorillagorilla* (G3QWX4); AnACE2: *Aotus nancymaae* (A0A2K5DQI6); ChaACE2: *Chlorocebus aethiops* (Q1LZX8); AmACE2: *Ailuropoda melanoleuca* (G1MC42); VuACE2: *Vombatus ursinus* (A0A4X2M679); UaACE2: *Ursus americanus* (A0A452R1Z9); UahACE2: *Ursusarctos horribilis* (A0A3Q7TE16); PmACE2: *Physeter macrocephalus* (A0A2Y9S5T9); LvACE2: *Lipotes vexillifer* (A0A340Y3Y6); BasACE2: *Balaenoptera acutorostrata scammoni* (A0A452CBT6); DlACE2: *Delphinapterus leucas* (A0A2Y9M9H3); TtACE2: *Tursiops truncatus* (A0A2U4AJL3); NaaACE2: *Neophocaena asiaeorientalis asiaeorientalis* (A0A341BCI8); CuACE2: *Callorhinus ursinus* (A0A3Q7N3M7); NsACE2: *Neomonachus schauinslandi* (A0A2Y9GEI9); TmlACE2: *Trichechus manatuslatirostris* (A0A2Y9E393); EllkACE2: *Enhydra lutriskenyoni* (A0A2Y9KLV0); ClACE2: *Chinchilla lanigera* (C7ECU0); MdACE2: *Monodelphis domestica* (F6WXR7); LpACE2: *Lynx pardinus* (A0A485NF12); PaACE2: *Pipistrellus abramus* (C7ECT9); MbACE2: *Myotis brandtii* (S7N573); DrACE2: *Desmodus rotundus* (K9INV8); RhpACE2: *Rhinolophus pusillus* (E2DHI9); RaACE2: *Rhinolophus alcyone* (A0A0N7IQX6); RlACE2(2): *Rhinolophus landeri* (A0A0P0IB69); MylACE2: *Myotis lucifugus* (G1PXH7), GgACE2: *Gallus gallus* (F1NHR4), ApACE2: *Anas platyrhynchos* (R0LHX5), MgACE2: *Meleagris gallopavo* (G1NPB8), CaaACE2: *Cathartes aura* (A0A091MDI4), OhACE2: *Ophiophagus hannah* (V8NIH2), CpbACE2: *Chrysemys picta bellii* (XP_023964517.1), CmACE2: *Chelonia mydas* (XP_007070561.1); and PsACE2: *Pelodiscus sinensis* (XP_006122891.1). On the basis of known 20 key sites in human ACE2 interacting with SARS-CoV-2 RBD,[11] we analyzed whether these sites were conserved on other ACE2 proteins. Phylogenetic and molecular evolutionary analysis of ACE2 protein was conducted using molecular evolutionary genetics analysis version X (MEGA-X).[12] Phylogenetic tree was generated with Jones-Taylor-Thornton evolutionary model using a maximum-likelihood method.

2.2 | Structure simulation of ACE2-RBD complex

On the basis of the structure of hACE2 with SARS-CoV-2 S RBD (PDB: 6LZG), the structure of SARS-CoV-2 S and ACE2 from *Bos taurus*, *Cricetulus griseus*, *Pelodiscus sinensis*, and *Ophiophagus hannah* were simulated by SWISS-MODEL online server[13] and analyzed by Chimera software version 1.14.[14]

3 | RESULTS

3.1 | Sequence alignment of ACE2

According to the recently resolved structure of the complex of human ACE2 and SARS-CoV-2 RBD, there are 20 key AAs in hACE2 for interacting with RBM.[11] We analyzed those AAs of ACE2 protein from a list of mammals, birds, turtles, and snake, as shown in Table 1. Next, a phylogenetic tree for mammalian ACE2 proteins was constructed by MEGA-X software. There were 16 *primates* ACE2, 5 *Bovidae* ACE2, 2 *Cricetidae* ACE2, and 3 *Cetacea* ACE2 (Table 1 and Figure 1A), possessing at least 90% (18/20) critical AAs. Pangolin ACE2 preserved only 70% (14/20) AAs. Nearly half of the key residues in turtles (CpbACE2, CmACE2, and PsACE2) and snake (OhACE2) were changed (Table 1). ACE2 from *Aves*, including *Gallus gallus*, *Anas platyrhynchos*, *Meleagris gallopavo*, and *Cathartes aura*, only matched 10 to 11 AAs (Table 1).

TABLE 1 Analysis of the key AAs in ACE2 for SARS-CoV-2 RBD binding

	AA position																			
ACE2	24	27	28	30	31	34	35	37	38	41	42	45	82	83	330	353	354	355	357	393	Matched AA
hACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
RhiACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
MacmACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
PoaACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
PtACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
PanACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
NlACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
CsACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
MfACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
PpACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
CaACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
MnACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
MalACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
GggACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
ChaACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
PrcACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	19
BtACE2	Q	T	F	E	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
OvaACE2	Q	T	F	E	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
MaACE2	Q	T	F	D	K	Q	E	E	D	Y	Q	L	N	Y	N	K	G	D	R	R	18
CgACE2	Q	T	F	D	K	Q	E	E	D	Y	Q	L	N	Y	N	K	G	D	R	R	18
ChACE2	Q	T	F	E	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
BibtACE2	Q	T	F	E	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
BmACE2	Q	T	F	E	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
PmACE2	Q	T	F	Q	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
DlACE2	Q	T	F	Q	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
NaaACE2	Q	T	F	Q	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
PhcACE2	Q	T	F	D	K	Q	E	E	D	Y	Q	L	N	Y	N	K	E	D	R	R	17
HgACE2	Q	T	F	D	K	Q	E	E	D	Y	Q	L	A	Y	N	K	D	D	R	R	17
ItACE2	L	T	F	D	K	Q	E	E	D	Y	Q	L	A	Y	N	K	G	D	R	R	17
BasACE2	Q	T	F	Q	K	H	E	E	D	Y	R	L	T	Y	N	K	G	D	R	R	17
CamdACE2	L	T	F	E	E	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
RlACE2	L	T	F	E	K	T	E	E	D	Y	Q	L	T	Y	K	K	G	D	R	R	16
SsACE2	L	T	F	E	K	L	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
FcACE2	L	T	F	E	K	H	E	E	E	Y	Q	L	T	Y	N	K	G	D	R	R	16
SsdACE2	L	T	F	E	K	L	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
OcACE2	L	T	F	E	K	Q	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
CjACE2	Q	T	F	D	K	H	E	E	D	H	E	L	T	Y	N	K	Q	D	R	R	16
DoACE2	L	T	F	D	N	Q	E	E	D	Y	Q	L	I	Y	N	K	G	D	R	R	16
UmACE2	L	T	F	E	K	Y	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16

(Continues)

TABLE 1 (Continued)

	AA position																				
ACE2	24	27	28	30	31	34	35	37	38	41	42	45	82	83	330	353	354	355	357	393	Matched AA
SbbACE2	Q	T	F	D	K	H	E	E	D	H	E	L	T	Y	N	K	Q	D	R	R	16
CciACE2	Q	T	F	D	K	H	E	E	D	H	E	L	T	Y	N	K	Q	D	R	R	16
AnACE2	Q	T	F	D	K	H	E	E	D	H	E	L	T	Y	N	K	Q	D	R	R	16
AmACE2	L	T	F	E	K	Y	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
UaACE2	L	T	F	E	K	Y	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
UahACE2	L	T	F	E	K	Y	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
LvACE2	R	T	F	Q	K	H	E	E	D	Y	Q	L	T	F	N	K	G	D	R	R	16
TtACE2	R	T	F	Q	K	R	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
LpACE2	L	T	F	E	K	H	E	E	E	Y	Q	L	T	Y	N	K	G	D	R	R	16
MpfACE2	L	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	K	R	D	R	R	15
ClfACE2	L	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	K	G	D	R	R	15
RpACE2	R	T	F	D	K	H	E	E	D	H	E	L	D	Y	N	K	D	D	R	R	15
LaACE2	L	T	F	D	T	Q	E	E	D	Y	Q	L	D	F	N	K	G	D	R	R	15
VvACE2	L	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	K	G	D	R	R	15
CpACE2	Q	T	F	D	E	L	K	E	D	Y	Q	L	A	Y	N	K	N	D	R	R	15
TsACE2	Q	T	F	D	K	Q	E	E	D	H	Q	L	S	Y	N	N	S	D	R	R	15
TmlACE2	L	T	F	D	T	Q	E	E	D	Y	Q	L	N	F	N	K	G	D	R	R	15
ClACE2	Q	T	F	D	N	E	K	E	D	Y	Q	L	A	Y	N	K	D	D	R	R	15
MuseACE2	L	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	K	R	D	R	R	14
PlACE2	L	T	F	E	N	N	E	E	E	Y	Q	L	T	Y	N	K	G	D	R	R	14
MjACE2	E	T	F	E	K	S	E	E	E	Y	Q	L	N	Y	N	K	H	D	R	R	14
PvACE2	L	T	F	E	K	T	E	E	D	Y	Q	L	A	Y	K	K	G	D	R	K	14
EcACE2	L	T	F	E	K	S	E	E	E	H	Q	L	T	Y	N	K	G	D	R	R	14
NpACE2	L	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	R	G	D	R	R	14
OgACE2	Q	T	F	D	N	R	E	E	E	H	Q	L	T	Y	N	K	D	D	R	R	14
VuACE2	R	E	F	E	T	K	E	E	E	Y	Q	L	T	F	N	K	G	D	R	R	14
NsACE2	L	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	K	H	D	R	R	14
ElkACE2	P	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	K	R	D	R	R	14
RhpACE2	L	K	F	N	D	S	E	E	D	Y	Q	L	N	Y	N	K	G	D	R	R	14
RmACE2	E	K	F	D	K	S	K	E	D	Y	E	L	N	Y	K	K	G	D	R	R	13
RsACE2	E	I	F	D	K	T	K	E	D	H	Q	L	N	Y	N	K	G	D	R	R	13
RatACE2	K	S	F	N	K	Q	E	E	D	Y	Q	L	N	F	N	H	G	D	R	R	13
MmACE2	N	T	F	N	N	Q	E	E	D	Y	Q	L	S	F	N	H	G	D	R	R	13
CuACE2	L	T	F	E	K	S	E	E	E	Y	Q	F	T	Y	N	K	H	D	R	R	13
RlACE2(2)	L	T	F	D	D	S	A	E	N	Y	Q	L	N	F	N	K	G	D	R	R	13
PcACE2	L	T	F	E	T	Y	E	Q	E	Y	Q	V	T	Y	N	K	G	D	R	R	12
RfACE2	L	K	F	D	D	S	E	E	N	H	Q	L	N	F	N	K	G	D	R	R	12
SusACE2	L	T	F	E	Q	H	E	Q	E	Y	L	V	A	Y	N	K	G	D	R	R	12

TABLE 1 (Continued)

	AA position																			
ACE2	24	27	28	30	31	34	35	37	38	41	42	45	82	83	330	353	354	355	357	393	Matched AA
MdACE2	D	T	F	D	D	A	K	E	E	H	Q	L	T	Y	N	K	N	D	R	R	12
DrACE2	E	T	F	E	N	T	E	E	E	Y	Q	L	T	Y	N	N	K	D	R	R	12
RaACE2	L	I	F	D	N	S	E	E	N	H	Q	L	N	F	N	K	G	D	R	R	12
OraACE2	E	Q	F	T	Q	K	Q	E	D	Y	Q	L	K	F	N	K	N	D	R	R	11
EeACE2	E	K	F	D	D	R	Q	E	N	Y	E	L	N	Y	N	N	G	D	R	R	11
MbACE2	K	I	F	E	N	S	K	E	D	H	E	L	T	Y	N	K	G	D	R	R	11
MylACE2	K	I	F	E	N	S	A	E	D	H	E	L	T	Y	N	K	G	D	R	R	11
GgACE2	E	T	F	A	E	V	R	E	D	Y	E	L	R	F	N	K	N	D	R	R	11
ApACE2	Q	M	F	A	E	V	R	E	D	Y	E	L	N	F	N	K	N	D	R	R	11
MgACE2	E	T	F	A	E	V	R	E	D	Y	E	L	R	F	N	K	N	D	R	R	11
CpbACE2	E	N	F	S	Q	V	R	E	D	Y	A	L	K	Y	N	K	K	D	R	R	11
CmACE2	E	N	F	S	Q	V	R	E	D	Y	A	L	K	Y	N	K	K	D	R	R	11
PsACE2	E	N	F	S	E	V	Q	E	D	Y	A	L	K	Y	N	K	K	D	R	R	11
PaACE2	E	R	F	V	K	H	E	E	N	H	E	L	G	F	D	K	N	D	R	R	10
CaaACE2	Q	I	F	E	E	P	R	E	N	Y	E	L	S	F	N	K	N	D	R	R	10
OhACE2	...	K	F	E	Q	A	R	T	D	Y	N	I	M	F	N	K	E	D	R	R	9

Note: hACE2, *Homo sapiens* (BAB40370.1), RhiACE2, *Rhinopithecus roxellana* (XP_010364367.2), MacmACE2, *Macaca mulatta* (NP_001129168.1), MuseACE2, *Mustela erminea* (XP_032187679.1), CamdACE2, *Camelus dromedarius* (XP_031301717.1), PlACE2, *Procyon lotor* (XP_031301717.1), PcACE2, *Paguma larvata* (AAX63775.1), RmACE2, *Rhinolophus macrotis* (ADN93471.1), RfACE2, *Rhinolophus ferrumequinum* (BAH02663.1), RsACE2, *Rhinolophus sinicus* (ADN93472.1), RlACE2, *Rousettus leschenaultii* (BAF50705.1), SsACE2, *Sus scrofa* (NP_001116542.1), MpfACE2, *Mustela putorius furo* (BAE53380.1), RatACE2, *Rattus norvegicus* (Q5EGZ1), MmACE2, *Mus musculus* (Q3URC9), ClfACE2, *Canis lupus familiaris* (J9P7Y2), FcACE2, *Felis catus* (A0A384DV19), MjACE2, *Manis javanica* (XP_017505752.1), RpACE2, *Rhinolophus pearsonii* (ABU54053.1), PvACE2, *Pteropus vampyrus* (XP_011361275.1), PoaACE2, *Pongo abelii* (NP_001124604.1), EcACE2, *Equus caballus* (F6V9L3), BtACE2, *Bos taurus* (Q58DD0), PtACE2, *Pan troglodytes* (A0A2J8KU96), OraACE2, *Ornithorhynchus anatinus* (F7FDA2), OvaACE2, *Ovis aries* (W5PSB6), PanACE2, *Papio Anubis* (A0A096N4X9), LaACE2, *Loxodonta africana* (G3T6Q2), SsdACE2, *Sus scrofa domesticus* (A0A220QT48), EeACE2, *Erinaceus europaeus* (A0A1S3APE5), OcACE2, *Oryctolagus cuniculus* (G1TEF4), NpACE2, *Nyctereutes procyonoides* (B4XEP4), VvACE2, *Vulpes vulpes* (A0A3Q7RAT9), PhcACE2, *Phodopus campbelli* (C7ECU7), MaACE2, *Mesocricetus auratus* (C7ECV1), CjACE2, *Callithrix jacchus* (F7CNJ6), SusACE2, *Suricata suricatta* (XP_029786256.1), HgACE2, *Heterocephalus glaber* (A0A0N8EUX7), DoACE2, *Dipodomys ordii* (A0A1S3GHT7), ItACE2, *Ictidomys tridecemlineatus* (XP_005316051.3), CpACE2, *Cavia porcellus* (XP_023417808.1), CgACE2, *Cricetulus griseus* (A0A061HZ66), ChACE2, *Capra hircus*(A0A452EVJ5); BibtACE2, *Bos indicus x Bos taurus* (A0A4W2H3A1), BmACE2, *Bos mutus* (L8I4I4), NlACE2, *Nomascus leucogenys* (G1RE79); CsACE2, *Chlorocebus sabaeus* (A0A0D9RQZ0); MfACE2, *Macaca fascicularis* (A0A2K5X283); PpACE2, *Pan paniscus* (A0A2R9BKD8); CaACE2, *Cercocebus atys* (A0A2K5KSD8); MnACE2, *Macaca nemestrina* (A0A2K6D1N8); MalACE2, *Mandrillus leucophaeus* (A0A2K5ZV99); TsACE2, *Tarsius syrichta* (A0A1U7TY97); PrcACE2, *Propithecus coquereli* (A0A2K6GHW5); UmACE2, *Ursus maritimus* (A0A452TT30); OgACE2, *Otolemur garnettii* (H0WMI5); SbbACE2, *Saimiri boliviensis boliviensis* (A0A2K6SBD4); CciACE2, *Cebus capucinus imitator* (A0A2K5PYM0); GggACE2, *Gorilla gorillagorilla* (G3QWX4); AnACE2, *Aotus nancymaae* (A0A2K5DQI6); ChaACE2, *Chlorocebus aethiops* (Q1LZX8); AmACE2, *Ailuropoda melanoleuca* (G1MC42); VuACE2, *Vombatus ursinus* (A0A4X2M679); UaACE2, *Ursus americanus* (A0A452R1Z9); UahACE2, *Ursusarctos horribilis* (A0A3Q7TE16); PmACE2, *Physeter macrocephalus* (A0A2Y9S5T9); LvACE2, *Lipotes vexillifer* (A0A340Y3Y6); BasACE2, *Balaenoptera acutorostrata scammoni* (A0A452CBT6); DlACE2, *Delphinapterus leucas* (A0A2Y9M9H3); TtACE2, *Tursiops truncatus* (A0A2U4AJL3); NaaACE2, *Neophocaena asiaeorientalis asiaeorientalis* (A0A341BCI8); CuACE2, *Callorhinus ursinus* (A0A3Q7N3M7); NsACE2, *Neomonachus schauinslandi* (A0A2Y9GEI9); TmlACE2, *Trichechus manatuslatirostris* (A0A2Y9E393); EllkACE2, *Enhydra lutriskenyoni* (A0A2Y9KLV0); ClACE2, *Chinchilla lanigera* (C7ECU0); MdACE2, *Monodelphis domestica* (F6WXR7); LpACE2, *Lynx pardinus* (A0A485NF12); PaACE2, *Pipistrellus abramus* (C7ECT9); MbACE2, *Myotis brandtii* (S7N573); DrACE2, *Desmodus rotundus* (K9INV8); RhpACE2, *Rhinolophus pusillus* (E2DHI9); RaACE2, *Rhinolophus alcyone* (A0A0N7IQX6); RlACE2(2), *Rhinolophus landeri* (A0A0P0IB69); MylACE2, *Myotis lucifugus* (G1PXH7), GgACE2, *Gallus gallus* (F1NHR4), ApACE2, *Anas platyrhynchos* (R0LHX5), MgACE2, *Meleagris gallopavo* (G1NPB8), CaaACE2, *Cathartes aura* (A0A091MDI4), OhACE2, *Ophiophagus hannah* (V8NIH2), CpbACE2, *Chrysemys picta bellii* (XP_023964517.1), CmACE2, *Chelonia mydas* (XP_007070561.1); and PsACE2, *Pelodiscus sinensis* (XP_006122891.1).
Abbreviations: AA, amino acid; ACE2, angiotensin-converting enzyme 2; RBD, receptor-binding domain; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

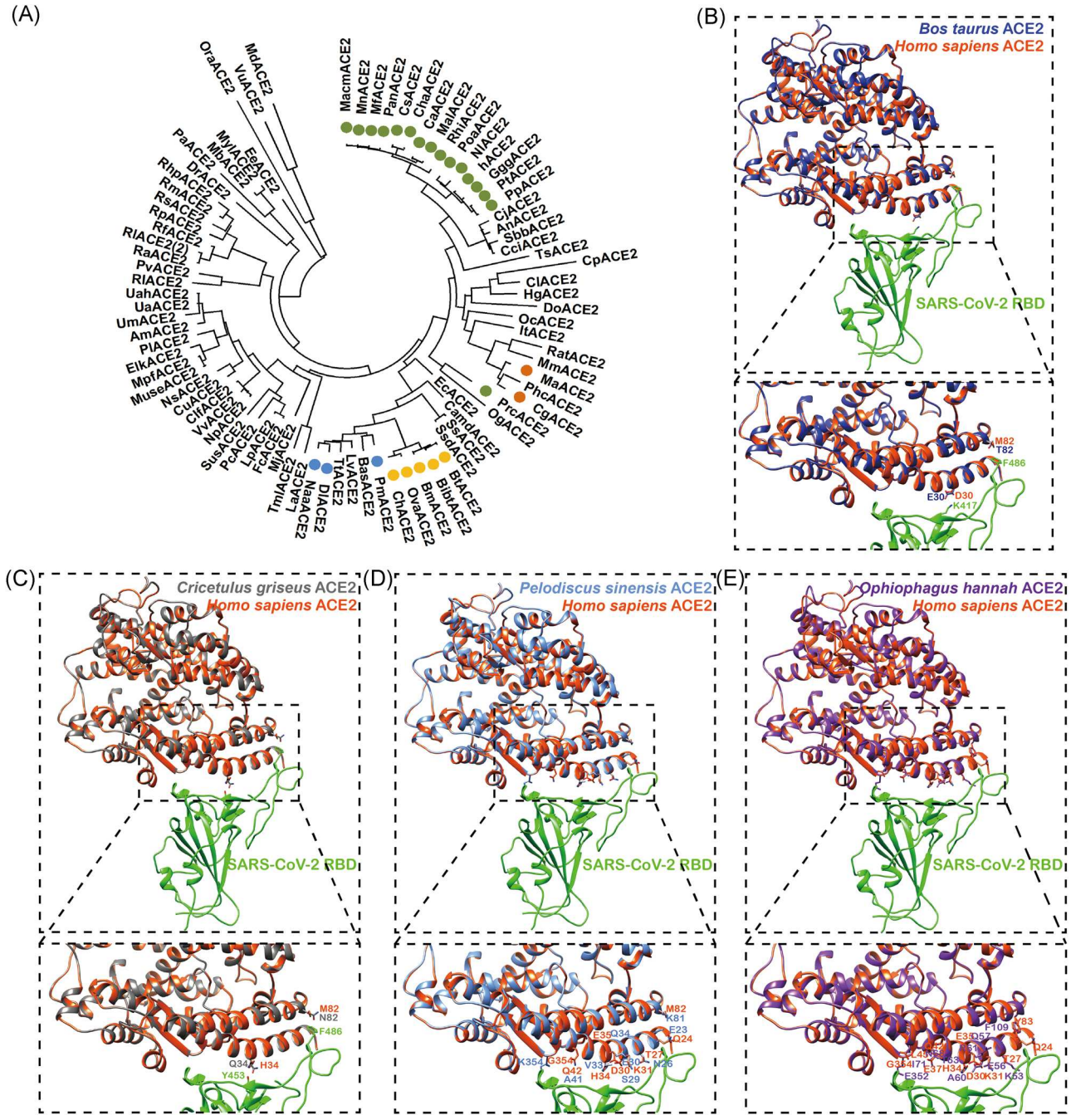

FIGURE 1 Structure simulation of SARS-CoV-2 RBD with ACE2 from different species. A, Phylogenetic tree of mammalian ACE2. ACE2 proteins from a total of 85 mammals were analyzed by MEGA-X and the phylogenetic tree was constructed using a maximum-likelihood method. The green, yellow, orange, and blue represent ACE2 from *Primates*, *Bovidae*, *Cricetidae*, and *Cetacea*, respectively. B, Structural simulation of the protein complex of *Bos taurus* ACE2 and SARS-CoV-2 RBD. *Bos taurus* ACE2, *Homo sapiens* ACE2, and SARS-CoV-2 RBD are in medium blue, orange red, and green, respectively. C, Structural simulation of the protein complex of *Cricetulus griseus* ACE2 and SARS-CoV-2 RBD. *Cricetulus griseus* ACE2, *Homo sapiens* ACE2, and SARS-CoV-2 RBD are in dim gray, orange red, and green, respectively. D, Structural simulation of the protein complex of *Pelodiscus sinensis* ACE2 and SARS-CoV-2 RBD. *Pelodiscus sinensis* ACE2, *Homo sapiens* ACE2, and SARS-CoV-2 RBD are in cornflower blue, orange red, and green, respectively. E, Structural simulation of the protein complex of *Ophiophagus hannah* ACE2 and SARS-CoV-2 RBD. *Ophiophagus hannah* ACE2, *Homo sapiens* ACE2, and SARS-CoV-2 RBD are in purple, orange red, and green, respectively. ACE2, angiotensin-converting enzyme 2; MEGA-X, Molecular Evolutionary Genetics Analysis version X; RBD, receptor-binding domain; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2

3.2 | Structure simulation of the protein complex of SARS-CoV-2 RBD and *Bovidae/Cricetidae*/turtle/snake ACE2

Recently, the structure of SARS-CoV-2 RBD with human ACE2 has been resolved. To investigate whether *Bovidae/Cricetidae* ACE2 maintained the binding affinity with SARS-CoV-2 RBD, we simulated the potential structure of the protein complex. T82 and E30 in *Bos taurus* ACE2 kept the contact to F486 and K417 in SARS-CoV-2 S (Figure 1B). N82 and Q34 in *Cricetulus griseus* ACE2 maintained the contact to F486 and Y453 in SARS-CoV-2 S (Figure 1C). We concluded that *Bovidae/Cricetidae* ACE2 could associate with SARS-CoV-2 S (Figure 1B,C).

To investigate the potential association between SARS-CoV-2 and ACE2 from turtle and snake, we simulated the potential structure of turtle/snake ACE2 with SARS-CoV-2 RBD. The AA correlated to hACE2 Q42 is changed to A (A41) in turtle (Figure 1D). We also noticed that the AA correlated to hACE2 H34 is changed to A (A60) in a snake (Figure 1E). When the contact AA was mutated to smaller AA (A), the contact force for protein-protein interaction will be reduced. Moreover, the corresponding AA of K31 was changed to E (E30) in turtle and Q (Q57) in snake ACE2 (Figure 1D). K31 in hACE2 was critical for SARS-CoV RBD binding and ACE2-K31D mutant abolished its association with SARS-CoV RBD.[15] Taken together, turtle and snake ACE2 are unlikely to bind to S protein of SARS-CoV-2.

4 | DISCUSSION

SARS-CoV, MERS-CoV, and SARS-CoV-2 have caused severe human infectious diseases in the last 2 decades. These three human coronaviruses originated from bats, but the intermediate hosts were different. SARS-CoV came from the *Paguma larvata*,[16] and the intermediate host for MERS-CoV is *Camelus dromedaries*.[17] The new coronavirus SARS-CoV-2 has recently caused a serious pandemic in China and other countries. However, it is not clear which animals are involved in the evolution of SARS-CoV-2 and which animals may be infected by SARS-CoV-2. RBD region in S protein of pangolin coronavirus is similar to that of SARS-CoV-2,[7,8] indicating the involvement of pangolin in the recombination of SARS-CoV-2. By analyzing the codon usage of SARS-CoV-2, people suggested that snake might be a potential host for SARS-CoV-2.[9] Another study indicated that turtle is a potential intermediate host for SARS-CoV-2 based on the key AAs in ACE2 for interacting with SARS-CoV RBD.[10] The late study raised the concerns of SARS-CoV-2 infection in the turtle aquaculture and pet turtle. Most of the coronaviruses hosts are mammals; with a few of exceptions are birds. Considering that all known hosts for coronaviruses are thermostatic animals, it is unlikely that reptiles will be infected with SARS-CoV-2.

There are 20 key AAs in ACE2 critical for binding S protein of SARS-CoV-2.[11] On the basis of these 20 AAs, we analyzed the corresponding AAs in ACE2 from a list of mammal, bird, turtle, and snake. We found that the ACE2 of turtles and snake lost the capability to associate with S protein (Table 1 and Figure 1D,E). These reptiles should be ruled out from the potential host list for SARS-CoV-2. *Aves* ACE2 was unlikely to associate with SARS-CoV-2 RBD because they lost the critical K corresponding to K31 in human ACE2 (Table 1). Pangolin ACE2 was predicted to recognize SARS-CoV-2 RBD less efficiently because it only preserved 14 of 20 critical AAs (Table 1). Interestingly, we found that ACE2 proteins from *Primates*, *Bovidae*, *Cricetidae*, and *Cetacea* were capable to recognize RBD of SARS-CoV-2 by maintaining the majority of key residues in ACE2 for associating with SARS-CoV-2 RBD. Swine ACE2 (CpACE2) with 15 of 20 matched critical AAs was shown to support SARS-CoV-2 entry.[6] *Bovidae/Cricetidae* ACE2 matched more AAs than swine ACE2, thus they should recognize SARS-CoV-2 RBD. It would strengthen our conclusion if we have biochemical evidence for the S-ACE2 interaction analysis for *Bovidae/Cricetidae* ACE2. On the basis of human ACE2 and SARS-CoV-spike complex structure model (PDB ID: 2AJF), we and others recently predicted that hamster ACE2 could associate with SARS-CoV-2 and hamster might be a candidate small animal model for SARS-CoV-2 infection.[18,19] Indeed, golden Syrian hamster (*Mesocricetus auratus*) has been established as a model to study the pathogenesis and transmission of COVID-19.[19] One of *Cetacea*, *Neophocaena asiaeorientalis asiaeorientalis* (Yangtze finless porpoise), lives in the middle and lower reaches of the Yangtze River and its lakes, where Wuhan located nearby.[20] It will be interesting to investigate whether Yangtze finless porpoise could be infected with SARS-CoV-2 or related coronavirus.

In conclusion, we found that *Bovidae/Cricetidae* ACE2 but not turtle/snake ACE2 could recognize SARS-CoV-2 RBD. More attention should be paid to *Bovidae* and *Cricetidae* in hunting the potential intermediate host for SARS-CoV-2.

ACKNOWLEDGMENTS

The authors would like to thank Dr Shan Gao for the discussion. This study is supported by grants from National Key Plan for Research and Development of China (2016YFD0500300), Shandong Academy of Medical Sciences Grant (2017-52), the Innovation Project of Shandong Academy of Medical Sciences, and Academic Promotion Program of Shandong First Medical University (2019LJ001). Molecular graphics and analyses performed with UCSF Chimera, developed by the Resource for Biocomputing, Visualization, and Informatics at the University of California, San Francisco, with support from NIH P41-GM103311.

CONFLICT OF INTERESTS

The authors declare that there are no conflict of interests.

AUTHOR CONTRIBUTIONS

LZ conceived the work. JL and XJ collected and analyzed the data. JL and YL contributed to graphics processing. LZ wrote the manuscript. All authors approved the final version for publication.

ORCID

Leiliang Zhang http://orcid.org/0000-0002-7015-9661

REFERENCES

1. Zhu N, Zhang D, Wang W, et al. A novel coronavirus from patients with pneumonia in China, 2019. *N Engl J Med*. 2020;382(8):727-733.
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How to cite this article: Luan J, Jin X, Lu Y, Zhang L. SARS-CoV-2 spike protein favors ACE2 from *Bovidae* and *Cricetidae*. *J Med Virol*. 2020;1–8. https://doi.org/10.1002/jmv.25817

From: Ebel,Greg
Sent: Thursday, October 08, 2020 1:02 PM EDT
To: Schountz,Tony epstein ecohealthalliance.org>
Subject: RE: R24

OK let me know if/when you'd want me to email him.
Greg

From: Schountz,Tony >
Sent: Thursday, October 08, 2020 10:36 AM
To: epstein ecohealthalliance.org>; Ebel,Greg
Subject: Re: R24

Yeah, it might be worth holding off until December to ask. □

T.

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Jon Epstein ecohealthalliance.org>
Sent: Thursday, October 8, 2020 8:28 AM
To: Ebel,Greg
Cc: Schountz,Tony
Subject: Re: R24

Sure, but I'd prefer to avoid sharing details of what we're doing at this stage, if possible.

Cheers,
Jon

Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
New York

(

On Wed, Oct 7, 2020, 5:49 PM Ebel,Greg > wrote:

> Hey,
>
> Do you all want me to reach out to Scott W about the WRCEVA R24?
>
> He might say no, but I'm fully OK with asking.
>
> Greg
>
> Gregory D. Ebel
> Professor, Department of Microbiology, Immunology and Pathology
> Director, Arthropod-Borne and Infectious Diseases Laboratory
> College of Veterinary Medicine and Biomedical Sciences
> Colorado State University

From: Schountz,Tony >
Sent: Wednesday, September 16, 2020 3:35 PM EDT
To: epstein ecohealthalliance.org>
CC: Schountz,Tony ; Ebel,Greg
Subject: Re: R24

Jon and Greg, my week has pretty much filled up, other than tomorrow morning from 8:30 to 11:00 MST. Next week has a number of openings, though.

Tony
—
Tony Schountz, PhD
Associate Professor
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Otherwise, suggest some times this week when you're free.

-Jon

On Mon, Sep 14, 2020 at 12:12 PM Schountz,Tony > wrote:

Hi Jon, we seemed to have missed you. We should reschedule this for later this week or perhaps next week.

Thanks,

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College of Veterinary Medicine
Colorado State University

On Sep 14, 2020, at 9:57 AM, Schountz,Tony > wrote:

Here's a Zoom link in case we need it. I'm limited to 30 minutes.

Topic: R24 Zoom Meeting
Time: Sep 14, 2020 10:00 AM Mountain Time (US and Canada)

Join Zoom Meeting
https://us02web.zoom.us/j/5861713088?pwd=RVJmb2VsenlWR1U3TkdiVGp4WUc2QT09

Meeting ID: 586 171 3088
Passcode: 4e5ZJe

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology

College of Veterinary Medicine
Colorado State University

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On Aug 31, 2020, at 7:19 AM, Jon Epstein ecohealthalliance.org> wrote:

Sorry, I have a meeting at that time. I'm free either the hour before or after that. Could we do 10AM MST?

On Fri, Aug 28, 2020 at 2:00 PM Schountz,Tony > wrote:

> How about September 14 at 9:00 AM MST?
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

From: Ebel,Greg >
Sent: Friday, August 28, 2020 11:57 AM
To: epstein @ecohealthalliance.org>; Schountz,Tony >
Subject: RE: R24

The morning of the 14th is OK for me.
Greg

From: Jon Epstein ecohealthalliance.org>
Sent: Friday, August 28, 2020 11:56 AM
To: Schountz,Tony >
Cc: Ebel,Greg
Subject: Re: R24

the 14th would work for me.
-Jon

On Fri, Aug 28, 2020 at 1:54 PM Schountz,Tony > wrote:

> Monday the 14th is open for me but the rest of the week is really tough.
> —
> Tony Schountz, PhD

Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Jon Epstein ecohealthalliance.org>
Sent: Friday, August 28, 2020 11:52 AM
To: Schountz,Tony
Cc: Ebel,Greg >
Subject: Re: R24

I'm actually off that week - we're moving the family back into NYC for the start of School (Sept 10th).
Could we meet the following week?

Thanks,
Jon

On Fri, Aug 28, 2020 at 1:45 PM Schountz,Tony wrote:

> Greg and Jon, I think we ought to schedule a conference call in a couple of weeks to hash out the R24 approach, namely to determine the goals and to identify people who need to be involved. How does the week of Sept 7 look? We're taking the kids hiking on Labor Day but otherwise my week is mostly open except for the morning of Thursday, September 10.
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--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

web: ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

--
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CC: Schountz,Tony
Subject: Re: R24

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Cheers,
Jon

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New York

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> Professor, Department of Microbiology, Immunology and Pathology
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> Director, Arthropod-Borne and Infectious Diseases Laboratory
>
> College of Veterinary Medicine and Biomedical Sciences
>
> Colorado State University

From: Ebel,Greg >
Sent: Friday, August 28, 2020 1:48 PM EDT
To: Schountz,Tony ; epstein ecohealthalliance.org>
Subject: RE: R24

I'm pretty sure I can do this on that week. I'm only really NOT available on the 10th.

Greg

From: Schountz,Tony
Sent: Friday, August 28, 2020 11:46 AM
To: Ebel,Greg ; epstein ecohealthalliance.org>
Subject: R24

Greg and Jon, I think we ought to schedule a conference call in a couple of weeks to hash out the R24 approach, namely to determine the goals and to identify people who need to be involved. How does the week of Sept 7 look? We're taking the kids hiking on Labor Day but otherwise my week is mostly open except for the morning of Thursday, September 10.

Tony

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Ebel,Greg
Sent: Tuesday, September 29, 2020 12:44 PM EDT
To: epstein ecohealthalliance.org>; Schountz,Tony >
Subject: RE: R24

That time works for me too. Can we get it on the calendar?
Greg

From: Jon Epstein ecohealthalliance.org>
Sent: Tuesday, September 29, 2020 10:38 AM
To: Schountz,Tony
Cc: Ebel,Greg
Subject: Re: R24

noon on the 7th (EDT) is open.
I asked Jean about research and for an example R24. She said she'd send one and get back to us regarding the limitations of an R24.
Cheers,
Jon

On Tue, Sep 29, 2020 at 12:21 PM Schountz,Tony wrote:

> Jon and Greg, how does Wed, Oct 7 between 9 AM and 3 PM work for you for the next meeting?
>
> Thanks,
>
> Tony
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University
>
> On Sep 16, 2020, at 7:35 PM, Schountz,Tony > wrote:
>
> Ok a week from tomorrow at 11/9 AM.
>
> Sent from my iPhone
>
> On Sep 16, 2020, at 5:41 PM, Jon Epstein @ecohealthalliance.org> wrote:
>
> Shall we say 9 MST /11 EDT ?
>
> Jonathan Epstein DVM, MPH, PhD
>
> Vice President for Science and Outreach
>
> EcoHealth Alliance
> New York
>
> (
>
> On Wed, Sep 16, 2020, 7:09 PM Schountz,Tony > wrote:
>
> > Yes, MST. Sorry.

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Sep 16, 2020, at 4:43 PM, Jon Epstein ecohealthalliance.org> wrote:

Is that mountain time?

Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
New York

On Wed, Sep 16, 2020, 6:27 PM Ebel,Greg > wrote:

> I could do those times on Thursday.
> Greg
>
> **From:** Schountz,Tony
> **Sent:** Wednesday, September 16, 2020 3:59 PM
> **To:** epstein ecohealthalliance.org>
> **Cc:** Ebel,Greg ; Schountz,Tony
>
> **Subject:** Re: R24
>
> Jon and Greg, do Tu or Th mornings, say 9 or 10, look good for you?
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University
>
> On Sep 16, 2020, at 3:22 PM, Jon Epstein ecohealthalliance.org> wrote:
>
> Me, too.
> Tuesday and thursday are fairly open if you want to suggest some times that work for you.
> -Jon
>
> On Wed, Sep 16, 2020 at 5:01 PM Ebel,Greg > wrote:
>
> > For me next week is a lot better.
> > Greg

From: Schountz,Tony
Sent: Wednesday, September 16, 2020 1:35 PM
To: epstein ecohealthalliance.org>
Cc: Schountz,Tony ; Ebel,Greg

Subject: Re: R24

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pwd=RVJmb2VsenlWR1U3TkdiVGp4WUc2QT09

Meeting ID: 586 171 3088
Passcode: 4e5ZJe

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> > > Disease Laboratory
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From: Ebel,Greg

Sent: Friday, August 28, 2020 11:57 AM
To: epstein ecohealthalliance.org>; Schountz,Tony

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> ---
>
> **From:** Jon Epstein ecohealthalliance.org>
> **Sent:** Friday, August 28, 2020 11:52 AM
> **To:** Schountz,Tony

Cc: Ebel,Greg

Subject: Re: R24

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Jon

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>

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> College of Veterinary Medicine
> Colorado State University

--

Jonathan H. Epstein DVM, MPH, PhD
Vice President for

From: 胡犇 <huben
Sent: Monday, October 01, 2018 7:36 PM EDT
To: Schountz,Tony >
Subject: Re: Re: Agenda of the 8th International Symposium of Emerging Viral Diseases

Dear Dr. Schountz:

I only need a short version.

Thanks.

Ben

-----原始邮件-----
发件人:"Schountz,Tony"
发送时间:2018-10-02 07:18:52 (星期二)
收件人: "胡犇" <huben
抄送:
主题: Re: Agenda of the 8th International Symposium of Emerging Viral Diseases

Hi Ben,

My arrival is flight NH 937 (Air Japan), Friday, Oct 19 at 10:00 PM.

My departure is flight NH 938, Tuesday, October 23 at 9:35 AM.

My CV is quite lengthy. Do you want me to send an abbreviated version?

Thank you,

Tony

> On Sep 28, 2018, at 9:17 PM, 胡犇 <huben wrote:
>
> Dear speaker:
>
> We have made the program for our emerging virus symposium. Your presentation is scheduled in the afternoon of 21st October, in the session "emerging viral pathogens".
>
> I have attached the program for your information.
>
> We have reserved accommodation for you at the conference venue, Optic Valley Plaza hotel. Please provide me your flight information once it is available, and we will arrange pick-up service at the airport.
>
> Also, please send me your update CV by 7th October, as we would like to include the CV of our speakers together with the abstracts in the conference proceedings.
>
> Thank you!
>
> Best wishes
>
> Ben Hu Ph.D
>
> Wuhan Institute of Virology, CAS
> Secretary of the 8th ISEVD
> <Program of the 8th ISEVD.pdf>

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology

From: 胡犇 <huben >
Sent: Friday, May 11, 2018 8:47 PM EDT
To: Schountz,Tony
CC: 石正丽 <zlshi ; 周鹏 <peng.zhou >
Subject: Re: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Dear Dr.Schountz:

Here is the hotel information:

name: Optics Valley Kingdom Plaza Hotel Wuhan,

address: No.1 Wu Jia Wan, Hongshan District, Wuhan, Hubei Province, China.

Best

Ben

-----原始邮件-----
发件人:"Schountz,Tony" >
发送时间:2018-05-12 00:01:20 (星期六)
收件人: "胡犇" <huben >
抄送: "Schountz,Tony" , "石正丽" <zlshi , "周鹏" <peng.zhou >
主题: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Hi Ben,

I have my flight booked and will arrive in Wuhan at 10:00 PM on October 19 (All Nippon Airways **NH 937**). Can you tell me the name and address of the hotel? I will need it for my visa and for my university administrators.

Thank you,

Tony

> On Apr 9, 2018, at 8:06 AM, 胡犇 <huben wrote:
>
> Dear Dr.Schountz:
>
> The 8th International Symposium on Emerging Viral Diseases will be held in October 20-22, 2018, in Wuhan, China. The biennial symposium is organized by Wuhan Institute of Virology, Chinese Academy of Sciences and has become an important event for leading Chinese and international virologists to discuss cutting-edge science on emerging viruses as well as to foster global collaborations.
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> Prof Zhengli Shi and Dr.Peng Zhou had a nice experience last year in Colorado when attending the symposium on bat-borne infectious diseases, and we know you have made great contributions to bat virus researches. We sincerely hope that you can attend the symposium. Please find enthe formal invitation letter for the meeting.
>
> If you have any question regarding the conference, please contact me.
>
> Thank you!
>
> Best regards
>
> Ben Hu Ph.D
>
> Research Assistant
>
> Secretary of the 8th International Symposium on Emerging Viral Diseases
>
> Wuhan Institute of Virology, Chinese Academy of Sciences

<Invitation letter Tony Schountz.pdf>

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: 胡犇 <huben >
Sent: Wednesday, August 08, 2018 9:38 PM EDT
To: Schountz,Tony
CC: 石正丽 <zlshi >
Subject: Re: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Hi Dr.Shountz:

There is no problem about the invitation letter with the official seal. I can prepare it today.

Is a scanned copy of this letter acceptable for visa application or the embassy must need an original copy?

Thanks

Ben

-----原始邮件-----
发件人:"Schountz,Tony"
发送时间:2018-08-09 02:15:14 (星期四)
收件人: "胡犇" <huben
抄送: "石正丽" <zlshi >
主题: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

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William Schountz

It would be helpful to get the letter by the end of next week because I need my passport back by September 14 for upcoming travel. I cannot get the passport back until I have the visa approved.

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Research Assistant

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Wuhan Institute of Virology, Chinese Academy of Sciences
Wuhan 430071, P.R. China

<Invitation letter Tony Schountz.pdf>

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—
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Colorado State University

From: 胡犇 <huben >
Sent: Wednesday, August 29, 2018 10:08 AM EDT
To: Schountz,Tony
Subject: Re: Re: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Dear Dr.Schountz:

May I ask whether your application for China visa goes well? Did the embassy accept the scanned copy of the invitation letter as supporting document?

If you successfully get the visa, please kindly update me.

Thanks.

Sincerely

Ben

-----原始邮件-----
发件人:"Schountz,Tony" >
发送时间:2018-08-09 10:00:26 (星期四)
收件人: "胡犇" <huben
抄送: "石正丽" <zlshi
主题: Re: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Thank you, Ben. My understanding is that it needs to be an original for the visa application.

Tony

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Wuhan 430071, P.R. China

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Tony Schountz, PhD
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Colorado State University

From: 胡犇 <huben >
Sent: Monday, August 13, 2018 7:13 AM EDT
To: Schountz,Tony
Subject: Re: Re: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases
Attachment(s): "Invitation letter William Schountz.jpg"

Dear Dr.Schountz:

Here is the scanned copy of the invitation letter with official seal. There are also some other speakers from US who requested this letter in our previous symposiums as well as in this year. They used the scanned copy for visa application.

However, if you confirm with the embassy that the scanned copy is not acceptable, I can send the original paper immediately. Do you need us to pay for the parcel or you can pay yourself upon receiving it?

Thanks

Sincerely

Ben

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> **发送时间:**2018-08-09 10:00:26 (星期四)
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Best regards

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Research Assistant

Secretary of the 8th International Symposium on Emerging Viral Diseases

Wuhan Institute of Virology, Chinese Academy of Sciences
Wuhan 430071, P.R. China

<Invitation letter Tony Schountz.pdf>

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WUHAN INSTITUTE OF VIROLOGY
THE CHINESE ACADEMY OF SCIENCES

Address:Xiaohongshan 44,Wuchang,Wuhan 430071,Hubei,P.R.China
Tel:+86-27-87199162 Fax: +86-27-87199162 http://www.whiov.ac.cn

August 9, 2018

William A. Schountz, Ph.D (Passport ID: 546272602)
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine, Colorado State University

Dear Dr. Schountz:

The 8th International Symposium on Emerging Viral Diseases (ISEVD) will be held in October 20-22, 2018 in Wuhan, China. The symposium is organized by Wuhan Institute of Virology, Chinese Academy of Sciences, and will cover a variety of topics including pathogen biology of emerging viruses, virus-host interaction, antiviral immunity, etc. This biennial symposium has become an important event for leading Chinese and international virologists to discuss cutting-edge science as well as to foster global collaboration.

It is our great pleasure to invite you to attend this symposium and present your work. As an invited speaker, your accommodation in Wuhan will be covered by the conference and your registration fee will be waived. Please note that we are regretfully unable to cover your travel expenses due to budget constrain.

We look forward to seeing you in Wuhan.

Sincerely Yours,

Xi Zhou, Ph.D
Senior Scientist & Professor
Wuhan Institute of Virology, CAS

Peng Zhou, Ph.D
Senior Scientist & Professor
Wuhan Institute of Virology, CAS

From: ￿ $ ￿￿ <huben >
Sent: Tuesday, June 20, 2017 11:03 PM EDT
To: Schountz,Tony >
Subject: Re: Re: Re: Requesting invitation letter for visa application

Dear Dr. Schountz:

The exciting conference is approaching. Although unfortunately I cannot attend the meeting due to the limited budget on international travel of our project, my colleagues, Prof. Zhengli Shi and Dr. Peng Zhou will go to Fort Collins and give two oral presentations.

May I ask for a pdf version of the conference program to forward to them?

Thank you so much!

Sincerely

Ben

> -----￿￿濮￿￿嵐欢-----
> ￿￿浠朵汉: "Schountz,Tony"
> ￿￿￿￿堕￿￿ 2017骞￿￿12￿￿￿￿￿涓￿
> ￿朵欢浜￿ "￿ $ ￿￿" <huben >
> ￿￿￿￿:
> 涓婚￿: Re: Re: Requesting invitation letter for visa application
>
> You're very welcome, Ben. I look forward to meeting all of you at the symposium.
>
> Tony
>
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

From: ￿ $ ￿￿ <huben >
Sent: Tuesday, April 11, 2017 7:34 PM
To: Schountz,Tony
Subject: Re: Re: Requesting invitation letter for visa application

Dear Dr. Schountz:
Thank you so much for your kind help!
Sincerely
Ben

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> ￿￿￿￿堕￿￿ 2017骞￿￿11￿￿￿￿￿浜￿
> ￿朵欢浜￿ "￿ $ ￿￿" <huben
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> Ben, I have attached a Word file that you can edit with the names and addresses of the four participants. So, just make a copy for each one and use them.
>
> Thank you,
>
> Tony

On Apr 11, 2017, at 3:56 AM, ﾟ筹ﾟ濡ﾟ<huben wrote:

Dear Dr.Schountz:
I am a researcher at Wuhan Institute of Virology, Chinese Academy of Sciences. My colleagues and I are studying bat viruses and we have submitted four abstracts to the 2nd International Symposium on Infectious Diseases of Bats which is going to be held in Fort Collins in June.
The title for the 4 abstracts are:
1) SARS coronavirus may have originated from frequent recombination events betwwen SARS-like coronaviruses in a single horseshoe bat habitat (oral)
2) Dampening of STING-dependent IFN production: an implication of virus tolerance in bats? (oral) ﾟﾟﾟﾟ noticed from the web that this abstract has already been confirmed as oral presentation)
3) Genomic characterization of diverse BatCoV HKU10 and three novel alphacoronaviruses (poster)
4) Genetically diverse filoviruses in Rousettus and Eonycteris spp. bats, China, 2009 and 2015. (poster)
As it is a unique conference specializing on our research area, we are very eager to attend. However, it usually takes at least two months for us to get the US visa due to the complicated procedure of applying for travel permit to Chinese Academy of Sciences and then one month of administrative processing by US embassy. So in order we can make our visit to Colorado in late June, we have to start the process of travel permit and visa application now.
To apply for a travel permit, we are required to submit an invitation letter from the conference organizer. I know for the bat-borne disease meeting, we will know the results of the acceptance of the abstract by May. But it will be late for us to apply for the travel permit and US visa.
Could you please kindly provides four invitation letters to us indicating we will attend the meeting and give presentations? (oral or posters)
It does not matter whether the abstracts will be finally selected as he invitation letters are only for visa application.
We deeply appreciate your understanding and assistance.
Thank you very much!
Best regards

Ben Hu Ph.D
Research Assistant
Wuhan Institute of Virology, CAS

ﾟﾟ/div>
Tony Schountz, PhD
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From: 胡犇 <huben >
Sent: Thursday, October 18, 2018 10:16 AM EDT
To: Schountz,Tony
Subject: Re: Re: Re:Re: Final Program of the 8th International Symposium on Emerging Viral Diseases

Dear Dr.Schountz:

I have an app via which I can follow the status of any flight.

So I can arrange with flexibility.

But hope everything will be fine.

Sincerely

Ben

-----原始邮件-----
发件人:"Schountz,Tony" < >
发送时间:2018-10-18 21:59:58 (星期四)
收件人: "胡犇" <huben
抄送:
主题: Re: Re:Re: Final Program of the 8th International Symposium on Emerging Viral Diseases

Hi Ben,

It looks like heavy thunderstorms for my arrival in Tokyo. Hopefully, they will not delay my connection to Wuhan. If I miss the flight to Wuhan, I will email you so that you can let the driver know. Otherwise, I should see him/her in about 24 hours!

Thanks,

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: 胡犇 <huben >
Sent: Wednesday, October 17, 2018 9:54 AM
To: Schountz,Tony
Subject: Re:Re: Final Program of the 8th International Symposium on Emerging Viral Diseases

Yes Dr.Schountz.

The pick-up from the airport to the hotel will be arranged.

Safe journey and see you soon.

Best

Ben

在 2018-10-17 23:41:10，"Schountz,Tony" > 写道：

>Hi Ben,
>
>
>I just want to verify a driver will pick me up at the airport upon my arrival and take me to the hotel.

>
>
>Thank you,
>
>
>Tony

From: 胡犇 <huben >
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To: Schountz,Tony
Subject: Re: Re: Requesting invitation letter for visa application

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Sincerely

Ben

-----原始邮件-----
发件人: "Schountz,Tony" >
发送时间: 2017年4月11日 星期二
收件人: "胡犇" <huben
抄送:
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Wuhan Institute of Virology, CAS

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Colorado State University

From: Schountz,Tony
Sent: Tuesday, September 01, 2020 4:26 PM EDT
To: Aleksei Chmura < ecohealthalliance.org>
CC: Schountz,Tony ; Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Re: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

Yes, that would work. Talk to you soon. I'm at the number below.

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Sep 1, 2020, at 2:22 PM, Aleksei Chmura ecohealthalliance.org> wrote:

Thanks, Tony!

That is good to read. Would 3pm Colorado (5pm NYC) today work for you - in approximately 40 mins?

If not, then what about tomorrow or Thursday at the same time?

Cheers,

-Aleksei

On Sep 1, 2020, at 16:20, Schountz,Tony > wrote:

Hi Aleksei,

I think a phone call would be better. I think she'd make a great addition to your team.

I'm available most of this week.

Tony
—
Tony Schountz, PhD
Associate Professor
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Colorado State University

On Aug 30, 2020, at 4:26 PM, Aleksei Chmura ecohealthalliance.org> wrote:

Dear Dr. Schountz,

We just interviewed Anna Fagre for a position here at EcoHealth Alliance as a Research Scientist and Project Manager. Our hiring committee thought she was terrific with the right background and attitude for our team. Anna listed you as a reference. If you would be

willing to send some comments about Anna, that would be terrific!

I have attached our position advertisement, so you may know more about the position - though based on her skillset, the specifics would evolve a bit. This position would focus primarily on our emerging infectious disease projects based in Southeast Asia including our recently awarded, NIAID funded EID-SEARCH program:

- https://www.ecohealthalliance.org/program/south-east-asia-research-collaboration-hub

I look forward to your reply and should a phone call be more convenient, we could do that as well.

On behalf of our whole committee, I sincerely appreciate your time.

-Aleksei

Aleksei Chmura, PhD
Chief of Staff

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-4182

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

<2020 Research Scientist and Project Manager Job Ad.pdf>

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> > -Aleksei
> >
> > **Aleksei Chmura, PhD**
> > *Chief of Staff*
> >
> > EcoHealth Alliance

520 Eighth Avenue, Suite 1200
New York, NY 10018-4182

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

<2020 Research Scientist and Project Manager Job Ad.pdf>

From: Ebel,Greg
Sent: Wednesday, April 01, 2020 1:04 AM EDT
To: epstein ecohealthalliance.org>; Schountz,Tony
Subject: RE: still working on bat section
Attachment(s): "C06 Update 2020.docx"

Hi Jon,

Thanks for the update. I'm working on the part of the document that is the pivot from the original C06 to the new scope. I'm attaching it in draft form in case you're interested in looking at it. Comments are welcome as always.

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Sent: Tuesday, March 31, 2020 11:02 PM
To: Ebel,Greg ; Schountz,Tony
Subject: still working on bat section

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I did get a letter of support from Vincent - just waiting for a signed copy.

Cheers,
Jon

--
Jonathan H. Epstein DVM, MPH, PhD
Vice President for Science and Outreach
EcoHealth Alliance
460 West 34th Street, Ste. 1701
New York, NY 10001

web: ecohealthalliance.org

Pathogens transmitted by bat and arthropod vectors continue to burden the health of humans around the world. Bat-associated pathogens, such as the currently circulating SARS-CoV-2, ebolaviruses, Nipah virus, rabies virus and others are among the most impactful and dreaded infections known. Malaria is perhaps the most deadly infection in the tropics. West Nile, chikungunya and Zika viruses have emerged as major global pathogens. Tick-transmitted infections such as Lyme disease and Powassan virus continue to emerge in temperate regions. Agents vectored by bat and/or arthropod vectors thus constitute some of the most feared, difficult and persistent problems affecting human health.

Therefore, Colorado State University (CSU) established the Arthropod-borne and Infectious Disease Laboratory (AIDL) in 1984 to counter these emerging threats. One of the many unique aspects of AIDL includes housing one of the only captive breeding colonies of bats for use in infectious disease research, and BSL2 and BSL3 insectaries. The pandemic spread of SARS-CoV-2 highlights the national need for this unique resource, and the central role that CSU now occupies in the ability of the US to study and design countermeasures against emerging viral threats of this type.

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This proposal, reviewed highly favorably in 2019 but not selected for funding, represents a unique opportunity to rapidly increase US capacity for housing, breeding and using bats in research. In particular, we propose to:

From: Jon Epstein ecohealthalliance.org>
Sent: Thursday, April 02, 2020 11:02 AM EDT
To: Ebel,Greg >
CC: Schountz,Tony >
Subject: Re: still working on bat section

Sure. And would appreciate if you could copy me on those communications as well.
Cheers,
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On Thu, Apr 2, 2020 at 12:51 AM Ebel,Greg > wrote:

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<C06 Update 2020.docx>

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Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street, Ste. 1701

From: Jon Epstein ecohealthalliance.org>
Sent: Wednesday, April 01, 2020 6:47 PM EDT
To: Schountz,Tony
CC: Ebel,Greg
Subject: Re: still working on bat section
Attachment(s): "C06 Update 2020_JHE.docx","Munster LoS_Ebel_signed.pdf"

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Tony Schountz, PhD
Associate Professor
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Department of Microbiology, Immunology and Pathology
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Colorado State University

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Emerging zoonotic ~~Pathogens~~viruses originating in bats ~~transmitted by bat and arthropod~~and vector-borne pathogens ~~vectors~~ continue to significantly threaten ~~burden~~ the health of humans and domestic animals around the world. Bat-associated pathogens, such as coronaviruses, including the currently circulating SARS-CoV-2~~,~~; filoviruses (e.g. Ebola and Marburg viruses), and henipaviruses (e.g. Nipah virus), ~~rabies virus and~~ others are among the most high consequence ~~impactful and dreaded infections~~viruses known. Malaria is perhaps the most deadly infection in the tropics. West Nile, chikungunya and Zika viruses have also emerged as major ~~global~~ pathogens globally. Tick-transmitted infections such as Lyme disease and Powassan virus continue to emerge in temperate regions as climate change expands the range tick vectors. Agents hosted by bats and~~/or arthropod vectors~~vector-borne pathogens thus constitute some of the most ~~feared~~important global health challenges and there is data to suggest that the rate of zoonotic disease emergence will continue to accelerate into the future.~~, difficult and persistent problems affecting human health.~~

To meet this challenge,~~Therefore~~, Colorado State University (CSU) established the Arthropod-borne and Infectious Disease Laboratory (AIDL) in 1984 to counter these emerging threats. One of the many unique aspects of AIDL includes housing one of the only captive breeding colonies of bats for use in infectious disease research, and BSL2 and BSL3 insectaries. One of the major challenges for studying the origins, transmissibility and pathogenesis of emerging bat-borne viruses is the lack of bat animal models. The species diversity of bats is second only to rodents among mammals, however, there are key species that have been associated with important groups of zoonotic viruses such as Ebola and Margburg virus, Nipah virus, and SARS and SARS-CoV2-related coronaviruses, and there is growing evidence that bats are physiologically and immunologically unique in their ability to tolerate viral infection, resist cancer, and have disproportionately long lifespans for their size. All of this makes the dearth of facilities capable of housing bats for basic research and the lack of available bat colonies in the United States for use in biomedical investigations a major impediment to basic infectious disease and translational medicine research. The current ~~pandemic spread o~~COVID-19 pandemic~~f SARS-CoV-2~~ highlights the national need for the~~is~~ ~~unique~~proposed facility as a scientific resource, and the central role that CSU now occupies in the ability of the US to study and design countermeasures against emerging viral threats. ~~of this type~~.

To support research into significant known and unknown emerging diseases, including those listed by the WHO R&D Blueprint as the ten most significant infectious disease threats to global health (half of which are bat-associated or vector borne viruses), CSU committed $22M in 2019 to construct a new building, the Center for Vector-Borne Infectious Diseases (CVID), to replace aging AIDL infrastructure. CVID construction is ongoing and we anticipate moving in in late 2020.

While CSU's commitment of $22M is laudable, it is insufficient to provide adequate housing for the additional bat colonies needed to address the urgent need for research into the biology and emergence of SARS-CoV-2, MERS CoV, Nipah virus, Ebola and yet-to-be discovered viral agents ("Disease X") which are statistically most likely to emerge from bat reservoirs. Further, additional infrastructure within the CVID is required in order to ensure that research focusing on bat-borne diseases is paired with adequate BSL2 and BSL 3 lab, tissue culture and other support space.

Commented [JE1]: There's little overlap here, so I'm trying to make sure they're read as two distinct and important categories of human health threats.

Commented [JE2]: I know it's NIAID, but including a One Health perspective here.

Commented [JE3]: Most human impact is from dog-associated rabies, not bats, so it's probably less relevant to this discussion of emerging viruses.

Commented [S4]: This seems out of place in the context of bats (before) and SARS-CoV-2 (after).

Commented [JE5]: I suppose it's too late to change the name of the facility? Can the bat wing (no pun intended) be given a name to reflect the research focus?

This proposal, which scored well~~reviewed highly favorably~~ in 2019 but was not selected for funding, represents a unique opportunity to rapidly increase US capacity for housing, breeding and using bats in biomedical research. In particular, we propose to:

- Develop a state-of-the art facility to house a breeding colony of *Pteropus* fruit bats known to be natural reservoirs for henipaviruses, filoviruses, and coronaviruses. This will be the first of its kind in the world, and will be a critically important resource for developing and generating reagents (e.g. cell lines, validated serology and PCR assays, etc…) studying basic genomics (groundbreaking work has begun in Singapore and Australia on bat viral tolerance using an Australian Pteropus species, and this will allow the US to actively accelerate this area of research by focusing on a natural reservoir for Nipah virus, filoviruses, and coronaviruses; build on the existing immunology and genomics work, and develop new lines of cancer and aging related research by engaging investigators from various centers at NIH, CSU, and around the world. Experimental work involving high containment pathogens (Nipah virus, Ebola, etc..) will be conducted through a partnership with NIAID Rocky Mountain Labs (see Munster letter of support) in Hamilton, MT.

- Import other key bat species (e.g. *Rhinlophus affinis*) and house native North American bat species for use in coronavirus research, including SARS CoV-2 within CVID.

Current Bat Research at CSU

Colorado State University has a breeding colony of Jamaican fruit bats (*Artibeus jamaicensis*), one of the most common and largest fruit bats in the New World. This colony was established in 2005 with funds from the NIAID Emerging Virus Disease Unit contract (AI25489) after it was determined that SARS-CoV was a bat-borne virus. Currently funded bat projects are to study SARS-CoV (CSU VPR funding), MERS-CoV (AI140442), bat influenza A viruses (AI134768), henipaviruses (DARPA G228-19-W7329) and rabies virus (DOE B634747). Our long-term goal for this colony is to make it the "bat version" of the laboratory mouse so that we can conduct experimental infections for other researchers, or provide bats to those who may need them for experiments at their institutions.

We have determined the species is susceptible to several viruses, including Zika virus (30716104), H18N11 bat influenza A virus (31527796), Middle East respiratory coronavirus (MERS-CoV) (26899616), Cedar henipavirus (unpublished), Tacaribe virus (22379103) and Bukakata virus (unpublished), the last two of which cause fatal diseases in the bats. We have also established primary cell lines from the species that are susceptible to MERS-CoV (26899616), Zaire ebolavirus (27354372), and Nipah, Hendra and Cedar henipaviruses (unpublished). We have generated a number of reagents, including monoclonal antibodies and recombinant cytokines, virological and immunological methods, large transcriptome data sets (23166587, 28959737), basic physiological parameters (32164795) and we have demonstrated that it can serve as a surrogate bat model organism for the study of bat-borne viruses. Importantly, a genome assembly to 30x coverage is available (NCBI PVKR01).

SARS-CoV Project. We performed an initial susceptibility study of three Jamaican fruit bats and found that all had low levels of viral RNA in oral swabs within a few days after intranasal

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Commented [JE6]: SARS COV-2?

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National Institute of Allergy and Infectious Diseases

ROCKY MOUNTAIN LABORATORIES

Division of Intramural Research
National Institute of Allergy
and Infectious Diseases
Laboratory of Virology
Virus Ecology Section

April 1st, 2020

Dear Dr. Auchincloss,

It is with utmost pleasure to be able to provide a letter of support for the CSU bat research center. Past outbreaks of bat-borne zoonotic viruses such as coronaviruses, henipaviruses and filoviruses, have had an enormous impact on human and wildlife health. The unpredictability of the zoonotic introductions of these bat-borne limits the potential for effective intervention strategies. Within my research at the NIAIDs Rocky Mountain Laboratories, I have directly focussed on bat-borne viruses such as Nipah virus, Ebola virus, MERS-CoV and now SARS-CoV-2. In particular we have extensive knowledge of bat infection models of ß-coronaviruses (MERS-CoV and WIV-1, in *Artibeus* and *Rousettus* bats) and Nipah virus (*Rousettus* bats) and are one of the few facilities which are completely set-up to perform bat studies in high and maximum containment (including long-term husbandry and on-site veterinary staff) and complete downstream immunological, genetic and virological analyses. In the absence of suitable breeding facilities at intramural NIAID, the addition of a centre focussed on *in vivo* bat research at CSU deserves the NIAIDs unconditional support.

I am underwriting my enthusiasm to continue to collaborate on the development of a bat resource center including breeding colonies of key bat species, at CSU. Having access to natural hosts for coronaviruses, henipaviruses and filoviruses would significantly advance research in infectious disease undertaken by my group and others at RML, and I am committed to working with Drs. Bowen and Schountz at CSU (long standing research collaboration on MERS-CoV) and Dr. Epstein of EcoHealth Alliance (long standing collaboration on the underlying ecological changes driving spillover events of Nipah virus) to develop and use the resources generated through this C06 proposal. The SARS-CoV-2 pandemic marks an occasion which should put renewed focus on detailed studies of bats as reservoirs of emerging diseases. After SARS-CoV-1, MERS-CoV and Ebola virus in West Africa, we have yet another high impact (both from public health as economic perspective) bat-borne disease which justifies the urgent need for facilities in the US for advanced bat infectious disease studies.

Please feel free to contact me with any remaining questions,

Sincerely,

Vincent Munster
Chief, Virus Ecology Section
Laboratory of Virology
Rocky Mountain Laboratories
NIAID/NIH

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Sent: Thursday, April 02, 2020 12:51 AM EDT
To: epstein ecohealthalliance.org>; Schountz,Tony < >
Subject: RE: still working on bat section

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From: 石正丽 <zlshi
Sent: Tuesday, October 30, 2018 10:14 PM EDT
To: Schountz,Tony
Subject: Re: Thank you!

Dear Tony,

Thanks you again for your comming and your excellent presentation.

It'll be great if we can form a collaboration project and do personal trainning in the future.

Best regards,

Zhengli,

> -----原始邮件-----
> **发件人:**"Schountz,Tony"
> **发送时间:**2018-10-31 00:11:10 (星期三)
> **收件人:** zlshi <zlshi
> **抄送:**
> **主题:** Thank you!
>
> Dear Zhengli,
>
> I want to thank you for the invitation to speak at the emerging infectious disease conference. It was a really great experience for me and I was pleased with the talks, posters and how well your team organized and ran the meeting. I hope I can return to the next meeting in two years as I am sure we will have much more data on bats and influenza virus, MERS-CoV and henipaviruses.
>
> I was so struck by the work at the Wuhan Institute of Virology that I spoke briefly to Peng about how your institute and our Arthropod-borne and Infectious Disease Laboratory (AIDL, http://csu-cvmbs.colostate.edu/academics/mip/aidl/Pages/default.aspx) group have so many similarities. I wonder if you might have an interest in forming a loose association between our groups? I don't know how we could manage this, but one feature I envision would be collaboration on relevant projects (e.g., arboviruses and bat-borne viruses) and training of students. So, if you think there might be interest amongst your group, perhaps we can have further discussions about it.
>
> Thank you very much!
>
> Tony
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

From: 周鹏 <peng.zhou >
Sent: Thursday, July 13, 2017 4:40 AM EDT
To: Schountz,Tony < >
Subject: Re:Greetings

Hi, Tony,

As you can see from Zhengli email, you are warmly welcomed !

Cheers,
Peng

在 2017-07-13 08:19:58, "Schountz,Tony" > 写道：

>Hi Peng,
>
>
>
>
>Thanks again for attending the symposium. I really appreciate your comments during the discussion as well as the questions. I hope to make the conference at your institution next year if I can manage to get travel funds.
>
>
>
>
>Thanks,
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>
>Tony
>
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>
>—
>Tony Schountz, PhD
>Associate Professor
>Arthropod-borne and Infectious Disease Laboratory
>Department of Microbiology, Immunology and Pathology
>College of Veterinary Medicine
>Colorado State University

From: 胡犇 <huben
Sent: Wednesday, October 17, 2018 11:54 AM EDT
To: Schountz,Tony
Subject: Re:Re: Final Program of the 8th International Symposium on Emerging Viral Diseases

Yes Dr.Schountz.

The pick-up from the airport to the hotel will be arranged.

Safe journey and see you soon.

Best

Ben

在 2018-10-17 23:41:10, "Schountz,Tony" > 写道：

>Hi Ben,
>
>
>I just want to verify a driver will pick me up at the airport upon my arrival and take me to the hotel.
>
>
>Thank you,
>
>
>Tony
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>
>
>On Oct 15, 2018, at 7:14 AM, 胡犇 wrote:
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>
>Dear speaker:
>
>
>We will have the 8th International Symposium on Emerging Viral Diseases in Wuhan soon this weekend.
>
>
>Please find enclosed the final program of the meeting, as minor changes have been made compared with the version that I previously sent to you.
>
>
>You will be accommodated in the venue hotel of the symposium, the Optics Valley Kingdom Plaza. Our student volunteers or myself will pick you up at Wuhan airport or Wuhan railway station when you arrive.
>
>
>We look forward to meeting you soon.
>
>
>Sincerely
>
>
>Ben Hu Ph.D
>Wuhan Institute of Virology, CAS
>Secretary of the 8th ISEVD
><Program of the 8th ISEVD_Final.pdf>
>
>
>—
>Tony Schountz, PhD
>Associate Professor
>Arthropod-borne and Infectious Disease Laboratory
>Department of Microbiology, Immunology and Pathology
>College of Veterinary Medicine
>Colorado State University

>

From: 胡犇 <huben >
Sent: Monday, October 22, 2018 2:24 AM EDT
To: Schountz,Tony
Subject: Re:Re: Final Program of the 8th International Symposium on Emerging Viral Diseases

Hi Dr Schountz,

Your flight will be on tomorrow morning at 9:35?

I will be at th hotel at 6:30. I will meet you at the hotel lobby then and ask a vehicle to send you to the airport.

Please also send me your boarding pass and I will print it for you and give you tomorrow morning.

Best

Ben

在 2018-10-22 11:44:15, "Schountz,Tony" > 写道：

>Hi Ben
>
>
>Do I need to schedule a ride to the airport tomorrow? Also do you know if I can print my boarding passes here at the hotel?
>
>
>Thanks
>
>
>Tony
>
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>Sent from my iPhone
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>On Oct 18, 2018, at 10:16 PM, 胡犇 <huben wrote:
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> Dear Dr.Schountz:
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> I have an app via which I can follow the status of any flight.
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>
> So I can arrange with flexibility.
>
>
> But hope everything will be fine.
>
> Sincerely
>
> Ben
>
>
>-----原始邮件-----
>发件人:"Schountz,Tony"
>发送时间:2018-10-18 21:59:58 (星期四)
>收件人: "胡犇" <huben
>抄送:
>主题: Re: Re:Re: Final Program of the 8th International Symposium on Emerging Viral Diseases
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>Hi Ben,
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>It looks like heavy thunderstorms for my arrival in Tokyo. Hopefully, they will not delay my connection

to Wuhan. If I miss the flight to Wuhan, I will email you so that you can let the driver know. Otherwise, I should see him/her in about 24 hours!
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>Tony
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>Colorado State University
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>From: 胡犇 <huben
>Sent: Wednesday, October 17, 2018 9:54 AM
>To: Schountz,Tony
>Subject: Re:Re: Final Program of the 8th International Symposium on Emerging Viral Diseases
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>Yes Dr.Schountz.
>
>The pick-up from the airport to the hotel will be arranged.
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>Safe journey and see you soon.
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>Best
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>Ben
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>在 2018-10-17 23:41:10, "Schountz,Tony" 写道：
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>>Hi Ben,
>>
>>
>>I just want to verify a driver will pick me up at the airport upon my arrival and take me to the hotel.
>>
>>
>>Thank you,
>>
>>
>>Tony
>

From: 胡犇 <huben >
Sent: Monday, August 06, 2018 7:27 PM EDT
To: Schountz,Tony
Subject: Re:Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Thanks a lot for the abstract, Dr.Schountz.

Best

Ben

在 2018-08-07 04:36:28, "Schountz,Tony" > 写道：

>Hi Ben,
>
>
>Attached is my abstract. I should have quite a bit more information for the talk as we have many bats infected with the virus and are getting some very interesting results.
>
>
>Thanks,
>Tony
>
>
>On Apr 9, 2018, at 8:06 AM, 胡犇 <huben wrote:
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>
>
>Dear Dr.Schountz:
>
>
>
>The 8th International Symposium on Emerging Viral Diseases will be held in October 20-22, 2018, in Wuhan, China. The biennial symposium is organized by Wuhan Institute of Virology, Chinese Academy of Sciences and has become an important event for leading Chinese and international virologists to discuss cutting-edge science on emerging viruses as well as to foster global collaborations.
>
>
>Prof Zhengli Shi and Dr.Peng Zhou had a nice experience last year in Colorado when attending the symposium on bat-borne infectious diseases, and we know you have made great contributions to bat virus researches. We sincerely hope that you can attend the symposium. Please find enthe formal invitation letter for the meeting.
>
>
>If you have any question regarding the conference, please contact me.
>
>
>Thank you!
>
>
>Best regards
>
>
>
>
>Ben Hu Ph.D
>
>
>Research Assistant
>
>
>Secretary of the 8th International Symposium on Emerging Viral Diseases
>
>
>Wuhan Institute of Virology, Chinese Academy of Sciences
>Wuhan 430071, P.R. China
>
><Invitation letter Tony Schountz.pdf>
>
>
>—
>Tony Schountz, PhD
>Associate Professor
>Arthropod-borne and Infectious Disease Laboratory

From: 胡犇 <huben
Sent: Saturday, May 12, 2018 11:37 AM EDT
To: Schountz,Tony
Subject: Re:Re: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

No need, Dr.Schountz. For invited speakers the rooms will be reserved by the conference.

Ben

在 2018-05-12 23:15:20, "Schountz,Tony" 写道：

>Thank you, Ben. Should I make my own reservation?
>
>
>
>
>Tony
>
>
>
>
>—
>Tony Schountz, PhD
>Associate Professor
>Arthropod-borne and Infectious Disease Laboratory
>Department of Microbiology, Immunology and Pathology
>College of Veterinary Medicine
>Colorado State University
>

>
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>
>From: 胡犇 <huben
>Sent: Friday, May 11, 2018 6:47 PM
>To: Schountz,Tony
>Cc: 石正丽; 周鹏
>Subject: Re: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases
>
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>
> Dear Dr.Schountz:
>
> Here is the hotel information:
>
> name: Optics Valley Kingdom Plaza Hotel Wuhan,
>
> address: No.1 Wu Jia Wan, Hongshan District, Wuhan, Hubei Province, China.
>
>
>
> Best
>
> Ben
>
>
>
>
>-----原始邮件-----
>发件人:"Schountz,Tony" <   >
>发送时间:2018-05-12 00:01:20 (   )
>收件人: "胡犇" <huben
>抄送: "Schountz,Tony"   , "石正丽" <zlshi   , "周鹏"
<peng.zhou@wh.iov.cn>
>主题: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases
>
>Hi Ben,
>
>
>I have my flight booked and will arrive in Wuhan at 10:00 PM on October 19 (All Nippon Airways NH 937).

Can you tell me the name and address of the hotel? I will need it for my visa and for my university administrators.
>
>
>Thank you,
>
>
>Tony
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>Dear Dr.Schountz:
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><Invitation letter Tony Schountz.pdf>
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>Tony Schountz, PhD
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>Colorado State University
>

>

From: 胡犇 <huben >
Sent: Monday, October 22, 2018 3:03 AM EDT
To: Schountz,Tony
Subject: Re:Re: Re:Re: Final Program of the 8th International Symposium on Emerging Viral Diseases

Dr Schountz

No you need not pay from your side.

I will pay the vehicle for you using a car-calling app.

Btw, you will share one vehicle with the Japanese speaker, Dr Saijo together, as you will fly with the same flight.

Cheers

Ben

在 2018-10-22 14:42:57, "Schountz,Tony" > 写道：

>Thank you, Ben. My boarding passes are attached as a single PDF (two passes).
>
>
>
>
>Will I need to pay the driver? If so, can it be done with my credit card? If not, I will need to get currency exchange and need to know how much it will cost.
>
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>
>
>Tony
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>—
>Tony Schountz, PhD
>Associate Professor
>Arthropod-borne and Infectious Disease Laboratory
>Department of Microbiology, Immunology and Pathology
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>Colorado State University
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>From: 胡犇 <huben >
>Sent: Monday, October 22, 2018 12:24 AM
>To: Schountz,Tony
>Subject: Re:Re: Final Program of the 8th International Symposium on Emerging Viral Diseases
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>>>
>>>Tony
>>

From: Aleksei Chmura ecohealthalliance.org>
Sent: Sunday, August 30, 2020 6:26 PM EDT
To: Schountz,Tony
CC: Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance
Attachment(s): "2020 Research Scientist and Project Manager Job Ad.pdf"

Dear Dr. Schountz,

We just interviewed Anna Fagre for a position here at EcoHealth Alliance as a Research Scientist and Project Manager. Our hiring committee thought she was terrific with the right background and attitude for our team. Anna listed you as a reference. If you would be willing to send some comments about Anna, that would be terrific!

I have attached our position advertisement, so you may know more about the position - though based on her skillset, the specifics would evolve a bit. This position would focus primarily on our emerging infectious disease projects based in Southeast Asia including our recently awarded, NIAID funded EID-SEARCH program:

- https://www.ecohealthalliance.org/program/south-east-asia-research-collaboration-hub

I look forward to your reply and should a phone call be more convenient, we could do that as well.

On behalf of our whole committee, I sincerely appreciate your time.

-Aleksei

Aleksei Chmura, PhD
Chief of Staff

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-4182

www.ecohealthalliance.org

EcoHealth Alliance

JOB ADVERTISMENT

POSITION TITLE: Research Scientist and Project Manager

POSITION SUMMARY

Reporting directly to the President, the Research Scientist will assist senior research scientists on our NIH-funded and projects to examine the dynamics of pathogen transmission within and among wildlife populations, livestock, and humans; as well as the risk of spillover, patterns of infection, phylogenetic relationships of emerging zoonotic diseases. The candidate should be self-motivated and proactive. The Research scientist will need to have a collaborative approach to research, a positive attitude towards solving complex problems, and creativity. This position is a critical part of our science base and the will actively and collaboratively engage in expanding the boundaries of our research as well as help create our 'think-tank' on emerging infectious diseases. Above all, a passion for understanding the process of zoonotic disease emergence is key.

RESPONSIBILITIES

- Collaborate and/or lead in the design and implementation of a multi-country field study of zoonotic disease emergence from bats, rodents, and primates as well as the role of human behavior in disease emergence and analyze the resulting data. Extensive foreign travel, particularly in southeast Asia will be expected.
- Work on modeling and other projects that broadly integrate evolutionary, ecological, and biodiversity data into emerging disease and zoonotic disease models.
- Liaise with EcoHealth Alliance and other scientists to generate hypotheses and to assist with development of models and plan avenues of scientific investigation
- Engage with EcoHealth Alliance scientists and consortium partners on our other projects as well as on federally funded programs on AI, Ebola, Nipah, RVFV, and other emerging diseases.
- Work closely with the President, science staff, and collaborators to design and execute analytical projects to understand the process of zoonotic disease emergence including examination of the roles of host-specific and evolutionary drivers of disease emergence.
- Represent EcoHealth Alliance and work with stakeholders and collaborators at local, national, and international levels.
- Manage Staff, liaise with international partners, and report proactively to funders
- Assist with grant and manuscript writing
- Be responsible for grant management and program coordination
- Use a strong fact basis and collaborative approach to formulate alternative and creative solutions to problems and sensitive issues.

QUALIFICATIONS

- Minimum of Ph.D. in: Biology, Ecology, Evolutionary Biology, Public Health, or related field in the life sciences
- Strong quantitative analytical skills
- Experience with statistical analyses, particularly using R
- Experience with phylogenetic and evolutionary analyses a plus.
- Previous experience in public health or infectious diseases
- Previous experience writing grants and with international grants and program administration of large projects with key components including field and laboratory work and analyses
- 1-to-3 years' experience working on projects funded by US Federal agencies as well as prior non-profit, academic, or equivalent positions
- Demonstrated writing and research skills including Publications in peer-reviewed scientific journals
- Ability to conduct literature reviews, data collation and cleaning, and exploratory data analyses
- Strong writing and verbal communication skills with a keen eye for detail
- Proven ability to work independently
- Self-driven, highly motivated, organized, and willing to perform research and administrative duties
- Strong interpersonal skills; a willingness to place team before self and a strong sense of diplomacy
- Previous experience in Southeast Asia is a plus
- Cultural sensitivity
- Willingness to work some mornings, evenings, weekends as necessary
- Fluency in written and spoken English required

At EcoHealth Alliance, our vision is a workplace with a diverse and talented staff where people want to come, to stay, do their best work, and grow. We recruit, employ, train, compensate and promote our staff without regard to race, ethnicity, color, religion, gender, gender identity or expression, sexual orientation, national origin, disability, age, veteran status, or socioeconomic status. This position is based at EcoHealth Alliance in New York City and will entail extensive domestic and international travel. EcoHealth Alliance offers a competitive salary and a comprehensive benefit package including health, dental, and vision coverage, and a 403(b) pension plan. EcoHealth Alliance is proud and deeply committed to being an equal opportunity employer. For further information about EcoHealth Alliance, please visit our website: www.ecohealthalliance.org.

HOW TO APPLY

Send an email with a *single* attachment in PDF format containing (a) a cover letter, (b) CV, and (c) three references to jobs@ecohealthalliance.org with "**2020 RESEARCH SCIENTIST AND PROJECT MANAGER JOB APPLICATION**" in the subject line. If you would like to be considered for more than one job position, please indicate that in your cover letter and list your order of preference. Emails without the subject line or with multiple attachments will not be reviewed. No formal text is required within the body of your email, since emails will not be evaluated. All inquiries will receive an automatic response confirming receipt. *Only* appropriately qualified candidates will be contacted. Closing date for this position: 15th July 2020.

Thank you for your interest in EcoHealth Alliance!

From: ￼ $ ￼￼ <huben
Sent: Tuesday, April 11, 2017 5:56 AM EDT
To: Schountz,Tony
Subject: Requesting invitation letter for visa application

Dear Dr.Schountz:

I am a researcher at Wuhan Institute of Virology, Chinese Academy of Sciences. My colleagues and I are studying bat viruses and we have submitted four abstracts to the 2nd International Symposium on Infectious Diseases of Bats which is going to be held in Fort Collins in June.

The title for the 4 abstracts are:

1) SARS coronavirus may have originated from frequent recombination events betwwen SARS-like coronaviruses in a single horseshoe bat habitat (oral)

2) Dampening of STING-dependent IFN production: an implication of virus tolerance in bats? (oral) 锛￼I noticed from the web that this abstract has already been confirmed as oral presentation)

3) Genomic characterization of diverse BatCoV HKU10 and three novel alphacoronaviruses (poster)

4) Genetically diverse filoviruses in Rousettus and Eonycteris spp. bats, China, 2009 and 2015. (poster)

As it is a unique conference specializing on our research area, we are very eager to attend. However, it usually takes at least two months for us to get the US visa due to the complicated procedure of applying for travel permit to Chinese Academy of Sciences and then one month of administrative processing by US embassy. So in order we can make our visit to Colorado in late June, we have to start the process of travel permit and visa application now.

To apply for a travel permit, we are required to submit an invitation letter from the conference organizer. I know for the bat-borne disease meeting, we will know the results of the acceptance of the abstract by May. But it will be late for us to apply for the travel permit and US visa.

Could you please kindly provides four invitation letters to us indicating we will attend the meeting and give presentations? (oral or posters)
It does not matter whether the abstracts will be finally selected as he invitation letters are only for visa application.

We deeply appreciate your understanding and assistance.

Thank you very much!

Best regards

Ben Hu Ph.D

Research Assistant

Wuhan Institute of Virology, CAS

From: Kevin Olival, PhD ecohealthalliance.org>
Sent: Thursday, June 22, 2017 2:46 PM EDT
To: Schountz,Tony >
Subject: Sorry, will get u an abstract soon...

Word limit? Last possible deadline time??

From: Jon Epstein ecohealthalliance.org>
Sent: Wednesday, April 01, 2020 1:01 AM EDT
To: Ebel,Greg ; Schountz,Tony <
Subject: still working on bat section
Attachment(s): "Los bat project_Munster.docx"

Greg and Tony,
I wasn't able to work on this much tonight. I'll pick it up tomorrow afternoon and will have you something by the end of the day.

I did get a letter of support from Vincent - just waiting for a signed copy.

Cheers,
Jon

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street, Ste. 1701

New York, NY 10001

)

web: ecohealthalliance.org

National Institute of Allergy and Infectious Diseases

ROCKY MOUNTAIN LABORATORIES

Division of Intramural Research
National Institute of Allergy
and Infectious Diseases
Laboratory of Virology
Virus Ecology Section

March 30, 2020

Dear Hugh Auchincloss,

It is with utmost pleasure to be able to provide a letter of support for the CSU bat research center. Past outbreaks of bat-borne zoonotic viruses such as coronaviruses, henipaviruses and filoviruses, have had an enormous impact on human and wildlife health. The unpredictability of the zoonotic introductions of these bat-borne limits the potential for effective intervention strategies. Within my research (https://www.niaid.nih.gov/research/vincent-j-munster-phd), I have directly focussed on bat-borne viruses such as Nipah virus, Ebola virus, MERS-CoV and now SARS-CoV-2. In particular we have extensive knowledge of bat infection models of ß-coronaviruses (MERS-CoV and WIV-1, in *Artibeus* and *Rousettus* bats) and Nipah virus (*Rousettus* bats) and are one of the few facilities which are completely set-up to perform bat studies in high and maximum containment (including long-term husbandry and on-site veterinary staff) and complete downstream immunological, genetic and virological analyses.

I am underwriting my enthusiasm to continue to collaborate on the development of a bat resource center including breeding colonies of key bat species, at CSU. Having access to natural hosts for coronaviruses, henipaviruses and filoviruses would significantly advance research in infectious disease undertaken by my group and others at RML, and I am committed to working with Drs. Bowen and Schountz at CSU (long standing research collaboration on MERS-CoV) and Dr. Epstein of EcoHealth Alliance (long standing collaboration on the underlying ecological changes driving spillover events of Nipah virus) to develop and use the resources generated through this C06 proposal. The SARS-CoV-2 pandemic marks an occasion which should put renewed focus on detailed studies of bats as reservoirs of emerging diseases. After SARS-CoV-1, MERS-CoV and Ebola virus in West Africa, we have yet another high impact (both from public health as economic perspective) bat-borne disease which justifies the urgent need for facilities in the US for advanced bat infectious disease studies.

Please feel free to contact me with any remaining questions,

Sincerely,

Vincent Munster

From: Virologica Sinica
Sent: Wednesday, July 19, 2017 2:57 AM EDT
To: Schountz,Tony <
Subject: To Dr.Schountz - Virologica Sinica, Volume 32, Issue 3

Dear Dr. Schountz,

It is my pleasure to present you the reviews, research articles and letters recently published in *Virologica Sinica*.

Your suggestions are welcome!

Zheng-Li Shi, Ph.D.
Editor-in-Chief, *Virologica Sinica*

Browse the website www.virosin.org for more information

Enjoy **rapid** & **free** publication in Virologica Sinica

Virologica Sinica is an academic journal which aims at presenting the cutting-edge basic and applied research on viruses all over the world. The journal publishes peer-reviewed original research articles and reviews, as well as commentaries and letters to the editor, to encompass the latest developments in all branches of virology, including research on animal, plant and microbe viruses. Virologica Sinica, the official journal of Chinese Society for Microbiology, will serve as a platform for the communication and exchange of academic information and ideas in an international context.
The journal is indexed by: Science Citation Index (SCI), JCR, PubMed/Medline, Scopus, BIOSIS, Google Scholar, and SCImago.

About the cover: In this issue, Xi-Juan Liu et al. reported the first observation of Hes1 oscillatory expression in human NPCs, and found HCMV infection disrupting the Hes1 rhythm and down-regulates its expression. The cover is adopted from a two-photon fluorescence image of Hes1 staining in NPCs (kindly provided by Xi-Juan Liu and Min-Hua Luo), and further processed with pseudo-color (in teal) at cytosol part. Like Hes1 rhythm, water lily also holds its own pattern of flowering rhythm. See page 188-198 for details.

Why Virologica Sinica?

- **Global visibility, available in Springer and covered by PubMed/Medline**
- **Rapid peer review and online publishing (approximately 3 weeks)**
- **Official journal of the Chinese Society for Microbiology**
- **No page or color charges, open-access options**
- **Free language editing**

2017, Vol. 32, Issue 3

Review

An update: Epstein-Barr virus and immune evasion via microRNA regulation

Free Full Text (HTML) ***Free*** Full Text (PDF)

Lielian Zuo, Wenxin Yue, Shujuan Du, Shuyu Xin, Jing Zhang, Lingzhi Liu, Guiyuan Li, Jianhong Lu

Epstein-Barr virus (EBV) is an oncogenic virus that ubiquitously establishes life-long persistence in humans. To ensure its survival and maintain its B cell transformation function, EBV has developed powerful strategies to evade host immune responses. Emerging evidence has shown that microRNAs (miRNAs) are powerful regulators of the maintenance of cellular homeostasis. In this review, we summarize current progress on how EBV utilizes miRNAs for immune evasion. EBV encodes miRNAs targeting both viral and host genes involved in the immune response. The miRNAs are found in two gene clusters, and recent studies have demonstrated that lack of these clusters increases the $CD4^+$ and $CD8^+$ T cell response of infected cells. These reports strongly indicate that EBV miRNAs are critical for immune evasion. In addition, EBV is able to dysregulate the expression of a variety of host miRNAs, which influence multiple immune-related molecules and signaling pathways. The transport via exosomes of EBV-regulated miRNAs and viral proteins contributes to the construction and modification of the inflammatory tumor microenvironment. During EBV immune evasion, viral proteins, immune cells, chemokines, pro-inflammatory cytokines, and pro-apoptosis molecules are involved. Our increasing knowledge of the role of miRNAs in immune evasion will improve the understanding of EBV persistence and help to develop new treatments for EBV-associated cancers and other diseases.

Research Article

Human cytomegalovirus infection dysregulates neural progenitor cell fate by disrupting Hes1 rhythm and down-regulating its expression

Free Full Text (HTML) ***Free*** Full Text (PDF)

Xi-Juan Liu, Xuan Jiang, Sheng-Nan Huang, Jin-Yan Sun, Fei Zhao, Wen-Bo Zeng, Min-Hua Luo

Human cytomegalovirus (HCMV) infection is a leading cause of birth defects, primarily affecting the central nervous system and causing its maldevelopment. As the essential downstream effector of Notch signaling pathway, Hes1, and its dynamic expression, plays an essential role on maintaining neural progenitor/stem cells (NPCs) cell fate and fetal brain development. In the present study, we reported the first observation of Hes1 oscillatory expression in human NPCs, with an approximately 1.5 hour periodicity and a Hes1 protein half-life of about 17(17.6±0.2) minutes. HCMV infection disrupts the Hes1 rhythm and down-regulates its expression. Furthermore, we discovered that depleting Hes1 protein disturbed NPCs cell fate by suppressing NPCs proliferation and neurosphere formation, and driving NPCs abnormal differentiation. These results suggested a novel mechanism linking disruption of Hes1 rhythm and down-regulation of Hes1 expression to neurodevelopmental disorders caused by congenital HCMV infection.

Research Article

Development of a reverse transcription quantitative polymerase chain reaction-based assay for broad coverage detection of African and Asian Zika virus lineages

Free Full Text (HTML) ***Free*** Full Text (PDF)

Yang Yang, Gary Wong, Baoguo Ye, Shihua Li, Shanqin Li, Haixia Zheng, Qiang Wang, Mifang Liang, George F Gao, Lei Liu, Yingxia Liu, Yuhai Bi

The Zika virus (ZIKV) is an arbovirus that has spread rapidly worldwide within recent times. There is accumulating evidence that associates ZIKV infections with Guillain-Barré Syndrome (GBS) and microcephaly in humans. The ZIKV is genetically diverse and can be separated into Asian and African lineages. A rapid, sensitive, and specific assay is needed for the detection of ZIKV across various pandemic regions. So far, the available primers and probes do not cover the genetic diversity and geographic distribution of all ZIKV strains. To this end, we have developed a one-step quantitative reverse transcription polymerase chain reaction (qRT-PCR) assay based on conserved sequences in the ZIKV envelope (*E*) gene. The detection limit of the assay was determined to be five RNA transcript copies and 2.94×10^{-3} 50% tissue culture infectious doses ($TCID_{50}$) of live ZIKV per reaction. The assay was highly specific and able to detect five different ZIKV strains covering the Asian and African lineages without nonspecific amplification, when tested against other flaviviruses. The assay was also successful in testing for ZIKV in clinical samples. Our assay represents an improvement over the current methods available for the detection ZIKV and would be valuable as a diagnostic tool in various pandemic regions.

Research Article

Rabies virus co-localizes with early (Rab5) and late (Rab7) endosomal proteins in neuronal and SH-SY5Y cells

Free Full Text (HTML) ***Free*** Full Text (PDF)

Waqas Ahmad, Yingying Li, Yidi Guo, Xinyu Wang, Ming Duan, Zhenhong Guan, Zengshan Liu, Maolin Zhang

Rabies virus (RABV) is a highly neurotropic virus that follows clathrin-mediated endocytosis and pH-dependent pathway for trafficking and invasion into endothelial cells. Early (Rab5, EEA1) and late (Rab7, LAMP1) endosomal proteins play critical roles in endosomal sorting, maturity and targeting various molecular cargoes, but their precise functions in the early stage of RABV neuronal infection remain elusive. In this study, the relationship between enigmatic entry of RABV with these endosomal proteins into neuronal and SH-SY5Y cells was investigated. Immunofluorescence, $TCID_{50}$ titers, electron microscopy and western blotting were carried out to determine the molecular interaction of the nucleoprotein (N) of RABV with early or late endosomal proteins in these cell lines. The expression of N was also determined by down-regulating Rab5 and Rab7 in both cell lines through RNA interference. The results were indicative that N proficiently colocalized with Rab5/EEA1 and Rab7/LAMP1 in both cell lines at 24 and 48 h post-infection, while N titers significantly decreased in early infection of RABV. Down-regulation of Rab5 and Rab7 did not inhibit N expression, but it prevented productive infection via blocking the normal trafficking of RABV in a low pH environment. Ultrathin sections of cells studied by electron microscope also verified the close association of RABV with Rab5 and Rab7 in neurons. From the data it was concluded that primary entry of RABV strongly correlates with the kinetics of Rab-proteins present on early and late vesicles, which provides helpful clues to explain the early events of RABV in nerve cells.

Research Article

Human endogenous retrovirus W env increases nitric oxide production and enhances the migration ability of microglia by regulating the expression of inducible nitric oxide synthase

Free Full Text (HTML) ***Free*** Full Text (PDF)

Ran Xiao, Shan Li, Qian Cao, Xiuling Wang, Qiujin Yan, Xiaoning Tu, Ying Zhu, Fan Zhu

Human endogenous retrovirus W env (HERV-W env) plays a critical role in many neuropsychological diseases such as schizophrenia and multiple sclerosis (MS). These diseases are accompanied by immunological reactions in the central nervous system (CNS). Microglia are important immunocytes in brain inflammation that can produce a gasotransmitter-nitric oxide (NO). NO not only plays a role in the function of neuronal cells but also participates in the pathogenesis of various neuropsychological diseases. In this study, we reported increased NO production in CHME-5 microglia cells after they were transfected with HERV-W env. Moreover, HERV-W env increased the expression and function of human inducible nitric oxide synthase (hiNOS) and enhanced the promoter activity of hiNOS. Microglial migration was also enhanced. These data revealed that HERV-W env might contribute to increase NO production and microglial migration ability in neuropsychological disorders by regulating the expression of inducible NOS. Results from this study might lead to the identification of novel targets for the treatment of neuropsychological diseases, including neuroinflammatory diseases, stroke, and neurodegenerative diseases.

Research Article

Detection of diverse viruses in alimentary specimens of bats in Macau

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Jie Liang, Xing-Lou Yang, Bei Li, Qi Liu, Qin Zhang, Hui Liu, Hon-Pio Kan, Kai-Chin Wong, Si-Nga Chek, Xiangyang He, Xingwen Peng, Zheng-Li Shi, Yi Wu, Libiao Zhang

Bats carry a variety of viruses, and some of them cause public health problems. Macau, which is famous for its gambling industry, has a complex population structure. The globalization in such an international metropolis has enhanced the chance of disease transmission. Therefore, surveillance of zoonotic viruses is necessary for the early warning of potential emerging infectious diseases. Here, we report the first surveillance of bat viruses in Macau. In this study, we collected 1004 samples involving 10 bat species from 7 sites from April 2015 to May 2016, and examined the presence of viruses using nucleic acid-based methods. Coronaviruses, adenoviruses and paramyxoviruses were detected in these samples, with a high prevalence of coronaviruses. While, none was positive for hepatitis A virus, hepatitis E virus or hantavirus. Co-infections are not common in those bat species, but coronavirus HKU6 and adenovirus can be found commonly occurred in *Myotis ricketti*.

Research Article

Phylogenetic analysis based on mitochondrial DNA sequences of wild rats, and the relationship with Seoul virus infection in Hubei, China

Free Full Text (HTML) ***Free*** Full Text (PDF)

Dong-Ying Liu, Jing Liu, Bing-Yu Liu, Yuan-Yuan Liu, Hai-Rong Xiong, Wei Hou, Zhan-Qiu Yang

Seoul virus (SEOV), which is predominantly carried by *Rattus norvegicus*, is one of the major causes of hemorrhagic fever with renal syndrome (HFRS) in China. Hubei province, located in the central south of China, has experienced some of the most severe epidemics of HFRS. To investigate the mitochondrial DNA (mtDNA)-based phylogenetics of wild rats in Hubei, and the relationship with SEOV infection, 664 wild rats were captured from five trapping sites in Hubei from 2000-2009 and 2014-2015. Using reverse-transcription (RT)-PCR, 41(6.17%) rats were found to be positive for SEOV infection. The SEOV-positive percentage in Yichang was significantly lower than that in other areas. The mtDNA D-loop and cytochrome b (*cyt-b*) genes of 103 rats were sequenced. Among these animals, 37 were SEOV-positive. The reconstruction of the phylogenetic relationship (based on the complete D-loop and *cyt-b* sequences) allowed the rats to be categorized into two lineages, *R.norvegicus* and *Rattus nitidus*, with the former including the majority of the rats. For both the D-loop and *cyt-b* genes, 18 haplotypes were identified. The geographic distributions of the different haplotypes were significantly different. There were no significant differences in the SEOVpositive percentages between different haplotypes. There were three sub-lineages for the D-loop, and two for *cyt-b*. The SEOV-positive percentages for each of the sub-lineages did not significantly differ. This indicates that the SEOV-positive percentage is not related to the mtDNA D-loop or *cyt-b* haplotype or the sub-lineage of rats from Hubei.

Letter

Retromer localizes to autophagosomes during HCV replication

Free Full Text (HTML) ***Free*** Full Text (PDF)

Peiqi Yin, Zhi Hong, Leiliang Zhang, Youyang Ke

In summary, we propose a model for the role of retromer in HCV replication. Upon HCV infection, retromer may provide double-membrane autophagosomal membranes for HCV replication. Our studies suggested a novel link between retromer and autophagy in HCV replication, which may provide new therapeutic targets for antiviral therapy.

Letter

Molecular typing of non-polio enteroviruses isolated from acute flaccid paralysis cases in Iran from 2010 to 2015

Free Full Text (HTML) ***Free*** Full Text (PDF)

Ahmad Nejati, Mohammad Farahmand, Hamideh Tabatabaie, Maryam Yousefi, Yaghoob Mollaei-Kandelous, Shohreh Shahmahmoodi

In summary, our findings showed that for correct identification of NPEVs, cell lines other than RD cells must be used. In addition, neutralization tests did not show high sensitivity for identification of all NPEVs. Finally, establishment of direct molecular tests with high sensitivity and specificity is needed to identify NPEV from patient and environmental samples.

Letter

Isolation and phylogenetic study of Rift Valley fever virus from the first imported case to China

Free Full Text (HTML) ***Free*** Full Text (PDF)

Yongxia Shi, Kui Zheng, Xiaobo Li, Liqiang Li, Shufen Li, Jinmin Ma, Jun Dai, Jingkai Ji, Shuai Yuan, Haorong Lu, Jiandong Li, Fangfang Sun, Xun Xu, Jicheng Huang

Here, laboratory detection, virus isolation, whole genome sequencing and phylogenetic analysis were performed to characterize the first imported case of Rift Valley fever virus infection returning from Angola.

Letter

CD95-CD95L interaction mediates the growth control of MHV68 immortalized B cells by cytotoxic T cells

Free Full Text (HTML) ***Free*** Full Text (PDF)

Sihan Dong, Lingbing Tan, Guifang Chen, Xiaozhen Liang

In conclusion, our current data demonstrate that MHV68-immortalized SL-1 cells can be recognized and controlled by specific cytotoxic T cells through CD95/CD95L-mediated apoptosis. This is in agreement with that CD4 T cells control the growth of EBV-infected cells through CD95/CD95L-mediated apoptosis, which suggests that the growth control of gammaherpesvirus-associated lymphoma cells by cytotoxic T cell shares conserved mechanism.

From: Tony Schountz on behalf of Schountz,Tony
Sent: Wednesday, February 19, 2020 6:09 PM EST
To: Schountz,Tony
BCC:

Subject: 3rd International Symposium on Infectious Diseases of Bats, 17-19 June 2020, Fort Collins, Colorado, USA

Dear Colleagues,

Registration is now open for the 3rd International Symposium on Infectious Diseases of Bats. With the emergence of yet another pathogenic coronavirus, we are planning to have an extended session to learn from one another about this new virus and I hope some of you can foster collaborative interactions while you are here. The URL for the meeting is:

http://www.batid.org

Please note a few important dates. **Abstract submission closes on April 17, 2020**. The format of the abstract is indicated on the web site and we ask that you follow it for purposes of continuity in the program. In addition, please send MS Word, Apple Pages or Rich Text files so that we can rapidly build the program. Please DO NOT send a PDF because they are much more difficult to integrate into the program. After you submit your abstract, you should receive a confirmation email. If you do not, please let me know and I'll resolve the issue.

Registration will close on May 1, 2020. Registration will be handled by the Colorado State University Conference Services with a direct link on the Bat ID web site. You can select registration only, or registration with dormitory housing on campus near the conference venue (Lory Student Center). Registration included breakfast for the two days, and the dormitory includes breakfast, too. If you prefer to stay in a hotel, the Fort Collins Hilton (on Prospect Avenue) and the Best Western University Inn are walking distance to campus. Links to these hotels are provided on the Registration page.

We also have the pleasure of hosting **This Week in Virology**. Vincent and crew will record an episode from the meeting.

Please let me know if you have questions or comments.

Thanks very much, and we are looking forward to seeing you again in Fort Collins.

Tony

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Nov 14, 2019, at 10:52 AM, Schountz,Tony > wrote:

Dear colleagues,

I am pleased to announce the **3rd International Symposium on Infectious Diseases of Bats** that will be held at Colorado State University in Fort Collins, Colorado, 17 June to 19 June, 2020. The previous meetings were quite successful and led to several new collaborations amongst participants. We hope we can continue to foster interactions and additional collaborations between groups. Please forward this email to colleagues and students that may be interested in the symposium.

We are currently finalizing details of the symposium but I wanted to send this email so that you can add the dates to your calendar if you are interested in attending. The American Society for Virology Annual Conference will also be hosted at CSU in 2020 and it ends on Wednesday, June 17 at noon. Thus, the Bat ID Symposium will follow with a reception on the evening of June 17th and two days of talks and posters on the 18th and 19th. As with previous meetings, we will end each day with an open discussion about bats and their infectious agents.

Should you have questions, please do not hesitate to contact me.

We look forward to hosting you next summer.

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony < on behalf of Schountz,Tony
Sent: Thursday, November 14, 2019 12:52 PM EST
To: Schountz,Tony
BCC:

Subject: 3rd International Symposium on Infectious Diseases of Bats, 17-19 June 2020, Fort Collins, Colorado, USA

Dear colleagues,

I am pleased to announce the **3rd International Symposium on Infectious Diseases of Bats** that will be held at Colorado State University in Fort Collins, Colorado, 17 June to 19 June, 2020. The previous meetings were quite successful and led to several new collaborations amongst participants. We hope we can continue to foster interactions and additional collaborations between groups. Please forward this email to colleagues and students that may be interested in the symposium.

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Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony
Sent: Wednesday, June 21, 2017 10:24 AM EDT
To: Kevin Olival, PhD ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>
Subject: Abstracts

Hi Jon and Kevin,

I don't seem to have abstracts for your bat ID talks. Could you (re)send them directly to me today or tomorrow?

Thanks

Tony

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Tony Schountz on behalf of Schountz,Tony
Sent: Monday, March 16, 2020 1:40 PM EDT
To: Wang Linfa ; 周鹏 <peng.zhou ; zlshi <zlshi
Subject: Asthma as a comorbidity for COVID-19?

Hi Zhengli, Linfa and Peng,

I have a graduate student who is working with SARS-CoV-2 and she informed me she has asthma. Of course, now I am concerned about this. I looked in the literature using various search terms but I could not find an indication whether asthma is a comorbidity associated with severe COVID-19 disease. Have you seen data from China or Singapore (or elsewhere) as to whether it might?

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony > on behalf of Schountz,Tony >
Sent: Monday, February 04, 2019 3:56 PM EST
To: Christian Drosten Wang Linfa >; Michelle Baker ; Susanna Lau ; Patrick Woo ; Martin Schwemmle ; Richard Yanagihara Jon Epstein ecohealthalliance.org>; 石正丽 <zlshi >
Subject: Bat conference advisory committee

Dear colleagues,

We're planning to host the third international bat infectious disease symposium June 18-20, 2020 here in Fort Collins. This coincides with the end of the 2020 ASV meeting that will also be in Fort Collins and which ends on June 17. I will submit an R13 proposal (Conference Support) to NIH in April to get a few thousand dollars to help with student travel awards for the conference. I hope you don't mind, but I would like to list each of you as members of the advisory committee. Probably not too much for you to do, but it will be helpful for the submission. Is that OK? If you plan to attend the bat symposium, I will waive your registration fee.

Thanks,

Tony

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Tony Schountz > on behalf of Schountz,Tony
Sent: Thursday, January 30, 2020 3:46 PM EST
To: 周鹏 <peng.zhou >; 石正丽 <zlshi
Subject: Bat ID conference

Dear Zhengli and Peng,

I was wondering if you will be attending the bat meeting after ASV. (I realize some of you may be at the Paris meeting instead.) If so, I'd like to list you as confirmed speakers. I'm awaiting a small grant decision from my university that would be used to waive your registration fee if you are a confirmed speaker. The decision is supposed to be made in the next week or two, so I won't be able to let you know for sure until then. I understand you are quite busy with the new coronavirus and that there may be travel issues, but if it is possible for you to make it, I would be most grateful.

Thank you,

Tony

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Tony Schountz > on behalf of Schountz,Tony >
Sent: Thursday, January 30, 2020 3:36 PM EST
To: Jon Epstein ecohealthalliance.org>; Kevin Olival ecohealthalliance.org>; Peter Daszak ecohealthalliance.org>
Subject: Bat ID meeting

Hi Peter, Jon and Kevin,

I was wondering if you will be at the bat meeting after ASV. (I realize some of you may be at the Paris meeting instead.) If so, Iâ€™d like to list you as confirmed speakers. Iâ€™m awaiting a small grant decision from my university that would be used to waive your registration fee if you are a confirmed speaker. The decision is supposed to be made in the next week or two, so I wonâ€™t be able to let you know for sure until then.

We also have a commitment from Vincent Racaniello to have a TWiV podcast from the meeting. ðŸ˜€

Thanks,

Tony
â€”
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony > on behalf of Schountz,Tony
Sent: Thursday, June 22, 2017 5:23 PM EDT
To: James.Aegerter@apha.gsi.gov.uk

Subject: Bat ID Symposium logistics
Attachment(s): "Campus map.pdf"

Dear Colleagues,

The symposium is one week away and I want to provide you with some logistical information for your arrival to Fort Collins.

1. Speakers. If you can email your presentation directly to me I will get it on the computer for the presentation**However, the file size must be less than 15 MB to accommodate our email server limit**. Otherwise, please bring your presentation on a USB drive if it is larger than 15 mb. We will have both Microsoft Power Point and Apple Keynote software for your presentations. **Bring your USB drive to the Thursday evening reception if you want to transfer it then.**

2. Poster presenters. The maximum size of the posters is 48” x 48” (120 cm x 120 cm). We will provide push pins to mount your poster on the easels. When you register, your poster will have a number assigned to it that corresponds to the easel number. Please mount your poster on that easel. **Bring your poster to the Thursday evening reception.**

3. Getting to Fort Collins. Those of you who are flying to Denver International Airport can schedule a ride with the **Green Ride Airport Shuttle** service. Please visit its web site (https://greenrideco.hudsonltd.net/) to make arrangements convenient for your flight schedules. There is a Green Ride desk in the main terminal at the airport with employees that can help you find the bus pickup. The bus ride is about 1 hour and 15 minutes. On the web site, in the box “Dropoff location” choose the appropriate destination from the pull-down menu. For those of you staying in the university dormitories it is “FC - Laurel Village”, the Hilton Hotel near campus is “FC - Hilton Ft Collins”, and the University Inn is “FC - Best Western University Inn”. And just to make you aware, afternoon and evening flights into Denver can be rather bumpy!

4. Weather and Climate. Fort Collins has lots of sunshine and is at 5000 ft/1500 meters. If you intend to be outdoors much you should bring sunscreen. We often get afternoon thunder showers in our otherwise dry climate but they are typically not more than an hour or two and it usually clears up afterwards. You may want to bring rain gear or a small umbrella. The current forecast is for the mid to high 80sF/low 30sC.

5. Getting to the UCA. The conference venue is the **University Center for the Arts (UCA)** (attached map, blue box, lower right). Oral and poster presentations will be in this building and directions will be posted inside. After you get settled in Thursday, please come to the UCA for the opening registration and social mixer by 5:30 PM. Walking paths (routes) are noted in blue hatched lines.

A. Laurel Village Alpine Dormitory. Those who are staying in campus housing, walk south to Plum Street and turn east to Meridian Avenue. Take Meridian Avenue south to Pitkin Street and take it east to Mason Street. Cross the railroad tracks and immediately turn right (south) just before the parking garage. Follow the path to just past the parking garage and turn left (east). This path leads to a **tunnel that passes under College Avenue** and comes out at the University Test Gardens (lots of flowers). Continue on this path and it will cross Remington Street to the UCA. **Allow 15-20 minutes to walk**.

B. Hilton Hotel. Proceed from the hotel to Prospect and Centre Avenue at the northwest corner of the Hilton Hotel parking lot. Cross Centre to the west and **take the tunnel under Prospect Avenue**. At Lake Street, turn right (east) to Mason Street. Cross the railroad tracks and immediately turn left (north). Just before the parking garage, turn right (east) and take the path that leads to a **tunnel that passes under College Avenue** and comes out at the University Test Gardens. Continue on this path and it will cross Remington Street to the UCA. **Allow 10 minutes to walk**.

C. University Inn Best Western Hotel. Take Elizabeth Street east to Remington Street (one block). Turn right (south) to Pitkin Street. Once you cross Pitkin Street, the University Center for the Arts is to your left. **Allow 5 minutes to walk.**

6. Registration packet. Your registration packet will include the program, name badge, water bottle and a pass for the Fort Collins MAX bus. The pass allows you to ride the bus through Saturday night. Registration also includes lunch for Friday and Saturday. If you are staying in the dorms you will also have breakfast provided at the dorm dining hall, Corbett Hall, which is just east of Alpine Hall where you are staying (please see the attached map).

If you have questions, please contact me and I will address them. Finally, I will be at the American Society for Virology meeting Saturday through Wednesday so my email access may be intermittent.

Thanks and see you next week.

Tony

—

Tony Schountz, PhD
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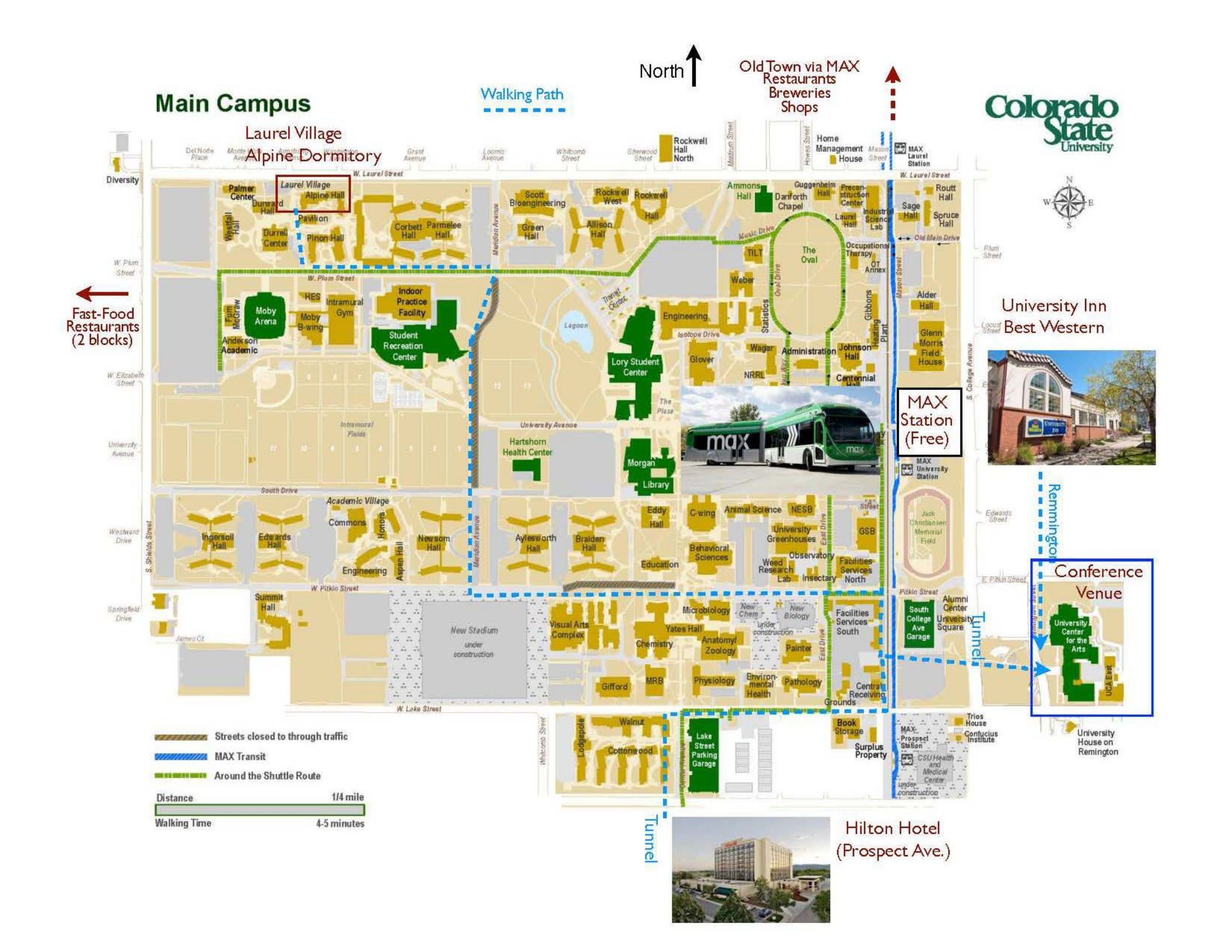
College of Veterinary Medicine
Colorado State University


Main Campus
North
Walking Path
Old Town via MAX
Restaurants
Breweries
Shops
Colorado State University
Laurel Village
Alpine Dormitory
Fast-Food Restaurants (2 blocks)
University Inn
Best Western
MAX Station (Free)
Conference Venue
Tunnel
Tunnel
Hilton Hotel (Prospect Ave.)
Remington
Streets closed to through traffic
MAX Transit
Around the Shuttle Route
Distance 1/4 mile
Walking Time 4-5 minutes

From: Schountz,Tony
Sent: Tuesday, June 27, 2017 3:54 PM EDT
To: James.Aegerter

CC:

BCC:
Subject: Bat ID Symposium program
Attachment(s): "Bat ID Program 2017 June 23.pdf"

All, please find attached a copy of the program.

See you in a few days.

Tony

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology

College of Veterinary Medicine
Colorado State University

From: Schountz,Tony
Sent: Thursday, June 22, 2017 3:23 PM
To: James.Aegerter

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Thanks and see you next week.

Tony
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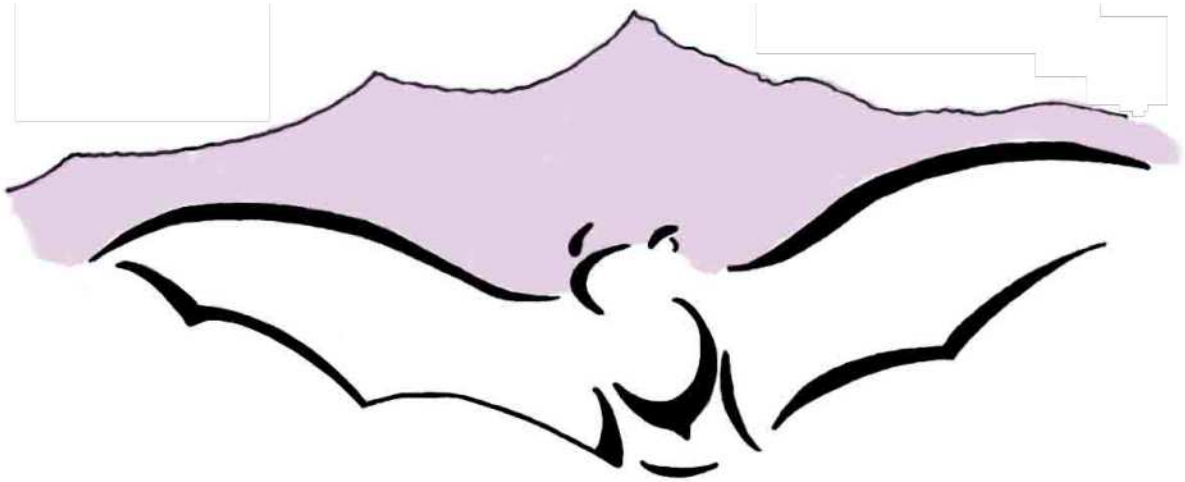
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

Infectious Diseases of Bats Symposium



June 29-July 1, 2017
University Center for the Arts
1400 Remington St
Colorado State University
Fort Collins, CO 80524

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Program

Venue: **University Center for the Arts**, Colorado State University

Thursday, June 29

5:30 p.m. Registration, PowerPoint file transfer, lobby, **University Center for the Arts**

6:00 p.m. Reception - *Wine, beer and snacks*, **University Center for the Arts**

Friday, June 30

7:00 a.m. Registration, University Center for the Arts

8:00 a.m. Tony Schountz. Colorado State University. **Welcoming remarks**

8:10 a.m. Session I - Filoviruses (Joseph Prescott, Moderator)

8:10 a.m. **Studies of horizontal transmission of Marburg virus among experimentally infected fruit bats**
Jonathan S. Towner[1,2], Amy J. Schuh[1], Brian R. Amman[1], Megan E. B. Jones[1,2], Tara K. Sealy[1], Uebelhoer LS, Spengler JR, Stuart T. Nichol[1]

[1]Viral Special Pathogens Branch, Centers for Disease Control and Prevention, Atlanta, USA, [2]Department of Pathology, College of Veterinary Medicine, University of Georgia, Athens, USA

8:30 a.m. **Investigations of Long-term Protective Immunity against Marburg Virus Reinfection in Egyptian Rousette Bats**
Amy Schuh, Amman BR, Sealy TK, Spengler JR, Nichol ST and Towner JS

Viral Special Pathogens Branch, Division of High-Consequence Pathogens and Pathology, Centers for Disease Control and Prevention, Atlanta, GA 30333, USA

8:45 a.m. **Innate immune response to filoviruses and the role of filoviral interferon-inhibiting domains in bat and human cells**
Ivan V. Kuzmin[1,2], Toni M. Schwarz[3], Philipp A. Ilinykh[1,2], Ingo Jordan[4], Thomas G. Ksiazek[1,2,5], Ravi Sachidanandam[6], Christopher F. Basler[3, 7], and Alexander Bukreyev[1,2,5]

[1] Department of Pathology, The University of Texas Medical Branch, Galveston, Texas, USA; [2] Galveston National Laboratory, The University of Texas Medical Branch, Galveston, Texas, USA; [3] Department of Microbiology, Icahn School of Medicine at Mount Sinai, New York, New York, USA; [4] ProBioGen AG, Berlin, Germany; [5] Department Microbiology & Immunology, The University of Texas Medical Branch, Galveston, Texas, USA; [6] Department of Oncological Sciences, Icahn School of Medicine at Mount Sinai, New York, New York, USA; [7] Current Address: Center for Microbial Pathogenesis, Institute for Biomedical Sciences, Georgia Research Alliance, Eminent Scholar in Virology, Georgia State University, Atlanta, Georgia, USA

9:00 a.m. **Broad based surveillance for ebolaviruses: PREDICT in Sierra Leone, Liberia, and Guinea.**
Brian Bird[1], Goldstein T[1], Anthony S[2], Gbakima A[3], Saylors K[3], Jean Louis F[3], Wolking D[1], Epstein J[4], Karesh W[4], Kreuder-Johnson C[1], Mazet J[1]

One Health Institute UC Davis School of Veterinary Medicine[1], Center for Infection and Immunity Columbia University[2], Metabiota Inc.[3], EcoHealth Alliance[4]

9:15 a.m. **Quantifying signatures of resistance and tolerance to filoviruses in bat cell lines**
Cara E. Brook[1], Melinda Ng[2], Esther Ndungo, Rohit K. Jangra, Andrew P. Dobson, Andrea L. Graham, Bryan T. Grenfell, C. Jessica E. Metcalf[1]*, Kartik Chandran[1]*
[1]Department of Ecology and Evolutionary Biology, Princeton University;
[2]Department of Microbiology and Immunology, Albert Einstein College of Medicine
*These senior authors contributed equally to this work.

9:30 a.m. **Serologic evidence of exposure to filoviruses in fruit bats, Singapore**
Laing ED[1], Ian H Mendenhall[2], Linster M[2], Low DHW[2], Chen Y[2], Yan L[1], Sterling SL[1], Borthwick S[2], Neves ES[2], Lim JSL[2], Skiles M[2], Lee BPY[4], Wang LF[2], Broder CC[1], Smith GJD[2, 5]

Uniformed Services University, Bethesda, MD, USA[1], Duke-National University of Singapore Medical School, Singapore[2], North Carolina State University, Raleigh, NC, USA[3], National Parks Board, Singapore[4], Duke Global Health Institute, Duke University, Durham, North Carolina, USA[5]

9:45 a.m. **Predicting undiscovered filovirus reservoirs and patterns of disease emergence**
David Hayman

Molecular Epidemiology and Public Health Laboratory, Hopkirk Research Institute, Massey University, New Zealand

10:00 a.m. Break

10:30 a.m. Session II - Coronaviruses A (Joel Rovnak, Moderator)

10:30 a.m. **Bats as possible animal origin of MERS-CoV**
Susanna K. P. Lau

Department of Microbiology, The University of Hong Kong, Hong Kong, China

10:45 a.m. **Rapid detection of MERS coronavirus ancestors in bats**
Prof. Patrick CY Woo

Department of Microbiology, The University of Hong Kong, Hong Kong.

11:00 a.m. **Global patterns in coronavirus diversity**
Simon J Anthony[1,2,3]; Johnson, C.K[4]; Greig, D.J[4]; Kramer, S[1,5]; Che, X[1]; Wells, H[1]; Hicks, A.L[1]; Joly, D.O[6, 7]; Wolfe, N.D[6]; Daszak, P[3]; Karesh, W[3]; Lipkin, W.I[1,2]; Morse, S.S[2]; PREDICT Consortium[8]; Mazet, J.A.K[4]; Goldstein, T[4]

[1]Center for Infection and Immunity, Mailman School of Public Health, Columbia University, 722 West 168th Street, New York, NY, 10032 (USA); [2]Dept of Epidemiology, Mailman School of Public Health, Columbia University, 722 West 168th Street, New York, NY (USA); [3]EcoHealth Alliance, 460 West 34th Street, NY, New York (USA); [4]One Health Institute & Karen C Drayer Wildlife Health Center, School of Veterinary Medicine, University of California Davis, California (USA); [5]Dept of Environmental Health Sciences, Mailman School of Public Health, Columbia University, 722 West 168th Street, New York, NY (USA); [6]Metabiota, Inc. One Sutter, Suite 600, San Francisco, CA, 94104 (USA); [7]Wildlife Conservation Society, New York, NY, (USA)

11:15 a.m. **SARS coronavirus may have originated from frequent recombination events between SARS-like coronaviruses in a single horseshoe bat habitat**
Ben Hu[1], Lei-Ping Zeng[1], Xing-Lou Yang[1], Xing-Yi Ge[1], Wei Zhang[1], Bei Li[1], Dong-Sheng Luo[1], Yun-Zhi Zhang[2], Mei-Niang Wang[1], Peter Daszak[3], Lin-Fa Wang[4], Jie Cui[1], Zheng-Li Shi[1]

[1] CAS Key Laboratory of Special Pathogens and Biosafety, Center for Emerging Infectious Diseases, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China; [2]Yunnan Institute of Endemic Diseases Control and Prevention, Dali, China; [3]EcoHealth Alliance, New York City, New York, USA; [4]Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore.

11:30 a.m. **A metagenomic approach identifying a MERS-related coronavirus in a bat from South Africa**
Marike Geldenhuys[1], Marinda Mortlock[1], Jaqueline Weyer[2], Oliver Bezuidt[3], Ernest Seamark[4], Teresa Kearney[5,6], Cheryl Gleasner [7], Tracey Erkkila[7], Helen Cui[7] and Wanda Markotter[1]

[1] Centre for Viral Zoonosis, Department of Medical Virology, Faculty of Health sciences, University of Pretoria, Pretoria, South Africa. [2] Centre for Emerging, Zoonotic and Parasitic Diseases,

National Institute for Communicable Diseases, Sandringham, South Africa. [3] Centre for Microbial Ecology and Genomics, University of Pretoria, Pretoria, South Africa. [4] AfricanBats NPC, South Africa and Centre for Wildlife Management, University of Pretoria, Pretoria, South Africa. [5] Animal, Plant and Environmental Sciences, University of the Witwatersrand, Johannesburg, South Africa

12:00 p.m. Lunch and Poster Session

2:00 p.m. Session III - Rhabdoviruses (Ashley Malmlov, Moderator)

2:00 p.m. **New insights into the antiviral innate immune response of *Desmodus rotundus***
Sarkis Sarkis, Marie-Claude Lise, Edith Darcissac, Stéphanie Dabo, Christine Neuveut, Benoît de Thoisy, Eliane Meurs, Anne Lavergne and Vincent Lacoste

Institut Pasteur de la Guyane, French Guiana/ France

2:15 p.m. **A comparative study of the autophagy pathway during virus infection of bat (natural) and human (accidental) host cells**
Eric D. Laing[1], Spencer L. Sterling[1], Dawn L. Weir[1], Sasha E. Larsen[2], Linfa Wang[3], Brian C. Schaefer[1], and Christopher C. Broder[1]

[1]Department of Microbiology, Uniformed Services University, Bethesda, MD, USA; [2]Department of Pharmacology, Uniformed Services University, Bethesda, MD, USA; [3]Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore

2:30 p.m. **Lagos bat virus in South Africa, 2013-2017**
Jessica Coertse[1], Le Roux, K.[2], Richardson, E.[3], White, W.[3], Markotter, W.[1]

[1]Centre for Viral Zoonoses, Department of Medical Virology, Faculty of Health Sciences, University of Pretoria, South Africa; [2]Allerton Provincial Veterinary Laboratory, Pietermaritzburg, KwaZulu-Natal, South Africa; [3]KwaZulu-Natal Bat Interest Group, KwaZulu-Natal, South Africa

2:45 p.m. **Characterization of a novel Rhabdovirus isolated from insectivorous bat (*Pipistrellus kuhlii*) in Italy**
Davide Lelli[1], Alice Prosperi[1], Chiara Chiapponi[1], Paola Debenedictis[2], Anna Maria Gibellini[3], Stefania Leopardi[2], Enrica Sozzi[1], Dino Scaravelli[4], Ana Moreno[1], Antonio Lavazza[1]

[1]Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna, Via Bianchi 9 - 25124 Brescia, Italy; [2]Istituto Zooprofilattico Sperimentale delle Venezie, OIE Collaborating Centre and National Reference Centre for Research on Infectious Diseases at the Animal-Human Interface, Viale dell'Università 10 - 35020 Legnaro (PD), Italy; [3]Wildlife Rehabilitation Center WWF of Valpredina via Pioda n.1, 24060 Cenate Sopra(BG), Italy; [4]University of Bologna, Department of Veterinary Medical Sciences, via Tolara di sopra 50 - 40064 Ozzano Emilia (BO), Italy

3:00 p.m. Session IV - Paramyxoviruses (Danielle Adney, Moderator)

3:00 p.m. **Age-specific dynamics of maternally- and infection- derived immunity within African bat populations**
Alison J Peel[1], Kate S Baker[2], David TS Hayman[3], Andrew A Cunningham[4], James LN Wood[5], Romain Garnier[5] and Olivier Restif[5]
[1] Environmental Futures Research Institute, Griffith University, Nathan, QLD, Australia; [2] Institute for Integrative Biology, University of Liverpool, UK; [3] Molecular Epidemiology and Public Health Laboratory, Hopkirk Research Institute, Massey University, Palmerston North, New Zealand; [4] Institute of Zoology, Zoological Society of London, Regent's Park, London, UK; [5] Department of Veterinary Medicine, University of Cambridge, Cambridge, UK

3:15 p.m. **Detection of rubula- and related viruses in an Egyptian fruit bat (*Rousettus aegyptiacus*) colony in South Africa**
Marinda Mortlock[1], Jacqueline Weyer[2], Janusz Paweska[2] and Wanda Markotter[1]

[1]Centre for Viral Zoonoses, Department of Medical Virology, Faculty of Health Science, University of Pretoria, South Africa; [2]Centre for Emerging, Zoonotic and Parasitic Diseases, National Institute for Communicable Diseases, Sandringham, Johannesburg, South Africa

3:30 p.m. Break

4:00 p.m. **Influenza-like virus and paramyxovirus screening in Brazilian bats**

Angélica Cristine Campos[1]; Luiz Gustavo Góes[1]; Cristiano Carvalho[2]; Guilherme Ambar[5]; Luciano M. Thomazelli[1]; Jhiovana Cristielly Costa[1]; Mariana Cristine de Souza[1]; Adriana Ruckert[3]; Débora C. Oliveira[3]; Luzia F. Martorelli[3]; Ana Paula Kataoka[3]; Marcelo S. Nardi[4]; Juliana L. Summa[4]; Roberta Marcatti de Azevedo[4]; Wagner A. Pedro[2]; Luzia H. Queiroz[2]; Ariovaldo P. Cruz-Neto[5] and Edison Durigon[1]

[1] Departamento de Microbiologia, Instituto de Ciências Biomédicas (ICB), Universidade de São Paulo (USP), São Paulo-SP; [2] Faculdade de Medicina Veterinária de Araçatuba, Universidade Estadual Paulista (UNESP), Araçatuba- SP; [3] Centro de Controle de Zoonozes (CCZ) do Município de São Paulo-SP; [4] Divisão Técnica de Medicina Veterinária e Manejo da Fauna Silvestre (DEPAVE-3), Secretaria do Verde e Meio Ambiente, Prefeitura do Município de São Paulo, São Paulo-SP; [5] Departamento de Zoologia, Instituto de Biociências, Universidade Estadual Paulista (UNESP), Rio Claro-SP

4:15 p.m. **Hendra virus dynamics and spillover**

Raina Plowright[1], Maureen Kessler[1], Alison Peel[2], Hamish McCallum[2], Peggy Eby[3]

[1]Department of Microbiology and Immunology, Montana State University; [2]Environmental Futures Research Institute, Griffith University, Queensland, Australia; [3]University of New South Wales, Australia.

4:30 p.m. Session V - Methodology in Bat-borne Viruses (Danielle Adney, Moderator)

4:30 p.m. **Using serology to understand the dynamics of concurrent viral infections in pteropid bats**

Jonathan H. Epstein[1], Noam Ross[1], Ariful Islam[1], Dan Crowley[1,2], Gary Crameri[3], Christopher Broder[4], Linfa Wang[5], and Peter Daszak[1].

[1]EcoHealth Alliance, NY USA; [2]Columbia University Mailman School of Public Health, NY USA; [3]CSIRO Australian Animal Health Laboratory, Geelong, VIC, AUS; [4]Uniformed Services University, MD USA; [5]Duke-NUS, Singapore

4:45 p.m. **Estimating viral richness and viral sharing in bats: integrating previously-published and newly-acquired field data**

Kevin J. Olival[1], Noam Ross[1], Evan A. Eskew[1], Anna R. Willoughby[1], Carlos Zambrana-Torrelio[1], Peter Daszak[1], and PREDICT Consortium[2]

[1] EcoHealth Alliance, New York, NY 10001, USA; [2] http://www.vetmed.ucdavis.edu/ohi/predict/publications/Authorship.cfm

5:00 p.m. **Open Discussion**

6:00 p.m. Recess

Saturday, July 1

7:30 a.m. Registration, North Ballroom, University Center for the Arts

8:00 a.m. Session II - Coronaviruses B (Rebekah Kading, Moderator)

8:00 a.m. **Optimised sampling efforts and screening assays identify several MERS-related coronaviruses in South African bats**

Wolfgang Preiser[1,2], Ndapewa L. Ithete[1], Nadine Cronjé[1], Tasnim Suliman[1]

[1]Division of Medical Virology, Faculty of Medicine & Health Sciences, University of Stellenbosch, South Africa; [2]National Health Laboratory Service (NHLS) Tygerberg, Cape Town, South Africa

8:15 a.m. **Coronavirus diversity in bats from urban, rural and forest areas of Atlantic and Amazon Forest biomes, Brazil.**
Luiz Gustavo Góes[1]; Angélica Cristine Campos[1]; Cristiano Carvalho[2]; Guilherme Ambar[5]; Douglas Oliveira[1]; Caroline Alvarenga[1]; Jhiovana Cristielly Costa[1]; Adriana Ruckert[3]; Débora C. Oliveira[3]; Luzia F. Martorelli[3]; Ana Paula Kataoka[3]; Marcelo S. Nardi[4]; Juliana L. Summa[4]; Roberta Marcatti de Azevedo[4]; Luzia H. Queiroz[2]; Ariovaldo P. Cruz-Neto[5] and Edison Durigon[1]

[1]Departamento de Microbiologia, Instituto de Ciências Biomédicas (ICB), Universidade de São Paulo (USP), São Paulo-SP; [2] Faculdade de Medicina Veterinária de Araçatuba, Universidade Estadual Paulista (UNESP), Araçatuba- SP; [3] Centro de Controle de Zoonozes (CCZ) do Município de São Paulo-SP; [4] Divisão Técnica de Medicina Veterinária e Manejo da Fauna Silvestre (DEPAVE-3), Secretaria do Verde e Meio Ambiente, Prefeitura do Município de São Paulo, São Paulo-SP; [5] Departamento de Zoologia, Instituto de Biociências, Universidade Estadual Paulista (UNESP), Rio Claro-SP

8:30 a.m. **Preliminary Evidence of a Novel Alphacoronavirus and Secondary Acquisition of Tymoviridae and Partitiviridae in Little Brown Bats (*Myotis lucifugus*) in Southcentral Alaska.**
Douglas Causey[1], Jonathan C. Rupp*[1], Maegan Lange[1], Megan Howard[2], Anitha Sundarajan[3], Jonny Sena[3], Faye D. Schilkey[3], Molly Murphy[4], Sarah Cooperman[1], Eric Bortz[1]

[1]Dept. of Biological Sciences, University of Alaska Anchorage; [2]Battelle Memorial Institute; [3]National Center for Genome Resources, Santa Fe NM; [4]Dept. of Veterinary Medicine, University of Alaska Fairbanks

8:45 a.m. **Are big brown bat cells different than human cells in their innate immune response to coronavirus and viral ligands?**
Arinjay Banerjee[1], Robert Brownlie[3], Noreen Rapin[1], Trent Bollinger[2], Darryl Falzarano[1,3] and Vikram Misra[1]

[1]Department of Microbiology, Western College of Veterinary Medicine, University of Saskatchewan, Canada. [2]Department of Pathology, Western College of Veterinary Medicine, University of Saskatchewan, Canada. [3]VIDO-InterVac, University of Saskatchewan, Canada.

9:00 a.m. **Session V - Influenza** (Corey Campbell, Moderator)

9:00 a.m. **Reverse genetic analysis of bat influenza viruses: A journey full of surprises.**
Martin Schwemmle

Institute of Virology, University of Freiburg Medical Center

9:30 a.m. **Towards understanding bat influenza A-like viruses**
Wenjun Ma[1], Bin Zhou[2], Jingjiao Ma[1], Qingfang Liu[1], Jinhwa Lee[1], Michael Duff[1], Juergen A. Richt[1], David E. Wentworth[2]
[1]Department of Diagnostic Medicine/Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan, Kansas, United States of America.
[2]Virology, J. Craig Venter Institute, Rockville, Maryland, United States of America.

9:45 a.m. **Experimental Infection of Jamaican Fruit Bats (*Artibeus jamaicensis*) with a Rescued Bat HL18NL11 Influenza A-like Virus**
Tony Schountz[1], Ashley Malmlov[1], Jingjiao Ma[2], Jinhwa Lee[2], Corey Campbell[1], Tawfik Aboellail[1], Ann Hawkinson[3] and Wenjun Ma[2]

[1]Department of Microbiology, Immunology and Pathology, College of Veterinary Medicine and Biomedical Sciences, Colorado State University; [2]Department of Diagnostic Medicine and Pathobiology, College of Veterinary Medicine, Kansas State University; [3]School of Biological Sciences, University of Northern Colorado

10:00 a.m. Break

10:00 a.m. Session VI - Ecology (Paul Cryan, Moderator)

10:30 a.m. **Seroprevalence of alphaviruses, flaviviruses and Rift Valley fever virus in Ugandan bats**
Rebekah C Kading[1,2], Kityo R[3], Mossel E[1], Borland E[1], Nakayiki T[4], Nalikka B[3], Nyakarahuka L[4], Ledermann J[1], Panella N[1], Gilbert A[5,6], Crabtree M[1], Kerbis Peterhans J[7], Towner J[8], Amman B[8], Sealy T[8], Nichol S[8], Powers A[1], Lutwama J[4], Miller B[1]

[1] Centers for Disease Control and Prevention, Division of Vector-borne Diseases, Arbovirus Diseases Branch, Fort Collins, CO. [2]Current Affiliation: Colorado State University, Department of Microbiology, Immunology and Pathology, Fort Collins, CO. [3]Makerere University, Department of Biological Sciences, Kampala, Uganda. [4]Uganda Virus Research Institute, Entebbe, Uganda. [5]Centers for Disease Control and Prevention, Division of High Consequence Pathogens, Rabies and Poxvirus Branch, Atlanta, GA. [6]Current Affiliation: United States Department of Agriculture, Animal and Plant Health Inspection Service, Fort Collins, CO. [7]College of Professional Studies, Roosevelt University &Collections & Research, The Field Museum of Natural History, Chicago, IL. [8]Centers for Disease Control and Prevention, Division of High Consequence Pathogens, Viral Special Pathogens Branch

10:45 a.m. **Presence of zoonotic bat pathogens correlate with reproductive seasons in South African bat populations**
Wanda Markotter[1], Muriel Dietrich[1], Teresa Kearney[2,3], Stewart McCulloch[1], Marinda Mortlock[1], Ernest Seamark[4,5] and Janusz Paweska[6]

[1] Centre for Viral Zoonoses, Department of Medical Virology, Faculty of Health Sciences, University of Pretoria, South Africa. [2] Ditsong National Museum of Natural History, Pretoria, South Africa. [3] Plant and Environmental Sciences, University of the Witwatersrand, Johannesburg, South Africa. [4] AfricanBats, Kloofsig, South Africa. [5] Centre for Wildlife Management, Faculty of Natural and Agricultural Sciences, University of Pretoria, Pretoria, South Africa. [6] Centre for Emerging, Zoonotic and Parasitic Diseases, National Institute for Communicable Diseases, Sandringham, South Africa.

11:00 a.m. **Body mass index of the Egyptian fruit bat, *Rousettus aegyptiacus*: An indicator of infection status**
Low J. de Vries[1], Stewart McCulloch[1], Janusz Paweska[2] and Wanda Markotter[1]

[1]Centre for Viral Zoonoses, Department of Medical Virology, Faculty for Health Science, University of Pretoria, South Africa; [2]Center for Emerging, Zoonotic and Parasitic Diseases, National Institute for Communicable Diseases, Sandringham, Johannesburg, South Africa

11:15 a.m. **Environmental constraints drive the viral diversity of two sympatric Amazonian bat species**
Arielle Salmier, Sourakhata Tirera, Benoit de Thoisy, Alain Franc, Edith Darcissac, Damien Donato, Christiane Bouchier, Vincent Lacoste and Anne Lavergne

Institut Pasteur de la Guyane, French Guiana/ France

11:30 a.m. **Seasonal and individual predictors of grey-headed flying fox (*Pteropus poliocephalus*) foraging movements in Adelaide, South Australia**
Cecilia A. Sánchez[1,2], Terry B. Reardon[3], Wayne S.J. Boardman[4] and Sonia Altizer[1,2]

[1]Odum School of Ecology, University of Georgia, Athens, GA, USA; [2]Center for the Ecology of Infectious Diseases, University of Georgia, Athens, GA, USA; [3]South Australian Museum, Adelaide, South Australia, Australia; [4]University of Adelaide, Adelaide, South Australia, Australia

11:45 a.m. **Uganda Bat calls library-developing a tool to survey arthropod-borne viruses associated with Chiroptera**
Robert Martin Kityo[1], Rebekah Kading[2], Betty Nalikka[1], Julius Lutwama[3]

[1]Makerere University, College of Natural Science – Department of Zoology, Entomology and Fisheries Science Kampala Uganda; [2]Colorado State University; [3]Uganda Virus research institute

12:00 p.m. Lunch

1:00 p.m. Session V - Immunology of Bats (Tony Schountz, Moderator)

1:00 p.m. **Dampening of STING-dependent IFN production: an implication of virus tolerance in bats?**
Jiazhen Xie[1], Chenxi Ma [1], Yang Li[1], Jie Cui[1], Linfa Wang [2], Zhengli Shi [1] and Peng Zhou[1*]

[1]Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan 430071, China; [2]Emerging Infectious programme, Singapore Duke-NUD Medical School, Singapore 169857, Singapore

1:15 p.m. **Regulation of immune activation and dampened inflammation in Pteropid bats**
Aaron T. Irving[1], Katarina Luko[1], Matae Ahn[1], Kong Pui San[1], & Lin-Fa Wang[1]

[1]Duke-NUS Medical School, Singapore

1:30 p.m. **Delineating the phenotype and function of the B cell population in the fruit-eating bat, *Pteropus Alecto.***
Pravin Periasamy[1,2], Martínez Gómez JM[1,2], Wang LF[3] , and Alonso S[1,2]

[1]Department of Microbiology and Immunology, [2]Immunology Programme, Yong Loo Lin School of Medicine, Life Sciences Institute, National University of Singapore, Singapore. [3]DUKE-NUS, Singapore.

1:45 p.m. **Integrative measures for assessing "health" in free-ranging bats – zoonotic and conservation implications from a One Health perspective**
DeeAnn M. Reeder, Kenneth A. Field

Department of Biology, Bucknell University

2:00 p.m. Session VI - White Nose Syndrome (Joel Rovnak, Moderator)

2:00 p.m. **Host-pathogen interactions during white-nose syndrome**
Ken Field[1], Sophia M Reeder[1], Jonathan M Palmer[2], Brent J Sewall[3], Jenni M Prokkola[4], Greg Turner[5], Thomas M Lilley[6], Marianne Gagnon[3], J Paul White[7], Joseph Johnson[8], Christopher Hauer[3], and DeeAnn M Reeder[2]

[1]Department of Biology, Bucknell University, Lewisburg, PA; [2]Center for Forest Mycology Research, Northern Research Station, US Forest Service, Madison, WI; [3]Department of Biology, Temple University, Philadelphia, PA; [4]University of Eastern Finland, Joensuu, Finland; [5]Wildlife Diversity Division, Pennsylvania Game Commission, Harrisburg, PA; [6]Institute of Integrative Biology, University of Liverpool, Liverpool L69 3BX, UK; [7]Wisconsin Department of Natural Resources, Madison, WI; [8]Biological Sciences, Ohio University, Athens, OH

2:15 p.m. **Resistance or Tolerance – How do European bats cope with *Pseudogymnoascus destructans*?**
Marcus Fritze[1,2],Voight CC[2], Czirjak GA[2], Puechmaille SJ[1,3]

[1] Zoology Institute,University of Greifswald,Soldmann-Str. 14, D - 17487 Greifswald, Germany; [2] Leibniz institute for Zoo and Wildlife Research, Alfred-Kowalke-Str. 17, 10315 Berlin, Germany and [3]School of Biology and Environmental Sciences, University College Dublin, Belfield, D4 Dublin Ireland

2:30 p.m. **Modeling the impact of White-nose syndrome on two western bat species**
C. Reed Hranac[1], Brandon J. Klüg-Baerwald[2], Yvonne A. Dzal[3], Cori Lausen[4], Jonathan C. Marshall[1,5], Sarah H. Olson[6] , David T. S. Hayman[1]

[1]Hopkirk Research Institute, Massey University, Private Bag, 11 222, Palmerston North 4442, New Zealand; [2] Department of Biology University of Regina, Regina, SK, Canada, 3737 Wascana Parkway, Regina, SK S4S 1T8; [3] Department of Zoology, University of British Columbia, Vancouver, BC, Canada #4200-6270 University Boulevard, Vancouver, BC V6T 1Z6, [4] Wildlife Conservation Society Canada, Kaslo, BC, Canada, P.O. Box 606, 202 B Ave, Kaslo, BC V0G 1M0; [5] Institute of Fundamental Sciences Massey University, Private Bag 11 222, Palmerston North 4442, New Zealand; [6] Wildlife Conservation Society, Wildlife Health Program 212 South Wallace Avenue, Suite 101, Bozeman, MT, 59715, USA

2:45 p.m. **Variable behaviors influence species susceptibility to disease – surviving white-nose syndrome.**
Paul M. Cryan

U.S. Geological Survey (USGS), USGS Fort Collins Science Center, 2150 Centre Ave., Bldg. C, Fort Collins, Colorado

3:00 p.m. Break

3:30 p.m. Session VI - Other Infectious Agents of Bats (Anna Fagre, Moderator)

3:00 p.m. **Emerging Insights into the Geographic Distribution, Genetic Diversity and Evolutionary Origin of Bat-borne Hantaviruses**
Satoru Arai[1], Se Hun Gu[2], Son Truong Nguyen[3], Vuong Tan Tu[3], Blaise Kadjo[4], Burton K. Lim[5], Joseph S. Masangkay[6], Saw Bawm[7], Joseph A. Cook[8], Shigeru Kyuwa[9], Keiko Tanaka-Taya[1], Shigeru Morikawa[1] and Richard Yanagihara[2]

[1]National Institute of Infectious Diseases, Tokyo, Japan; [2]University of Hawaii at Manoa, Honolulu, HI, USA; [3]Institute of Ecology and Biological Resources, Vietnam Academy of Science and Technology, Hanoi, Vietnam; [4]University of Félix Houphouët-Boigny, Abidjan, Côte d'Ivoire; [5]Royal Ontario Museum, Toronto, Canada; [6]University of the Philippines Los Baños, Laguna, Philippines; [7]University of Veterinary Science, Nay Pyi Taw, Myanmar; [8]University of New Mexico, Albuquerque, New Mexico, U.S.A.; [9]University of Tokyo, Tokyo, Japan;

3:15 p.m. **Neotropical Bats that Co-habit with Humans Function as Dead-End Hosts for Dengue Virus**
Amanda Vicente-Santos[1,2], Andres Moreira-Soto[1,4], Claudio Soto-Garita[1], Luis Guillermo Chaverri[3], Andrea Chaves[2], Jan Felix Drexler[4,5], Juan Alberto Morales[6], Alejandro Alfaro-Alarcón[6], Bernal Rodríguez-Herrera [2] and Eugenia Corrales-Aguilar [1*]

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3:30 p.m. **Novel Gammaherpesvirus in Bats: discerning the secrets of these oncogenic viruses**
Sonu Subudhi, Noreen Rapin, Janet Hill[1] and Vikram Misra

Department of Veterinary Microbiology, University of Saskatchewan, Saskatoon, Canada

3:45 p.m. **Experimental Infection of Jamaican Fruit Bats (*Artibeus jamaicensis)* with Zika Virus**
Ashley Malmlov[1], Kaitlyn Miedema[1], Tawfik Aboellail[2], Corey L Campbell[1], Miles Eckley[1], Nunya Chotiwan[1], Rebekah C. Gullberg[1], Rushika Perera[1] and Tony Schountz[1]

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4:00 p.m. **Long-term monitoring of *Bartonella* bacteria in a captive colony of fruit bats and experimental evidence of bat flies as vectors of bartonella**

Clifton McKee[1,2], Colleen Webb[1], Michael Kosoy[2], Ying Bai[2], Lynn Osikowicz[2], Richard Suu-Ire[3], Yaa Ntiamoa-Baidu[4], Andrew Cunningham[5], James Wood[6], David Hayman[7]

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4:15 p.m. **Open Discussion**

5:00 p.m. Adjourn

POSTER PRESENTATIONS

1. James N. Aegerter, Ashley C. Banyard, Anthony R. Fooks, Graham C. Smith·
Predicting the epizootiology of temperate bat disease: Is it all about the bats?

2. Danielle E. Anderson, Kristmundur Sigmundsson, So Young Kim, Brian Ho Wenkae, Jasmine Tan[1] and Lin-Fa Wang. **Comparative loss of function screens highlight common cellular pathways required by mumps virus for replication in bats and humans**

3. Victoria Avanzato, Neeltje van Doremalen, Christine Carrington, Janine Seetahal, Tony Schountz, Vincent Munster
Development Implementation of a RT-PCR Assay to Detect Henipaviruses in Trinidad Bats

4. Jonathan C. Rupp, Maegan Lange, Megan Howard, Anitha Sundarajan, Jonny Sena[3], Faye D. Schilkey, Molly Murphy, Douglas Causey, Eric Bortz.
Genomic characterization and pathogenic potential of a novel evolutionarily-divergent alphacoronavirus isolated from *M. lucifigus* bats in Alaska.

5. Douglas Causey, Jonathan C. Rupp, Maegan Lange, Megan Howard, Anitha Sundarajan, Jonny Sena, Faye D. Schilkey, Molly Murphy, Eric Bortz
Preliminary Evidence of Secondary Acquisition of Tymoviridae and Partitiviridae in Little Brown Bats (*Myotis lucifugus*) in Southcentral Alaska.

6. Marcy Kanuka, Ashley Malmlov, Christine Cornish, Kathleen Parker, Cassandra Tang Wing, Diana Stone, Tony Schountz and Sonia Cheetham
Molecular Screening of Zika and Dengue Viruses in Bats (*Artibeus jamaicensis, Glossophaga longirostris and Molossus molossus*) from Grenada, West Indies.

7. Diana Stone, Christine Cornish, Amy C. Lyons, Yan-Jang S. Huang, Dana L. Vanlandingham, Stephen Higgs, Bradley Blitvich, Abiodun A. Adesiyun, Sharlene Santana, Leith Leiser-Miller, Sonia Cheetham.
Serologic evaluation of Alphavirus and Flavivirus exposure in bats in Grenada

8. Fagre AC, Kityo R, Lee J, Mossel E, Crabtree, M, Nalikka B, Nakayiki T, Kerbis J, Gilbert, A, Bergren, N, Nyakarahuka L, Lutwama J, Stenglein M, Byas A, Malmlov A, Bergren N, Rice L, Miller B, Schountz T & Kading, RC.
Isolation and molecular characterization of Bukakata orbivirus, a novel virus from a Ugandan bat, and associated pathology in experimentally infected Jamaican fruit bats (*Artibeus jamaicensis*)

9. Robert J. Fischer, Seth D. Judson, Sarah H. Olson, Vincent J. Munster
Using GIS to Guide Ebola Virus Disease Ecology Field Investigations

10. Hannah Frank, David Enard, Chase Mendenhall, Ji-Yeun Lee, Ellie Armstrong, Stefan Prost, Seth Judson, Jamieson O'Marr, Gretchen Daily, Dmitri Petrov, Scott Boyd and Elizabeth Hadly[1,6,7]
Bat - infection interactions: Signals of evolution, ecology, immunity and deforestation

11. Yupadee Hengjan, Didik Pramono, Hitoshi Takemae, Ryosuke Kobayashi, Karla Cristine Doysabas, Keisuke Iida, Takeshi Ando, Supratikno, Chaerul Basri Yuli Sulistya Fitriana, Eko M.Z. Arifin, Yasushige Ohmori, Ken Maeda, Srihadi Agungpriyono and Eiichi Hondo
Daytime behavior of *Pteropus vampyrus* and *Acerodon jubatus* in the natural habitats: a cue of viral transmission

12. Yutthana Joyjinda, Supaporn Wacharapluesadee, Prateep Duengkae, Apaporn Rodpan, Teerada ponpinit, Thongchai Kaewpom, Sangchai Yingsakmongkol, Kevin J Olival, Thiravat Hemachudha
The study of whole spike gene of bat coronavirus from Thailand using Next Generation Sequencing

13. Jun Li & Vincent Munster
Assessment of the cross-species potential of two emerging coronaviruses, SARS-CoV and MERS-CoV, by Protein-Protein Molecular Docking analyses

14. Kessler MK, Kamath PL, Smith CS, Goldspink LK, Plowright RK
Hendra virus phylogeography in eastern Australia

15. Tamar Kutateladze, Lela Urushadze, Davit Putkaradze, Magda Dgebuadze, Giorgi Babuadze, Ioseb Natradze, Lillian Orciari, and AndresVelasco-Villa
Viral Zoonosis in Georgian Bats

16. Aiah Lebbie, Jonathan Towner, Ibrahim Bakarr Brian Amman, Amy Schuh, Jonathan Johnny, Tara Sealy, James Graziano, Celine Taboy, John Klena, Immah Conteh, Stuart Nichol, Alusine Koroma, Ibrahim Foday and Richard Wadsworth
Forestalling Future Outbreaks: Enhancing Capacity for Surveillance of Viral Hemorrhagic Fever Viruses in Sierra Leone

17. Matovu Benard, Nalikka Betty and Kityo Robert
Ecological aspects of bats in a cave frequented by members of the local community in Kaptum Cave in eastern Uganda.

18. Rebekah McMinn, Michael Letko, Neeltje van Doremalen, Kerri Miazgowicz, Vincent Munster[1]
Middle East respiratory syndrome coronavirus spike plasticity in the context of the common vampire bat (*Desmodus rotundus***) DPP4 receptor.**

19. Alison J. Peel, Victoria Boyd, Raina K. Plowright, Olivier Restif, Gary Crameri, John Giles, Hamish McCallum, Konstans Wells
Viral community dynamics of Australian Flying foxes

20. Ponpinit T, Wacharapluesadee S, Duengkae P, Kaewpom T, Yinsakmongkon S, Rodpan A, Hemachudha T
The glycoprotein of Nipah virus in Thai bats associated with Nipah virus in Bangladesh

21. Jonathan C. Rupp, Maegan Lange, Megan Howard, Anitha Sundarajan, Jonny Sena, Faye D. Schilkey, Molly Murphy, Douglas Causey, Eric Bortz.
Genomic characterization and pathogenic potential of a novel evolutionarily-divergent alphacoronavirus isolated from *M. lucifigus* **bats in Alaska.**

22. Salmier A., de Thoisy B., Crouau-Roy B., Lacoste V. and Lavergne A.
Spatial pattern of genetic diversity and selection in the MHC class II DRB of three Neotropical bat species

23. Ken Cameron, Stephanie Seifert, Shauna Milne-Price, Alain Ondzie, Trent Bushmaker, Jean-Vivien Mombouli, Sarah Olson and Vincent J. Munster
Establishing a field collection scheme to investigate the role of African fruit bats as the natural reservoir of ebolaviruses

24. Lela Urushadze, Ying Bai, Lynn Osikowicz, Ioseb Natradze, Ketevan Sidamonidze, Davit Putkaradze, and Michael Kosoy
Co-infection in Georgian Bats

25. Megan E. Vodzak, MS, MPH, Ohnmar Aung, MBBS, MA , Marc T. Valitutto, VMD, Kyaw Y. N. Tun, BVSc, MSc, PhD , Heather S. Davies, MS , Michael E. von Fricken, PhD, MPH Suzan Murray, DVM, DACZM, and Dawn M. Zimmerman, DVM, MS
Caves of Myanmar: a high-risk human-wildlife interface for zoonotic disease

26. Supaporn Wacharapluesadee, Prateep Duengkae, Aingorn Chaiyes, Sangchai Yinsakmongkon[3] Pattarapol Maneeorn[4], Patcharakiti Phengsakul, Wachirapon Khumbucha, Thongchai Kaewpom, Apaporn Rodpan, Thiravat Hemachudha
Prevalence Patterns of Coronaviruses in Lyle's flying fox (*Pteropus lylei*) in Thailand

27. Xing-Lou Yang, Yun-Zhi Zhang, Ren-Di Jiang, Hua Guo, Wei Zhang, Bei-Li, Ning Wang, Li-Wang, Cecilia Waruhiu, Ji-Hua Zhou, Shi-Yue Li, Peter Daszak, Lin-Fa Wang, Zheng-Li Shi
Genetically Diverse Filoviruses in *Rousettus* and *Eonycteris* spp. Bats, China, 2009 and 2015

28. Miles Eckley, Ann Hawkinson, Tyler Sherman, Tony Schountz, Corey L Campbell
Development of a monoclonal antibody to Jamaican fruit bat CD3γ.

29. Candace Cotter, Tony Schountz, Corey L Campbell.
Bats and Immunity: Anti-Viral IFNγ Responses Differ Among Hosts.

30. Janine F.R. Seetahal, Orchid M. Allicock, Stephen C. Sameroff, Christopher Oura, Vernie Ramkissoon, W. Ian Lipkin, Christine V.F. Carrington
Virome analysis of neotropical bats on the Caribbean island of Trinidad

31. Periasamy P, Martínez Gómez JM, Wang LF, and Alonso S.
Delineating the phenotype and function of major lymphocyte populations in the fruit-eating bat, Pteropus Alecto.

32. Cara E. Brook, Hafaliana C. Ranaivoson, Christopher C. Broder, Andrew A. Cunningham, Andrea L. Graham, Jean-Michel Héraud, Louise Wong, James L.N. Wood, Andrew P. Dobson, C. Jessica E. Metcalf
Seasonal serological signals in viral infections for Madagascar fruit bats

Oral Presentation Abstracts

Studies of horizontal transmission of Marburg virus among experimentally infected fruit bats
Jonathan S. Towner[1,2], Amy J. Schuh[1], Brian R. Amman[1], Megan E. B. Jones[1,2], Tara K. Sealy[1], Uebelhoer LS, Spengler JR, Stuart T. Nichol[1]

[1]Viral Special Pathogens Branch, Centers for Disease Control and Prevention, Atlanta, USA, [2]Department of Pathology, College of Veterinary Medicine, University of Georgia, Athens, USA

Objectives: To investigate under experimental conditions the dynamics of Marburg virus replication in a known reservoir host and determine if 1) the virus can be transmitted from infected bats to immunologically naïve bats in the absence of arthropod vectors, and 2) identify the route(s) of virus shedding and therefore likely exposure. **Methods**: Using age-matched captive borne juvenile bats, we inoculated a total of 12 animals with Marburg virus 371 bat isolate and co-housed these animals with 24 naïve contact bats for 9 months under BSL-4 conditions and tested for evidence of virus shedding and transmission. **Results**: Marburg virus shedding was detected in oral, rectal and urine specimens from the inoculated bats through 19 days post infection. During the same time frame, Marburg virus was detected in oral specimens from contact bats, indicating that they were orally exposed to the virus from the inoculated animals. In the late study phase, we found that Marburg virus was horizontally transmitted from the donor bats to naïve contact bats by finding Marburg virus RNA in blood and oral specimens from contact bats, followed by the detection of Marburg virus IgG antibodies in these same animals. **Conclusions**: This study demonstrates, in the absence of any arthropod vectors, 1) direct filovirus transmission from a natural reservoir to another animal, 2) Marburg virus is shed primarily in saliva and urine, and perhaps feces, with some bats acting as super-shedders accounting for more than 80% of the cumulative virus shed, and 3) that this virus/reservoir host system can serve as an bona-fide experimental model for investigating how filoviruses are maintained long-term in nature and what drivers might influence occasional spillover to humans and other animals.

Investigations of Long-term Protective Immunity against Marburg Virus Reinfection in Egyptian Rousette Bats
Schuh AJ, Amman BR, Sealy TK, Spengler JR, Nichol ST and Towner JS

Viral Special Pathogens Branch, Division of High-Consequence Pathogens and Pathology, Centers for Disease Control and Prevention, Atlanta, GA 30333, USA

Objectives: The Egyptian rousette bat (ERB; *Rousettus aegyptiacus*) is as a known natural reservoir host for Marburg virus (MARV). Following infection of ERBs with MARV, virus-specific IgG antibodies rapidly decline and by 3 months post infection the bats are MARV seronegative. Therefore, it is unclear whether reinfection plays a role in MARV maintenance. **Methods:** To address this question, ERBs that had been “naturally” or experimentally infected with MARV 17 to 24 months prior were challenged with homologous virus. Following challenge, evidence of MARV replication in the blood and viral shedding from the oral mucosa was monitored for 14 days, MARV IgG antibody responses were monitored for 21 days and tissues obtained at necropsy at 21 days were tested for the presence of MARV RNA. **Results:** No evidence of MARV replication in the blood or shedding from the oral mucosa was detected in either group of bats through 14 days post inoculation. A robust MARV IgG antibody response occurred by seven days post inoculation in all bats, indicating the occurrence of a secondary immune response. **Conclusions:** This study demonstrates that both “natural” and experimental infection of ERBs with MARV induces long-term protective immunity against reinfection and suggests that other factors such as the twice-yearly influx of susceptible juveniles, large colony sizes and population connectivity, drive MARV transmission dynamics in wild populations of ERBs.

Innate immune response to filoviruses and the role of filoviral interferon-inhibiting domains in bat and human cells
Ivan V. Kuzmin[1,2], Toni M. Schwarz[3], Philipp A. Ilinykh[1,2], Ingo Jordan[4], Thomas G. Ksiazek[1,2,5], Ravi Sachidanandam[6], Christopher F. Basler[3, 7], and Alexander Bukreyev[1,2,5]

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Objectives: Innate immune responses in bat (Rousettus aegyptiacus) and human cells to the filoviruses Marburg (MARV) and Ebola (EBOV) were investigated to determine the ability of these viruses to subvert antiviral insults from different host species.
Methods: The innate immune response to filoviruses in bat and humans cells was profiled by deep sequencing and also analyzed by qRT-PCR. Bat mRNAs encoding IFNalpha, beta, gamma, lambda, and interferon stimulated genes (ISG) 54 and 56, were cloned and examined for their antiviral effect in response to MARV and EBOV infection in bat and human cells. Rates of infection and the effects of the major filoviral IFN-inhibiting domains (IID), VP35 and VP24, were analyzed in cells from both host species.
Results: We demonstrated that EBOV and MARV replicate to similar levels in all tested cell lines, indicating that permissiveness for EBOV at cell and organism levels do not necessarily correlate. Filoviruses, particularly MARV, induced a potent innate immune response in rousette cells that was generally stronger than in human cells. Both EBOV VP35 and VP24 IID were found to suppress the innate immune response in rousette cells, but only VP35 IID appeared to promote virus replication. Along with IFN-alpha and IFN-beta, IFN-gamma was demonstrated to control filovirus infection in bat cells but not in human cells suggesting host species specificity of the antiviral effect. The antiviral effects of bat IFNs appeared not to correlate with induction of bat ISG54 and ISG56, which were detected in human cells expressing bat IFN-alpha and IFN-beta.
Conclusions: Rousettus aegyptiacus cells mount robust innate immune responses to filovirus infection. Filovirus IIDs are active in both rousette and human cells; however, the VP35 IID plays a greater role in promotion of viral replication in rousette cells than in human cells. IFN-gamma plays a greater role in control of filovirus infections in rousette non-immune cells than in human cells. At least in part, the antiviral effect of IFN-gamma results from 'cross talk' leading to activation of the type I IFN response. The data are useful for understanding the interactions of filoviruses with natural (Rousettus aegyptiacus) and accidental hosts (humans).

Broad based surveillance for ebolaviruses: PREDICT in Sierra Leone, Liberia, and Guinea
Bird B[1], Goldstein T[1], Anthony S[2], Gbakima A[3], Saylors K[3], Jean Louis F[3], Wolking D[1], Epstein J[4], Karesh W[4], Kreuder-Johnson C[1], Mazet J[1]

One Health Institute UC Davis School of Veterinary Medicine[1], Center for Infection and Immunity Columbia University[2], Metabiota Inc.[3], EcoHealth Alliance[4]

Objectives: Developing and operationalizing strategies to reduce zoonotic pathogen spillover, amplification, and spread are nowhere more relevant than in Sierra Leone, Guinea, and Liberia. The devastating loss of lives associated with the Ebola virus outbreak revealed the urgent need for increased animal and public health sector capacity strengthening. Put into historical context, this epidemic was more than 60 times larger than any previous Ebola outbreak, spread to 7 additional countries, and stretched emergency response efforts to the utmost limits of capacity. **Methods**: PREDICT is working to improve understanding of wildlife reservoirs, spillover hosts, and origins of these viruses; ascertain the potential of virus-spillover into other non-typical hosts, such as livestock or companion animals; gain a greater understanding of high-risk human behavioral activities; and improve disease surveillance and laboratory capacities through workforce development in line with Global Health Security Agenda priorities. **Results**: Due to the impact on these three countries, USAID's PREDICT Project developed a focused effort to better address the threat of ebolaviruses by investigating the virus' animal origins, while strengthening in-country capacity to build and reinforce emerging disease surveillance and detection systems. In each country, teams are conducting concurrent sampling of from multiple animal taxa (dogs, cats, livestock, wildlife) and applying broad based molecular approaches to detect all known and other potential novel ebolaviruses. As of April 2017, over 6,500 animals have been sampled including over 3,500 bats in the three countries, with laboratory testing underway. Without identifying reservoirs of infection and how widely they are distributed across the region, prevention programs to reduce transmission from animals to people will have limited impact, and it is likely that future spillover of ebolaviruses from animals into humans will continue to occur. **Conclusions**: As we have seen over the years in Central and Eastern Africa where filovirus outbreaks have repeatedly occurred, effective control of these rare "spillover" events is possible and, when the right technical capacities are in place, these outbreaks can even be limited to a small number of human cases.

Quantifying signatures of resistance and tolerance to filoviruses in bat cell lines
Cara E. Brook[1], Melinda Ng[2], Esther Ndungo, Rohit K. Jangra, Andrew P. Dobson, Andrea L. Graham, Bryan T. Grenfell, C. Jessica E. Metcalf[1]*, Kartik Chandran[1]*

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[2]Department of Microbiology and Immunology, Albert Einstein College of Medicine
*These senior authors contributed equally to this work.

Objectives: Previous work has demonstrated that a single amino acid change in the filovirus receptor, NPC1, in *Eidolon helvum* cells make them refractory to Ebola virus infection, hinting at a possible coevolutionary history between virus and bat host. We sought to expand on this nascent evidence of the evolution of pathogen resistance. **Methods:** We carried out a series of plaque assays, in which we challenged bat (EidNi/41.3, RoNi/7.1, PaKiT01), U2OS, and Vero cell lines with multicycle replicating pseudotype Ebola and Marburg filoviruses. Because of the agar overlay inherent to the plaque assay, viral transmission was restricted to neighboring cells. We visualized this transmission by photographing the timecourse of infection spread across the cell monolayer, and processing the images to quantify the proportion infected at a given time point as the proportion of photograph illuminated by GFP-tagged virus. We then fit spatially-structured traditional epidemiological models to the resulting data, in order to disentangle the mechanisms underpinning diverse trajectories of tolerance and resistance in different virus-cell line relationships. **Results:** Our modeling highlights diverse, species-specific evolutionary relationships between particular bat cell lines and particular filoviruses, which necessitate mechanisms of pathogen resistance in order to recapture data trajectories in some cases (chiefly *E. helvum* and Ebola and *P. alecto* and Marburg) and mechanisms of tolerance in others. **Conclusions:** Our work highlights the power of interdisciplinary approaches, combining quantitative epidemiology with cell biology and adds to growing evidence suggestive of unique species-specific coevolution between bats and filoviruses.

Serologic evidence of exposure to filoviruses in fruit bats, Singapore
Laing ED[1], Mendenhall IH[2], Linster M[2], Low DHW[2], Chen Y[2], Yan L[1], Sterling SL[1], Borthwick S[2], Neves ES[2], Lim JSL[2], Skiles M[2], Lee BPY[4], Wang LF[2], Broder CC[1], Smith GJD[2, 5]

Uniformed Services University, Bethesda, MD, USA[1], Duke-National University of Singapore Medical School, Singapore[2], North Carolina State University, Raleigh, NC, USA[3], National Parks Board, Singapore[4], Duke Global Health Institute, Duke University, Durham, North Carolina, USA[5]

Objectives: Bats are known natural hosts of Nipah virus and Maburg virus, and the collective evidence suggests that bats are also the natural hosts of ebolaviruses. Reston virus, an *Ebolavirus* species, is known to circulate in species of bats in the Philippines. To examine whether ebolaviruses and marburgviruses are more broadly present in Southeast Asia, we tested sera from three fruit bat species endemic in Singapore and widely distributed throughout Southeast Asia for evidence of past exposure to known species of ebolaviruses and marburgviruses. **Methods:** Sera were collected from the above-mentioned bat species from 2011 to 2016 in Singapore to screen for evidence of exposure to filoviruses. Venous blood was diluted 1:10 in 1×PBS and tested using a Bio-Plex® bead-based multiplex assay that simultaneously probes sera for immunoglobulins specific to the viral envelope glycoprotein from representative strains of all previously described *Ebolavirus* and *Marburgvirus* spp. We employed methods developed by Peel AJ *et al.* to establish a median fluorescence intensity (MFI) cutoff value. We screened 409 samples with this *Ebolavirus/Marburgvirus* spp. Bio-Plex® assay. **Results:** Positive results indicated that bats were previously infected with viruses related to the ebolaviruses from which the virus surface proteins were derived. Of the species tested, 10% of *Eoncyteris spelaea*, 8% of *Cynopterus brachyotis*, and 4% of *Penthetor lucasi* had positive sera results for antibodies specific to ebolaviruses.
Conclusion: These serological results demonstrated that viruses related to ebolaviruses have previously infected all three species of fruit bats, and may circulate in the populations, but we have not detected the virus in any samples. We conducted next generation sequencing on urine and feces, bat cell lines and screened numerous samples from bats in Singapore and have detected no evidence of the virus. As there is no evidence of Ebola virus disease in humans in Singapore or Southeast Asia, we think that these serological findings are evidence of novel, yet undescribed viruses related to known ebolaviruses.

Predicting undiscovered filovirus reservoirs and patterns of disease emergence
David Hayman[1]

[1]Molecular Epidemiology and Public Health Laboratory, Hopkirk Research Institute, Massey University, New Zealand

Objectives: How can we discover unidentified filovirus hosts and where should we be searching for the viruses? Filoviruses *Ebolavirus* (EBOV) and *Marburgvirus* cause hemorrhagic fevers with high mortality rates, posing significant threats to public health and wildlife conservation. The viruses have sporadically emerged over the last 40 years at least, and yet the hosts of EBOV in particular remain poorly known and characterized. Here different studies help inform field surveillance through the identification of bat traits that predict filovirus reservoirs and ecological processes that facilitate emergence. **Methods:** Different modeling approaches were used. A mathematical model with seasonal birthing synthesized filovirus and bat data to determine if biannual birthing

might facilitate pathogen persistence. Regression analyses on serological data tested the model predictions. A machine learning approach provided additional information on bats, integrating multiple host trait data. Fragmentation analyses using satellite land cover data and Ebola virus disease outbreak index cases in humans (i.e. spillover from wildlife reservoirs) tested the hypothesis that forest fragmentation was correlated with emergence. **Results:** Synthesis of filovirus and bat data through models suggests bi-annual breeding and longer incubation periods, such as reported for Egyptian fruit bats and EBOV in experimental studies, allow viral persistence in bat colony sizes often found in nature. Serological data and machine learning approaches support the findings, with bats from species with two annual birth pulses more likely to be seropositive (odds ratio 4.4, 95% confidence interval 2.5-8.7) than those with one, suggesting biannual birthing may allow filovirus persistence. Machine learning algorithms suggest species' geographic range overlap may facilitate filovirus persistence. Finally, fragmentation analyses suggest Ebola virus disease outbreaks occurred mostly in hotspots of forest fragmentation. **Discussion:** These analyses suggest surveillance for filoviruses, especially ebolaviruses, might be targeted to young bats from species with biannual birthing in areas of fragmented forested habitat. The link between forest fragmentation and EBOV outbreaks suggests there is common ground between biodiversity conservation and disease risk mitigation. Together these results will help the research community identify where, when and in which species to continue the search for filovirus hosts.

Bats as possible animal origin of MERS-CoV

Susanna K. P. Lau

Department of Microbiology, The University of Hong Kong, Hong Kong, China

Objectives: Bats are important reservoir for emerging viruses including coronaviruses. Although dromedary camels are believed to be the immediate animal source of the recent MERS epidemic, the evolutionary origin of MERS-CoV remains obscure. While horseshoe bats are the primary reservoir of ancestors of SARS-CoV, the possible role of bats in the emergence of MERS-CoV is less clear. When MERS-CoV was first discovered, it was found to be most closely related to *Tylonycteris* bat CoV HKU4 (Ty-BatCoV HKU4) and *Pipistrellus* bat CoV HKU5 (Pi-BatCoV HKU5) previously discovered in lesser bamboo bat (*Tylonycteris pachypus*) and Japanese pipistrelle (*Pipistrellus abramus*) respectively in Hong Kong. Subsequently, two other lineage C betacoronaviruses, BtVs-BetaCoV/SC2013 and Coronavirus Neoromicia/PML-PHE1/RSA/2011 (NeoCoV) were also detected in bats from China and Africa respectively. Interestingly, a lineage C betacoronavirus, Erinaceus CoV VMC/DEU, has also been found in European hedgehogs, which are phylogenetically closely related to bats, in Europe. Although NeoCoV represents the closest bat counterpart of MERS-CoV in most genome regions, the spike (S) protein, important for host receptor binding, is genetically divergent from that of MERS-CoV. On the other hand, Ty-BatCoV HKU4 possessed an S protein being most closely related to MERS-CoV. The spike of Ty-BatCoV HKU4, but not that of Pi-BatCoV HKU5, was able to utilize the MERS-CoV receptor, human dipeptidyl peptidase 4 (hDPP4) or CD26, for cell entry. These findings suggested that bats may be the primary host of the ancestor of MERS-CoV. **Methods**:To better understand the evolutionary path of MERS-CoV, we collected bat samples from various regions in China. **Results**: Diverse CoVs were detected, including a potentially novel lineage C betacoronavirus. Compared to Ty-BatCoV HKU4 and Pi-BatCoV HKU5, the virus was even more closely related to MERS-CoV and NeoCoV in most regions of its genome. In contrast, the S1 region was less closely related MERS-CoV than Ty-BatCoV HKU4 but more closely related to MERS-CoV than Pi-BatCoV HKU5. To determine if this virus can utilize hDPP4 as receptor, binding experiments using S1-receptor-binding domain (RBD), cell entry studies using pseudovirus assays and structural modelling of the RBD-hDPP4 interphase were performed. **Conclusions**: The results suggested a stepwise evolutionary process among lineage C betacoronaviruses in gaining the ability to bind hDPP4, and support a bat origin of MERS-CoV.

Rapid detection of MERS coronavirus ancestors in bats

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Objectives: Since its first appearance in 2012, the Middle East Respiratory Syndrome (MERS) has affected more than 25 countries in four continents with more than 1,300 cases and a high fatality rate of more than 30%. A novel lineage C betacoronavirus (betaCoV), MERS-CoV, has been confirmed to be the etiological agent. Human dipeptidyl peptidase 4 (hDPP4) was found to be the cellular receptor for MERS-CoV. Subsequent detection of MERS-CoV and its antibodies in dromedaries in various countries in the Middle East and North Africa have implied that these animals are probably the reservoir for MERS-CoV. Other lineage C betaCoVs in bats [e.g. *Tylonycteris* bat CoV HKU4 (Ty-BatCoV-HKU4), *Pipistrellus* bat CoV HKU5 (Pi-BatCoV-HKU5)] and hedgehogs were found to be closely related to MERS-CoV. So far, detection of MERS-CoV and discoveries of its closely related CoVs are most efficiently achieved through RT-PCR. Although RT-PCR is highly sensitive, its turn-around-time is about four hours and the test requires expensive equipment, stringent laboratory set-up and personal attention to prevent laboratory PCR product cross contamination which may lead to false-positive results.

Methods: Recently, we have developed a monoclonal antibody-based rapid nucleocapsid protein (NP) detection assay for on-site diagnosis of MERS-CoV, which can be finished in 30 minutes. **Results and Conclusions**: This rapid test is highly specific for MERS-CoV for human and dromedary samples, as samples containing other human CoVs (HCoV-OC43, HCoV-229E, HCoV-NL63 and HCoV-HKU1) or dromedary CoV UAE-HKU23 all showed negative results. However, we hypothesize that the rapid test can pick up betaCoVs closely related to MERS-CoV; and hence would be useful for the discovery of MERS-CoV ancestors. To test this hypothesis, we examine the usefulness of this rapid test to detect four alphaCoVs and four lineage B, C and D betaCoVs in fecal samples of bats.

Global patterns in coronavirus diversity

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Objectives: Since the emergence of SARS-CoV and MERS-CoV it has become clear that bats are important reservoirs of coronaviruses (CoVs). Despite this, only 16% of all CoV sequences in Genbank come from bats. The remaining 84% largely consist of known pathogens of public health or agricultural significance, indicating that current research effort is heavily biased towards describing known diseases rather than the 'pre-emergent' CoV diversity circulating in bats. Our study addresses this critical gap, and focuses on the evolutionary and ecological drivers of CoV diversity in resource poor countries, where the risk of zoonotic emergence is believed to be highest. **Methods**: We surveyed the diversity of CoVs in multiple host taxa from 20 countries in Africa, Asia and Latin America to explore the factors driving viral diversity at a 'global' scale. Partial CoV sequences were identified using consensus PCR, which was chosen in part because it could be easily implemented in resource poor settings. Sequences were then parsed into phylogenetic clusters (operational taxonomic units) and analyzed using ecological and epidemiologic approaches. **Results**: In total we identified sequences representing 100 discrete clusters, 91 of which were found in bats, and showed that patterns of CoV diversity correlate with those of bat diversity. This cements bats as the major evolutionary reservoirs and ecological drivers of CoV diversity. Preliminary co-phylogenetic reconciliation analysis indicated that frequent host switching has contributed to CoV evolution, and that regional variation exists in the dynamics of this process. **Conclusions**: Overall our study represents a model for exploring global viral diversity and advances our fundamental understanding of CoV biodiversity and the potential risk factors associated with zoonotic emergence.

SARS coronavirus may have originated from frequent recombination events between SARS-like coronaviruses in a single horseshoe bat habitat

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Objectives: Horseshoe bats are recognized as the natural reservoirs of Severe Acute Respiratory Syndrome coronavirus (SARS-CoV), as an increasing number of SARS-like coronaviruses (SL-CoV) have been detected in this bat family since 2005. However, knowledge gaps remain between currently known bat SL-CoVs and the direct progenitor of SARS-CoV. Further information is needed to better understand where and how SARS-CoV originated from bat reservoirs. **Methods:** We have conducted a 5-year surveillance of SL-CoV in a cave inhabited by horseshoe bats in Yunnan, China. Full-length genome sequencing of 11 novel bat SL-CoVs discovered in this single location was performed and genomic characterization, phylogenetic analysis and recombination analysis were conducted. Efficiency of human ACE2 usage was also evaluated in HeLa cells for several newly identified strains. **Results:** Our findings revealed that genetically diverse bat SL-CoVs were circulating in this single location, including different strains with high sequence similarity to SARS-CoV in the highly variable N-terminal

domain (NTD) and receptor-binding domain (RBD) of S protein and the ORF8 region, respectively. Meanwhile, compared with other SL-CoVs, strains identified from this cave exhibited higher sequence similarity to SARS-CoV in the non-structural proteins. Evidence supported that frequent recombination events have occurred within the S gene and around ORF8 between bat SL-CoVs in this cave and may have promoted the generation of the pandemic SARS-CoV. Cell entry studies demonstrated that different newly identified SL-CoVs with variants of S protein are all able to use human ACE2 as the receptor, which represent a potential risk of emergence if given the opportunity to spillover. **Conclusions:** We have identified an epicenter of SL-CoVs where the director progenitor of SARS-CoV likely originated via sequential recombination events. These findings offered important new insight into understanding the geographical and evolution origin of SARS-CoV and highlights the need to pursue the surveillance of bat SL-CoVs to make better preparation for future emergence of SARS-like disease in humans.

A metagenomic approach identifying a MERS-related coronavirus in a bat from South Africa

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A Middle East Respiratory Syndrome (MERS) related coronavirus was previously detected in a Cape serotine bat (*Neoromicia capensis*) from the KwaZulu Natal Province in South Africa. Though the virus showed significant similarity to human MERS coronavirus (MERS-CoV), it was too divergent to be considered the direct progenitor of the virus causing human MERS-CoV outbreaks. **Objectives:** As part of a broader viral discovery surveillance program investigating excreted zoonotic viruses from bats, we implemented metagenomic techniques to collectively screen the virome of 60 *Neoromicia* bats constituting 6 species from 4 South African provinces sampled from 2007-2015. **Methods:** Using a viral particle enrichment methodology, total nucleic acids from faecal and rectal specimens were sequenced on Illumina's MiSeq and NextSeq500. Coding complete genome sequencing was performed with further amplicon sequencing on Illumina's MiSeq. Bayesian (BEAST) phylogenetic comparisons and pairwise estimations were performed with full genome representatives of all 4 betacoronavirus lineages. **Results:** We detected a MERS-related betacoronavirus from the same *Neoromicia* species. The virus shared a 97.2% overall nucleotide identity to another *Neoromicia* MERS-related virus identified in South Africa, and 85.5-85.6% nucleotide identity to human and camel (alternative hosts) strains of MERS-CoV. Significant discrepancies between bat-borne and human/camel MERS-CoV genomes were attributed to the low (63.7-64.3%) amino acid similarities of the spike genes, which is responsible for receptor attachment. Genome comparisons between betacoronavirus lineages of emerging viruses, namely MERS-CoV and the equivalent Severe Acute Respiratory Syndrome (SARS) coronaviruses, indicate that the relative phylogenetic distances between *Neoromicia* MERS-related strains and human/camel MERS-CoV are far greater than the distances between SARS-related bat viruses and human SARS viruses. **Conclusions:** Continued surveillance within the *Neoromicia* genus may yield additional MERS-related viruses sharing greater similarity to the human and camel MERS strains (as was shown with detected SARS-related bat viruses). Alternatively, if the progenitor of MERS-CoV originated from the *Neoromicia* genus, the currently identified diversity would suggest that significant receptor adaptation was required within dromedary camels (or unknown intermediate hosts) prior to being transmitted to humans. Continued viral surveillance in regions inhabited by both these hosts may aid in understanding the emergence of MERS.

New insights into the antiviral innate immune response of *Desmodus rotundus*

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The common vampire bat, *Desmodus rotundus*, is the main reservoir of rabies virus in South America. Mechanisms that allow persistence of viruses in bats are not well-defined. During the last decade, innate immunity has emerged as one of the implicated mechanisms. As a non-model organism, no tools were available regarding *D. rotundus*, there was therefore a crying need for characterizing their immune system. Given that the interferon (IFN) system provides the first line of defense upon viral recognition, we investigated the IFN-I response in an immortalized cell line, established from a *D. rotundus* embryonic lung, stimulated with synthetic

dsRNA (poly I:C). We observed that stimulation induced high levels of expression of all PRRs involved in dsRNA recognition, as well as a rapid up-regulation of both IFN-α1 and β. Furthermore, in characterizing some of the ISGs such as OAS1, PKR and ADAR, we identified two OAS1 genes, tentatively named *OAS1a* and *OAS1b*. Upon stimulation, *OAS1b* appeared to be the most inducible ISG tested. These results not only provide evidence of the intact signaling pathway of the IFN-I in our cellular model, but also that *OAS1b* may be a major player in antiviral activity in *D. rotundus*. In the frame of the present work, we generated a sum of insightful tools specific of the common vampire bat useable to the study of a number of different viruses, the first of which is the rabies virus.

A comparative study of the autophagy pathway during virus infection of bat (natural) and human (accidental) host cells

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Objectives: In contrast to other terrestrial animals, infection of bats with ebolaviruses and henipaviruses does not cause symptomatic disease. Whether bats have antiviral mechanisms to control these infections or how these viruses persist at a cellular level is largely unknown. Autophagy is a cellular protein homeostatic process, which has been implicated as a cell-autonomous innate defense mechanism against a broad array of intracellular infections. Bats are longer lived compared to other similarly sized mammals and increased proteostatic processes have been observed in long-lived mammalian species. **Methods:** In this study, we performed an investigation of autophagy in cell lines from the black flying fox (*Pteropus alecto*), a natural host of Hendra virus and Australian bat lyssavirus (ABLV), and human cells. ABLV, a neurotropic virus, was used as a model bat-borne virus to examine the interactions between an intracellular virus infection and autophagy in host cells. **Results:** Autophagy activation was observed in *P. alecto* brain tissue-derived primary and secondary cells infected with replication competent ABLV 1 and 2 days post infection. Compared to a human neuroblastoma cell line, *P. alecto* kidney and brain cells exhibited a higher level of basal autophagy. Treatment of bat and human cell lines with pharmacological activators of autophagy reduced ABLV replication. Quantification of ABLV titers and protein levels after infection of bat and human cells lines demonstrated that bat cells were less permissive to ABLV infection. Lentiviral knockdown of autophagy-related gene-5 (ATG-5) in bat and human cell lines did not result in a significant silencing of the autophagy pathway, however, a trending increase of ABLV replication levels was observed in the ATG-5 knockdown cells. Pre- and post-infection treatment of human neuroblastoma cells with BEZ235, an mTOR- and PI3K-inhibitor, significantly decreased virus replication in a dose-dependent manner. **Conclusions:** To our knowledge this is the first study to explore whether the autophagy pathway has a role as an antiviral defense mechanism during virus infection in bats. Ongoing experiments aimed at the interplay between autophagy and apoptosis will be critical to supporting our hypothesis that autophagy is an antiviral defense mechanism in bats.

Development of a minimally invasive individual identification technique for continuous monitoring of African bat species

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Objectives; An ever increasing number of potentially zoonotic diseases are associated with bat populations throughout the world, and as such the continuous monitoring and surveillance of these populations has become essential, not only for disease epidemiology but also in order to address the lack of knowledge available for biology, ecology and life histories of the majority of bat species. This requires the development of an ethically acceptable, cost effective, durable and reliable marking system to facilitate monitoring of individual bats. In order to address annual population structure, potential movement patterns and individuals' infection or exposure status we tested the ability to uniquely mark 11 bat species from six families, ranging in mass from 4g to 120g, using wing tattoos. Specific serological monitoring of Lagos bat virus exposure in *Rousettus aegyptiacus,* focussing on the presence and duration of neutralising antibodies has been undertaken since 2012. **Methods;** Non-toxic black ink was applied into the interdermal layers of the propatagial membrane of the bat by means of a tattoo system with nine-pronged needles. The tattooing procedure was performed on individual bats from a captive colony of *R.*

aegyptiacus (n=287) and free-flying, wild populations of the aforementioned species (n=2559). The robustness and longevity of this system was assessed from recaptures of tattooed individuals representing four of the above species in the wild, and observations of the captive colony of *R. aegyptiacus*. **Results;** This technique provides a simple, durable and cost effective marking system for both immediate and medium term monitoring, with no observed detrimental effects to the individuals to date. The longest periods between application and observation of tattoos has been; 927 days for *R. aegyptiacus*, 292 days for *N. thebaica*, 126 days for *M. natalensis* and 89 days for *Rh. smithersii.* Over 100 *R. aegyptiacus* recapture events have demonstrated individuals' seroconversion, antibody maintenance and loss against LBV. **Conclusion;** This technique has shown potential to facilitate monitoring individual bats' infection or exposure status in both captive and wild settings, with individual seroconversion and titer loss against LBV being observed, as well as providing an effective mark-recapture identification for population and movement studies.

Characterization of a novel Rhabdovirus isolated from insectivorous bat (*Pipistrellus kuhlii*) in Italy
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Objectives: *Rhabdoviridae* is one of the most ecologically diverse families of RNA viruses with clinical importance. Herein we report the isolation and the genome characterization of a novel rhabdovirus detected from a bat collected within a survey implemented in Italy on emerging viruses of bats. **Methods:** A fresh carcass of an adult female of *Pipistrellus kuhlii* spontaneously dead in a wildlife rehabilitation center in Northern Italy was fully necropsied. Tissue samples from different organs (lung, hearth, intestine) were subjected to viral isolation on cell culture. Virus identification was performed using negative staining electron microscopy (nsEM) and NGS sequencing. Molecular and phylogenetic analyses were performed. **Results:** Anamnesis reported sensory depression, inappetence, normal body mass and injuries of patagium consistent with a cat bitten. The death occurred three days after the admission to the rehabilitation center and no pathological lesions indicative of infectious diseases were observed at necropsy. CPE was observed on VERO cells inoculated with a pool of organs and nsME performed on cells supernatants revealed characteristic bullet-shaped viral particles referable to rhabdovirus. Tests aimed to exclude rabies and related lyssaviruses resulted negative. The complete genome size was 11,780 nt comprised 5 genes encoding the canonical rhabdovirus structural proteins and an additional transcriptional unit (U1) encoding a small protein (157 aa) located between the G and L genes (3'-N-P-M-G-U1-L-5'). BLAST analysis showed the highest nucleotide identity (65%) to Le Dantec virus (LDV) (human, 1965 Senegal) the prototype strain of the putative genus Ledantevirus. The most highly conserved protein L shared 70% and 69% of aa identity with LDV and Keuraliba virus (KEUV) (gerbil, 1968 Senegal) respectively. Phylogenetic tree based on full-genome sequence confirm the belonging of the new isolate to the ledantevirus group. **Conclusions:** A novel rhabdovirus was identified from *Pipistrellus kuhlii*, the most common species in urban areas in Italy. This finding represents (beside lyssaviruses) the only bat-borne rhabdovirus isolated in Europe. Specific diagnostic tools for viral detection will be set up for epizootiological investigations aimed to define the viral ecology and diffusion in bats population in Italy, in order also to further characterize and clarify its zoonotic potential.

Age-specific dynamics of maternally- and infection- derived immunity within African bat populations
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Objectives: Predicting and managing spillover of emerging infectious diseases to domestic animals and humans depend on data on reservoir host distribution, ecology and immunology as well as the mechanisms governing pathogen transmission among its populations. However, such data are generally sparse. This is exemplified by old-world fruit bats, which have been linked to an increasing number of zoonotic viruses, but whose ecology is

challenging to study and immunology has only recently begun to be elucidated. Even where appropriate data are available, fission-fusion population structures make it challenging to separate out the dynamical effect of pathogen reintroduction into the study population through movement from the transmission dynamics expected within a closed population. Island populations provide ideal natural experiments and involve simplifications analogous to the assumptions often made in modelling studies (e.g. single, closed population of a single species), allowing exploration of underlying processes. Here, building on an extensive body of work on straw-coloured fruit bats (*Eidolon helvum*), we aim to further elucidate fundamental processes governing viral dynamics, including the role of maternally-derived antibodies (MatAb). **Methods:** We focus on two viruses for which *E. helvum* is a reservoir (Lagos bat virus (LBV) and African henipavirus) and look for evidence of the presence of MatAb in wild *E. helvum* from continental and island populations. We use rare age-specific data to model waning rates of maternally- and infection- derived antibodies. These results then informed the parameterisation of a stochastic seasonal birth model to explore population-level persistence in the presence of MatAb, in both naive and non-naive populations. **Results:** Statistical modelling supported age as the strongest determinant of seroprevalence for both henipavirus and LBV, in addition to highly significant correlations between mother-offspring pairs. Age-specific seroprevalences predicted rapid loss of maternal immunity and effectively lifelong infection-induced immunity (particularly for LBV). The inclusion of MatAb had considerable implications on viral persistence within populations in a dynamic birth pulse model. **Conclusions:** This study helps to better understand endemic viral dynamics in bat populations, and the implications of considering the presence of MatAb in broader wildlife disease systems.

Detection of rubula- and related viruses in an Egyptian fruit bat (*Rousettus aegyptiacus*) colony in South Africa

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Objectives: More than 22 viral families have been associated with bats globally, eight of which with the Egyptian fruit bat (*Rousettus aegyptiacus*) occurring across sub-Saharan Africa and parts of the Middle East. Among numerous other zoonotic viruses, this species has also been associated with zoonotic henipaviruses (family *Paramyxoviridae*). More recently, a newly described zoonotic rubulavirus, Sosuga virus, was detected in this species from Uganda. The occurrence and diversity of these viruses remain unknown in Southern Africa. **Methods:** A broadly reactive hemi-nested RT-PCR assay targeting the *Avula-Rubulavirus* genera within the *Paramyxoviridae* family was used for nucleic acid detection. Spleen and kidney samples from bats collected during 2012-2016 from a cave in the Limpopo Province of South Africa, were retrospectively screened for the presence of rubulavirus RNA. Virus isolation, next-generation Illumina sequencing and amplicon sequencing were used to obtain full gene or genome sequences for comparison. **Results:** A total number of 137 bats were screened of which 5.84% of spleen samples tested positive. We detected several rubulavirus-related viruses grouping in a sister clade to the *Rubulavirus* genus. This clade contains other bat-associated rubulaviruses including the zoonotic Sosuga virus. Additionally, a co-infection with a virus closely related to human mumps virus was detected in one of the bats sampled. Preliminary results also suggest seasonality of these viruses in the colony, as positive individuals were predominantly detected in winter months. This phenomenon coincides with the loss of maternal antibodies i.e. an influx of susceptible individuals into the colony. **Conclusion:** The first evidence of bat-associated rubulaviruses from *R. aegyptiacus* in South Africa, some of which are related to know human pathogens, are reported. Additionally, a considerable diversity was detected from a small sample size. Enhanced surveillance might shed light on the prevalence of these viruses within the targeted colony. Considering the potential excretion of these viruses during the winter months might be the next step in determining their transmission potential. This is of importance as the specific cave is situated within a rural settlement surrounded by free-roaming livestock and is frequented by humans for religious practices.

Influenza-like virus and paramyxovirus screening in Brazilian bats

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Objectives: Bats are recognized as natural reservoirs of emergent viruses related to severe human disease outbreaks including Rabies, Nipah, Hendra and SARS coronavirus. Since the discovery of Hendra and Nipah emergent paramyxovirus in late 1990s in flying foxes bats from Australia and Asia, others bat-borne paramyxovirus have been identified in bats across the globe including bats species from Australia, Asia, Africa and America. Recently, new members of the influenza A virus where detected in bats from Guatemala and Peru, amplifying the host variety of Influenza virus A group. Despite the recent detection of Influenza-A and Paramyxovirus in South American bats and the spill-over events of paramyxovirus from bats to humans only few studies had analyzed the occurrence of influenza-like virus and paramyxovirus in Brazilian's bats. These study aims to analyze the occurrence and diversity of influenza-like virus and paramyxovirus in Brazilian bats. **Methods:** A total of 1071 samples including distinct tissues (intestine, lung, kidney and spleen), rectal and oral swabs, and serum (821 individuals/47 species) from urban area and Atlantic Forest biome were analyzed. The Total Nucleic Acid was extracted and cDNA synthesis was performed. Samples were screened by Pan-Flu PCR assay targeting the Influenza PB1 gene and by a Semi-Nested Pan-paramyxovirinae PCR assay targeting the L gene. **Results:** PCR fragments for both assays were observed in electrophoresis analysis. The amplicons were purified and sequenced by Sanger method. Sequencing confirmed the presence of 3 distinct Paramyxovirus lineages in eight bats. Morbillivirus-like was detected in insectivorous bat's *Molossus rufus* (intestine) and *Myotis nigricans* (lung)*;* Unclassified Paramyxovirus and one possible Henipa-like virus was found in hematophagous bats *Desmodus rotundus* in kidney samples*.* **Conclusions:** This study report the lack of detection of influenza-like in a high number of bat samples and may indicate the absence or the lower prevalence of these virus group in bats from Brazil. Our results also suggest the presence of paramyxovirus genotypes in bats commonly found in rural and urban area, including a probably Henipa-like virus in hematophagous bats, species that already had been described as vectors of rabies and others paramyxovirus with unknown zoonotic potential.

Hendra virus dynamics and spillover

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Hendra virus provides a model system for understanding the dynamics of emerging bat viruses and spillover. One factor constraining our ability to study Hendra virus spillover is the limited knowledge of the biology of the virus within its reservoir hosts. We present three different hypotheses for how within-host pathogen dynamics in bats may interact with among host factors to drive dynamics of emerging bat virus spillover. These hypotheses include: pulsed viral excretion due to seasonal epidemics, local persistence due to waning immunity within bats, or episodic shedding from persistently infected bats. We discuss the evidence for each hypothesis and show that differentiation among these scenarios is essential for predicting and managing spillover.

Using serology to understand the dynamics of concurrent viral infections in pteropid bats

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Objectives: Fruit bats of the genus *Pteropus* are reservoirs for henipaviruses throughout their range. *Pteropus medius* is the natural reservoir for Nipah virus in India and Bangladesh, and mechanisms of spillover to humans primarily involves contamination of date palm sap with excreta. Serological dynamics have provided insight into patterns of Nipah virus infection in this host, but other viruses, including Nipah-like viruses have been identified through pathogen discovery techniques. Little is known about infection patterns of other viruses within this species, or their likelihood of infecting other animals or people. **Methods**: We screened sera from a single population of *P. medius* in Bangladesh collected quarterly over six years for IgG antibodies against henipaviruses (NiV, HeV, CEDV), filoviruses (EBOV, MARV), and Menangle virus, using assays containing virus-specific solubilized glycoproteins or F proteins in a Luminex platform. **Results and Conclusions:** Here we present preliminary observations of comparative temporal patterns for multiple viral agents that suggest co-circulation in this population. We also discuss challenges in interpretation of serology

when studying viral infections in wildlife, particularly when multiple antigenically related viruses may be present.

Estimating viral richness and viral sharing in bats: integrating previously-published and newly-acquired field data

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Objectives: A handful of studies published over the last 8 years have sought to identify the host, ecological, and evolutionary factors that best explain species-level differences in viral richness in bats. Similarly, a few studies have also aimed to answer the golden question: Do bats carry a significantly larger number of total viruses, or a larger number or proportion of zoonotic viruses than other mammals? Our objective is to address these critical questions using statistical models and large datasets collated from the literature and acquired from the field. **Methods:** We collated data from the past 75 years of published for over 2800 mammal-virus associations, representing 754 mammal species and 586 ICTV-named viral species. We fit a series of generalized additive models to these data to identify and examine the functional form of significant predictor variables for total and zoonotic viral richness. Using our best-fit models we also estimate expected viral richness for each host species under a scenario of 'maximum' research effort. We map these viruses in geographic space. We also use species accumulation curves to estimate viral richness from standardized, field-acquired data from the USAID PREDICT project (http://www.healthmap.org/predict/). Network models and statistics were used to compare patterns of viral sharing among bats between the literature and field-acquired datasets. **Results:** For the all mammal analyses: The best-fit model for total viral richness per wild mammal species explained 49.2% of the total deviance, and included a per-species measure of disease-related research effort, phylogenetically corrected body mass, geographic range, mammal sympatry, and taxonomy (order) After controlling for research effort, the proportion of zoonotic viruses per species is predicted by phylogenetic relatedness to humans, host taxonomy and human population within a species range—which may reflect human–wildlife contact. We demonstrate that bats harbor a significantly higher proportion of zoonotic viruses than all other mammalian orders. For the bat field-acquired data we show significant differences in viral richness estimates across bat genera and viral family, as well as differences in the rates of saturation. Clustering in bat host-virus networks follow some predictable patterns and identify additional bat species to target for viruses of interest. **Conclusions:** These host-specific analyses and estimates of viral richness, including the unobserved or 'missing' viruses, allow us to better identify and target which species and regions should be preferentially targeted to characterize the global bat virome.

Optimised sampling efforts and screening assays identify several MERS-related coronaviruses in South African bats

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Objectives: Bats are considered reservoir hosts for all mammalian alpha- and beta-coronaviruses (α-, β-CoV). Following the emergence of SARS in 2002/03 and the subsequent identification of *Rhinolophus sinicus* as the likely ancestral SARS-CoV source, a wide diversity of bat CoV has been described worldwide. We work in transdisciplinary collaborations with ecologists and zoologists to define CoV diversity and ecology in South African bats. In addition to general "opportunistic" surveillance, species-specific studies of *Neoromicia capensis* and *Rhinolophus spp* are conducted, including longitudinal studies of bat colonies to determine shedding patterns and diversity of viruses present. **Methods:** Since 2011, 24 different bat species have been sampled along rainfall and altitudinal gradients across different biomes; namely Fynbos, Forest, Nama Karoo, Grassland, and Savanna. Sample types include faecal pellets, saliva and urine swabs, and when voucher specimens are sacrificed for museum collections, also blood and organs. Sequences of the 816bp RGU fragment (Drexler et al., 2010) for species classification were used to construct ML trees in MEGA v7. **Results:** An improved screening method greatly increased the CoV detection rate. Of 686 samples tested, 92 from 9 bat species were screening-positive: 66 for α-CoV, 19 for β-CoV, and 7 for both. The majority of sequences identified are α-CoVs, with ~20% prevalence for *N. capensis*. Preliminary analyses of partial RdRp, nucleocapsid and spike gene fragments of novel β-CoV identified in Neoromicia and Pipistrellus bats are closely related to BtCoV PML-PHE1/RSA/2011 (NeoCoV), previously found by us in a *N. capensis* and belonging to the same viral species as the recently emerged MERS-CoV, responsible for the ongoing

outbreak in the Arabian Peninsula. **Conclusions:** Extensive, dedicated sampling efforts allowed detection of α- and β-CoV from a wide range of bat species across large parts and different biomes of South Africa. An improved screening PCR approach yielded significantly more positive samples. There is substantial CoV diversity in southern African bats, including, most importantly, additional MERS-CoV-related CoV, which will hopefully help to address the unresolved question of the origin of this zoonotic pathogen.

Coronavirus diversity in bats from urban, rural and forest areas of Atlantic and Amazon Forest biomes, Brazil.

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Objectives: Epidemiological and phylogenetic studies indicate that four out of six coronavirus capable of infecting humans are the result of spill over events of virus from bats to humans. Despite the great diversity of coronaviruses in bats, the large number of bat species in Brazil (15% of the world's bat diversity) and the presence regions classified as hotspot for zoonotic pathogen emergence only few studies have analyzed the circulation of coronaviruses in Brazilian's bats. This study aims to evaluate the diversity of CoV circulating in bats in Brazil, covering different species, habitats, and life history of the hosts. **Methods:** We analyzed 840 bats from 53 species and five bat families with a pancoronavirus detection assay. Intestine, lungs, serum and rectal/oral swabs were obtained from bats from forest, urban, and rural areas located in the Atlantic and Amazon Forest biomes. **Results:** Distinct coronavirus lineages were detected in in bats from all sites screened. The coronavirus RNA was detected in 27 individuals from eleven bat species including *Artibeus lituratus(4), Carollia perspicillata (5), Eumops glaucinus(1), Glossophaga soricina (3), Mimon crenulatum(1), Molossus rufus(2), Molossus molossus (1), Myotis nigricans(1), Myotis riparus (1), Phyllostomus discolor(1)* and *Sturnira lilium (7)*. The analysis of coronavirus phylogenetic relation from nucleotide sequences obtained showed the circulation of the 25 Alphacoronavirus genotypes (α-CoV) and two Betacoronavírus (β-CoV), distributed in thirteen lineages (eleven α-CoV and two β-CoV). Results indicate the presence of a great coronavirus diversity in bats from Brazil including potential new and already described lineages. We describe the detection of a bat coronavirus genetically related with Alphacoronavirus-1 species, which are a group of closely related viruses with an evolutionary history of recombination and cross-species transmission between domestic and livestock animals. We also report the circulation of Betacoronavirus lineage "C", related to emergent highly pathogenic coronavirus CoV-MERS, in South American bats commonly found in urban areas, representing the first detection of coronavirus Clade C in this subcontinent. **Conclusions:** Our report points to the great diversity of CoV genotypes in New World bats, more specifically in the Atlantic Forest Biome, providing a better understanding of CoV diversity, host range and biogeographic distribution.

Preliminary Evidence of a Novel Alphacoronavirus and Secondary Acquisition of Tymoviridae and Partitiviridae in Little Brown Bats (*Myotis lucifugus*) in Southcentral Alaska.

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Objective: We sought to analyze the virome of the most common bat species in Alaska, *Myotis lucifugus*, the little brown bat. Swabs, tissue, and fecal samples were collected from habitats in close proximity to barns, farm buildings, and human habitations in southcentral Alaska. **Methods**: Total RNA extracts were screened by RT-PCR and CoV ORF1a, and primary RNA samples were used in library preparation for short-read, paired-end next generation sequencing on an Illumina HiSeq platform. **Results**: Sanger sequencing of amplicons confirmed the presence of an alpha-coronavirus phylogenetically related to

persistent alphacoronaviruses detected in bats in Colorado and the Rocky Mountains. Aligning to a reference *M. lucifigus* virus from Colorado, bat alphacoronavirus CDPHE15/USA/2006, we assembled a full-length genome (28,515nt) identifying the novel alphacoronavirus/bat/Alaska/s7/2014. A high degree of thermodynamically stable stem-loop RNA structures are predicted by Mfold within 700nt of 5' and 3' termini of genome**.** While nucleotide conservation to the Colorado virus was 96%, notable amino acid differences were identified in coronavirus proteins. In two distinct bat samples, preliminary results indicate the likely presence of tymovirus (eg. Dulcama mottle virus) probably acquired through ingestion of insects feeding on infected plants. In addition, initial results indicate presence of alpha-partitivirus closely aligned to *Rosellina*-type associated with spruce/alder and other partitivirus-like sequences. Secondary acquisition of virus obtained by feeding or incidental infection by fungi (eg. gamma-partitivirus associated with *P. destructans*) has been previously described for bats collected from similar ecological settings (eg. Thapa et al. 2016). **Conclusions**: We continue to further refine these initial for better resolution of the virome of Alaska bats.

Are big brown bat cells different than human cells in their innate immune response to coronavirus and viral ligands?

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Objectives: Bats are hosts for viruses such as those that closely resemble coronaviruses (CoV) that cause severe acute respiratory syndrome (SARS), Middle East respiratory syndrome (MERS) and porcine epidemic diarrhoea (PED). Despite the serious nature of these diseases in other mammalian hosts, bats naturally infected with CoV or experimentally infected with MERS-CoV do not demonstrate clinical signs of disease. We challenged big brown bat (*Eptesicus fuscus*) cells and human cells with MERS-CoV or viral ligands to study the differences in their interferon and inflammatory responses. **Methods:** *E. fuscus* kidney cell line and bone marrow derived cells, human fibroblast and epithelial cells were challenged with either MERS-CoV or poly(I:C), a double stranded RNA surrogate. Transcripts for several innate immune response genes were quantified using qRT-PCR. Interaction between the bat TNF promoter and a potential repressor of the promoter, c-Rel, was detected by chromatin co-immunoprecipitation and bat c-Rel, TLR3, RIGI and MDA5 transcripts were knocked-down using specific siRNA. **Results:** Both human and bat cells, when stimulated with poly(I:C), contained higher levels of transcripts for interferon beta than unstimulated cells. In contrast, only human cells expressed robust amount of RNA for TNFα, a cell signaling protein involved in systemic inflammation. We further observed that poly(I:C) signaled primarily through TLR3 in big brown bat cells. We examined the bat TNFα promoter and found a potential repressor (c-Rel) binding motif. We demonstrated that c-Rel binds to the putative c-Rel motif in the promoter and knocking down c-Rel transcripts significantly increased basal levels of TNFα transcripts. Both human and bat cells support replication of MERS-CoV to comparable levels. **Conclusions:** We have identified a novel transcription repressor, c-Rel, that inhibits an increase in TNFα transcripts in bat cells after poly(I:C) stimulation. We have also showed for the first time that poly(I:C) signals through TLR3 in bat cells. We are currently studying the modulation of the innate immune response in bat cells by MERS-CoV and individual MERS-CoV and bat coronavirus proteins. Identifying adaptations in the bat innate immune response might allow us to extrapolate the knowledge in identifying potential drug targets in spill-over species, such as humans.

Reverse genetic analysis of bat influenza viruses: A journey full of surprises.

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Our understanding of conventional influenza A viruses was recently challenged by the identification of two novel genome sequences of influenza A-like viruses from bat specimens by next-generation sequencing. Serological surveys indicate that these viruses circulate in various bat species in Central and South America. However, no viable viruses could be isolated from bats, impeding further characterization of these viruses. Interestingly, analysis of the viral surface proteins revealed that the entry machinery of these viruses differ significantly from all known conventional influenza A viruses and may only support entry into bat cells. This talk will summarize recent progress obtained by reverse genetic analysis of bat influenza A-like viruses, including the observation that the host tropisms of these viruses might be larger than anticipated.

Towards understanding bat influenza A-like viruses

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Objectives: Bats harbor many viruses, which are periodically transmitted to humans resulting in outbreaks of disease (e.g., Ebola, SARS-CoV). Recently, bat influenza A-like virus HL17NL10 and HL18NL11 sequences were identified; however, no viruses were isolated from bats. This discovery aroused great interest in understanding the evolutionary history and pandemic potential of bat-influenza virus. **Methods**: Using synthetic genomics, we rescued a modified bat-influenza virus that had the HA and NA coding regions replaced with those of A/PR/8/1934 (H1N1). **Results**: This modified bat-influenza virus replicated efficiently in vitro and in mice, resulting in severe disease. The results indicate that internal genes of bat influenza A-like viruses are functional to support virial genome transcription and virus replication. Mini-genome replication studies and virus reassortment experiments demonstrated that bat influenza A-like virus has very limited genetic and protein compatibility with Type A or Type B influenza viruses, yet it readily reassorts with another divergent bat influenza A-like virus. **Conclusions**: In conclusion, our data indicate that the bat influenza A-like viruses recently identified are authentic viruses that pose little, if any, pandemic threat to humans; however, they provide new insights into the evolution and basic biology of influenza viruses.

Experimental Infection of Jamaican Fruit Bats (*Artibeus jamaicensis*) with a Rescued Bat HL18NL11 Influenza A-like Virus

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Objectives: Nucleotide sequences of two novel influenza A-like viruses, HL17NL10 and HL18NL11, were recently discovered in New World little yellow shouldered fruit bats (*Sturnira lilium*) and flat-faced fruit bats (*Artibeus planirostris*), respectively. Serological studies indicated high prevalence to these viruses among many species of Phyllostomidae leaf-nosed fruit bats of Central and South America, including Jamaican fruit bats (*Artibeus jamaicensis*). **Methods**: Infectious viruses have not been isolated from bats, therefore an infectious clone of HL18NL11 was generated by reverse genetics technologies that produced particles resembling influenza viruses from transfected cells by electron microscopy. Susceptibility of Jamaican fruit bats to rescued HL18NL11 bat influenza A-like virus was determined during a 28-day challenge experiment via intranasal inoculation. **Results**: The bats exhibited no overt clinical signs of disease nor fever. However, rectal swabs had up to 10^4 $TCID_{50}$ equivalents of HL18NL11 vRNA by real-time PCR in each bat on days 2, 4 and 7 post inoculation, but not day 15 or 28, and in the lungs of one of the bats on day 28 when they were euthanized. Serology showed moderate antibody titers to nucleoprotein by ELISA. Histopathology revealed mild pathology, particularly in the one bat with detectable vRNA in its lung. This bat's lungs showed multifocal mild-to-moderate histiocytic and lymphoplamacytic interstitial pneumonia. Pleocellular infiltrates were especially prominent around adventitia of pulmonary arterioles. Immunohistochemistry with mouse antibody to recombinant H18N11 nucleoprotein revealed virus antigen in the lungs of this bat. **Conclusions**: This is the first study to demonstrate susceptibility to bat influenza viruses and suggests that viral persistence up to 28 days may occur in some bats, supporting the hypothesis that Jamaican fruit bats may be a natural reservoir host of the HL18NL11 virus.

Seroprevalence of alphaviruses, flaviviruses and Rift Valley fever virus in Ugandan bats

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Objectives: Arboviruses including Rift Valley fever virus (RVFV), chikungunya virus (CHIKV) and Sindbis viruses have previously been isolated from naturally-infected East African bats, however the role of bats in arbovirus transmission cycles is poorly understood. The aim of this study was to investigate the exposure history of Ugandan bats to a panel of arboviruses. **Methods**: Insectivorous and fruit bats were captured from multiple locations throughout Uganda between 2009 – 2013. All bat captures were conducted under the approval of IACUC protocols 1731AMMULX (Maramagambo samples) and 010-015 (all other samples). Bats were captured using harp traps or mist nets, taking appropriate biosafety precautions. All serum samples were frozen at -80°C until they were tested for neutralizing antibodies against West Nile virus (WNV), yellow fever virus (YFV), Dengue 2 virus (DENV-2), Zika virus (ZIKAV), CHIKV, o'nyong-nyong virus (ONNV), Babanki virus (BABV), and RVFV by plaque reduction neutralization test (PRNT). **Results**: Sera from up to 626 bats were screened for neutralizing antibodies against each virus. Key findings include the presence of antibodies against ONNV in approximately 15% (44/303) of Egyptian rousette bats (*Rousettus aegyptiacus*) from Maramagambo forest in western Uganda, and antibodies against RVFV in Ethiopian epauletted fruit bats (*Epomophorus labiatus*) captured from Kawuku (5/52) and Egyptian rousette bats from Kasokero cave (3/54). **Conclusions**: Antibodies reactive to flaviviruses were widespread across bat taxa and sampling locations.The data presented demonstrate the widespread exposure of bats in Uganda to arboviruses, and highlight particular virus-bat associations that warrant further investigation.

Presence of zoonotic bat pathogens correlate with reproductive seasons in South African bat populations
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In 2003 we initiated passive surveillance on bats in South Africa with the initial objective to identify rabies–related lyssaviruses, but this has since expanded to include several other possible zoonotic viral and bacterial pathogens. The project has identified viruses in the following families; *Rhabdo, Paramyxo, Bunya, Filo*, *Adeno-, Herpes-, Picorna, Orthomyxo, Circo, Parvo, Papilloma* and *Coronaviridae* as well as the following bacterial pathogens; *Leptospira*, *Rickettsia and Bartonella.* **Objectives:** To determine longitudinal circulation of pathogens we initiated seasonal sampling from 2012 in two cave systems in South Africa. This sampling specifically focused on the reproductive seasons of *Rousettus aegyptiacus* and *Miniopterus natalensis*. **Methods:** Serum was analysed for rabies related lyssavirus, Lagos bat virus, antibodies using a virus neutralization assays. Tissue, urine saliva and fecal samples were tested for the presence of viral nucleic acids using RT-PCR/PCR specific for several viral families. Illumina MiSeq 16S rRNA gene sequencing on low-biomass individual bat samples was used to identify bacterial pathogens. **Results:** Longitudinal studies, specifically focused on measuring the presence of LBV antibodies in *Rousettus aegyptiacus*, indicated cyclic fluctuation of antibodies with a marked increase shortly after the parturition period, which identified this as a high risk period for spill-over. We showed that seasonal bat reproduction is a major driver shaping temporal variations in microbial community structure. A strong temporal shift in oral, fecal and urinary microbiota was also associated with bat reproduction, with significant associations between the microbiota and the sex, or reproductive status. **Conclusion**: This cumulative evidence can be used to indicate periods of increased viral and bacterial circulation, which can be used to make public and veterinary health decisions on spill-over risks.

Body mass index of the Egyptian fruit bat, *Rousettus aegyptiacus*: An indicator of infection status
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Body mass in conjunction with forearm length has long been used to determine body mass indices for bats. These indices have been further linked to diseases detected in bats, with a low body mass index being a potential indicator of infected bats. **Objectives**: We correlated body measurements to body mass, enabling us to determine

the best measurement that could be used to build body mass indices which can be correlated to disease status of *Rousettus aegyptiacus.* **Methods**: This study focuses on the Egyptian fruit bat (*Rousettus aegyptiacus*) in the Limpopo Province of South Africa. Data was gathered over a two year period, 2015 and 2016, and consisted of measurements of various body parts. **Results**: Wilcoxon Matched pair tests indicated a significant difference in body weight between the two sampling years (V = 34476, p = 0.002466). A strong correlation was found between body mass and forearm length when both years are considered (S = 17252000, p-value < 2.2e-16), as well as for the first (S = 3487900, p-value < 2.2e-16) and second year (S = 1250500, p-value < 2.2e-16) of the study with a strong correlation value; R > 0.78 in all cases. The correlation between mass and forearm length was significant for both males and females during both years (p-value < 2.2e-16), but the correlation value was always lower for females. Other body measurements correlated significantly with body mass, but only forearm length showed a strong correlation. **Discussion**: Forearm length is thus an indicator of body mass in Egyptian fruit bats, as has been found for insectivorous bats. As such, body mass in conjunction with forearm length could be used to build body mass indices, which could be used as a preliminary indicator of disease status for *Rousettus aegyptiacus.*

Environmental constraints drive the viral diversity of two sympatric Amazonian bat species
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Amazonia is a major biodiversity hotspot which encompasses a great diversity of bat species, as well as a wide variety of climates and vegetation formations. Landscape characteristics (*e.g*. climate, vegetation structure, anthropogenic disturbances) are relevant predictors of species richness and influence the host-pathogens relationships. However, the effects of contrasting environmental conditions on the viral diversity harbored by Amazonian bats have yet to be investigated. Through a metagenomic approach we characterized the viral diversity of two sympatric Amazonian bat species: the common vampire bat, *Desmodus rotundus* (*Phyllostomidae*) and the insectivorous bat, *Molossus molossus* (*Molossidae*). Then, through a statistical approach, we assessed the impact of the landscape characteristics by comparing the viral richness harbored by different populations of vampires and insectivorous bats inhabiting different environments (*e.g.*, forests, edge habitats, anthropized and urban areas). We identified 10,983 viral sequences related to 48 viral families known to infect a wide range of hosts (*i.e.*, bacteria, plants, insects and vertebrates). Most viruses detected reflect the dietary habits, especially within the insectivorous bat species which presented the highest diversity of plant and insect-related viral families. Diversity tests and phylogenetic relationships reconstructed for several mammal-related viral families (*e.g.*, *Bunyaviridae*, *Circoviridae*, *Foamyviridae*, *Herpesviridae*, *Papillomaviridae*) revealed a preferential transmission route within phyla of bats, as well as a potential association of viral diversity with the host's gut microbiota. Three structuring poles related to species traits and environments were identified, explaining the distribution of viral diversity and showed a strong correlation between the type of environment, host phylogeny, diet and viral diversity. The substantial viral richness detected in forest environments is likely due to a wider diversity of prey and favored by more frequent contacts between hosts and overlapping habitats. These findings provide significant insight into viral bat diversity in Amazonia and emphasize that environmental constraints and host features are the main drivers of viral diversity in bat species.

Seasonal and individual predictors of grey-headed flying fox (*Pteropus poliocephalus*) foraging movements in Adelaide, South Australia
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Objectives: The distribution of flying foxes in Australia is influenced by the unpredictable availability of their preferred diet, especially eucalypt blossoms. Recently, human activities, including destruction of native habitat and planting of non-native vegetation that provides predictable foraging, have altered the distribution and movements of flying foxes. The consequences of this change are important for both bat and human health, given that bats are reservoirs of Australian bat lyssavirus and Hendra virus, both of which cause fatal disease in humans. In 2010, grey-headed flying foxes (*Pteropus poliocephalus)* established a permanent roost in Adelaide, South Australia, several hundred kilometers outside their previous range. Despite incurring juvenile mortality due to extreme heat events, the population now numbers approximately 7000 and is expected to continue growing. **Methods:** As part of a larger study to characterize the health and behavior of the Adelaide flying fox population, we deployed lightweight GPS loggers on bats to track their foraging movements. Loggers recorded a bat's position every 30 seconds when flying and every 45 minutes when stationary, and also recorded acceleration,

speed, and altitude data. Forty foraging sites were ground-truthed to identify feeding resources. **Results:** Five flying foxes were tracked in winter 2016 and 9 in summer 2017, resulting in 112 nights of movement data. Bats exhibited individual variation in movement patterns, with some foraging repetitively, and others ranging more widely over the landscape. The nightly distance traveled depended on the interaction between sex and the ratio of weight to forearm length, but not on season. In the summer, bats foraged predominantly on urban resources, with figs and eucalypts being especially popular. **Conclusions:** This work provides insight into a recently-established, understudied bat population and is useful both to local Adelaide stakeholders as well as other urban citizens seeking to manage the bats that share their space. Foraging on urban resources, especially in residential yards, could increase the chances for disease transmission from flying foxes to humans and pets. Individual predictors of movement should be considered when building models of bat movement and disease risk.

Uganda Bat calls library-developing a tool to survey arthropod-borne viruses associated with Chiroptera
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Objectives: We continue to conduct studies of bats in different parts and habitats of Uganda with a number of particular goals: -

i. To continue to understand the occurrence and ecology of bats that may be reservoirs and/or vectors of viruses in Uganda (BM presentation),
ii. To develop a micro-chiroptera calls Library for the country
iii. Continue the development a fast approach that can be used to quickly survey and identify the bat fauna of different parts of Uganda.
iv. To investigate the roles of different species of bats in the ecology of viruses (RK presentation),

Methods: Through a DTRA supported project we particularly targeted to understand bat ecology and their potential roles in virus ecology. This was done through graduate training and research, training in field techniques of capture and processing of bats for detection of and characterization of viruses a pillar institutional players and a compilation of reference calls of micro-chiropteran bats for Uganda. Field biosurveillance training was held with participants from NADDEC, UVRI and Makerere University at Zika forest. A graduate student now preparing his dissertation, was recruited and completed an ecological study on bats in the Kaptum cave. Insect bats are captured using Mist nets, Herp traps and Hand net capture at roost sites. Bats are either free flown, ziplined or light tagged and hand released from which voucher calls are collected. Collected calls are processed using Kaleidoscope Pro version 31.7 for large files that need to be split for examination and processing in Sonobat4.0.6p. **Results**: Cumulatively, voucher calls for 50 species of micro chiropteran bats (over 50% of the Ugandan species) have been collected. Several of these are represented by multiple bats that way taking care of potential intra specific variations, potential ecological variations each of which could affect the call produced by the species. This presentation specifically shares our findings on call characteristics for a sample of the species and highlights the great overlap in signatures for species of Molosid bats, species of the Genus *Scotophilus*, while showing very nicely segregated call signals for Hipposiderid, Rhinolophid and a good number of verspertilionid bats. **Conclusions**: Our next steps are to attempt to collect voucher calls from species we haven't, collect additional calls from species already recorded but from few individuals, and to work with partners to develop a tool that could be used to rapidly identify calls collected from bat detection surveys from different parts of the country.

Dampening of STING-dependent IFN production: an implication of virus tolerance in bats?
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Objectives: Bats are known to harbour a number of zoonotic viruses, many of which are highly pathogenic in human but result in no clinical symptoms in bats. The mechanism of how bats coexist with viruses is still largely unknown. We previously reported the contraction of type I IFN locus and unusual constitutively expression of IFNA in bats. We hypothesis this may help bat to inhibit virus replication. However, as immune response can also do harm to the host, then how bats tolerate viruses and viral induced immune responses become a question. **Methods:** To address this question, we scanned a list of DNA and RNA sensors in bats. We then focus on STING, which played a key role in multiple DNA sensing pathways, for understanding how bats tolerate DNA viruses. We also tested the functionality of bat STING in a list bat immune or non-immune cells. **Results and Conclusions:** We found some of the viral DNA sensors are under faster evolution, implying a change of function. Further experimental data also confirmed the dampening of viral DNA sensing, more specifically STING- dependent IFN production pathway. We then identified a ubiquitous key point mutation in all bat species tested, which hugely

decreased the cGAS-STING sensing ability (80%) by gain-of-function studies. Lastly, we restored the functionality of STING and STING-dependent viral DNA sensing pathway by changing this site to human. We conclude that bat naturally own a dampened STING-dependent IFN production, probably to avoid over responses to virus. This observation provides a model of how bats tolerance thus long-term hosting these viruses.

Regulation of immune activation and dampened inflammation in Pteropid bats
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Objective: Natural reservoir hosts can maintain low-level infection of pathogens without succumbing to severe disease. Several bat species host viruses such as Ebola, SARS, Nipah, Hendra, and other pathogenic viruses and while these same infections cause mass-inflammation in humans and other animals they are mostly asymptomatic in the bat. As such, bats are a unique model for studying the host control of systemic inflammation. **Methods:** We utilised bat cell lines, primary cells and tissue with qPCR, Western Blot, FACS analysis, NGS transcriptomics and cellular proteomics to profile pathways and characterise signalling mechanisms. **Results:** Through studying immune activation to flaviviruses, influenza and reovirus, along with natural stimulants of innate immunity such as TLR and RLR ligands we are beginning to characterize key differences to their human counterparts for PRRs.. There appears to be differences also in the kinetics and activation signals required for Interferon activation also. In addition, our data, from investigation of primary bat immune cells and studying bat homologs, suggests that inflammasome activation pathways may be altered with dampened activation of downstream inflammation. **Conclusion:** Along with fundamental differences to cell biology, this may indicate an evolutionary adaptation that while supporting flight, may cause susceptibility to infection yet maintain a symbiotic state with several pathogens. Initial observations show several key mutations, altered kinetics and a decrease in sensitivity to induce signaling all appear to be involved. From this we can gain understanding into a mechanism for controlling excess inflammation in humans.

Delineating the phenotype and function of the B cell population in the fruit-eating bat, Pteropus Alecto.
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Objective: The unique ability of bats to act as reservoir for viruses that are highly pathogenic to humans suggests unique properties and functional characteristics of their immune system. However, the lack of bat specific reagents, in particular antibodies, has limited our knowledge of bat's immunity.
Methods: Here, using cross-reactive antibodies, we report the phenotypic and functional characterization of B cells based on anti-mouse I-Ab (MHC-II) and anti-bat IgG. **Results**: Using flow cytometry, we show their distribution amongst the major lymphoid organs and scanned electron micrographs of these sorted population reveal that they are morphologically similar to human and murine B cells. In addition, a large population of these cells test positive for CD19 mRNA, tested using SmartFlare RNA probes, and anti-human CD19 antibody. Uniquely, these cells are able to show an increase in calcium uptake upon cross-linking of their B cell receptor with the addition of secondary donkey anti-goat antibody, which is specific for the goat anti-bat IgG. We also demonstrate T cells and myeloid cells do not release calcium in the presence of IgG and secondary antibody. Furthermore, we also demonstrate that injecting LPS for 5 hrs show an increase in MHC-II$^+$IgG$^+$ B cell population in the spleen and blood. This demonstrates a T-independent B cell activation amongst the B cell population. In addition, this population of cells do not respond to Poly (I:C) stimulation. We also performed single cell RNA sequencing on sorted MHC-II$^+$IgG$^+$CD19$^+$ positive cells to identify various B cell subsets based on their gene signature. Initial analysis reveal that these cells show increased expression of CD19 and do not express CD3, CD8 and CD11b. **Conclusions**: Here, we demonstrate for the first time the phenotype and function of B cells in *Pteropus Alecto.* This provides us with a platform to isolate and further elucidate the role of these cells in infectious models.

Integrative measures for assessing "health" in free-ranging bats – zoonotic and conservation implications from a One Health perspective

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Objectives: Risks of zoonotic spillover are likely related to the overall health of the animal host. For bat hosts of viral zoonotic diseases, the relationship between health and spillover risk is complex, with poor health possibly favoring transmission by increasing viral load and shedding but also decreasing animal mobility and human-host contact. Unfortunately, determining the health status of free-ranging bats is fraught with difficulty. Challenges exist not only in deciding which diagnostic measures to use, but also in interpreting the results of these measures. Furthermore, without the ability to measure fitness in these long-lived mammals, our understanding of the consequences of "good" or "bad" health for a free-ranging bat is poor. Our objective is to provide a framework for defining bat health that will facilitate bat studies and will enhance our understanding of spillover risk, ecosystem health, and human health. **Methods:** We combined an extensive literature review of health metrics in free-range wildlife, including bats, with our own long-term field studies and experiences studying bat physiology and disease. **Results:** Literature review and our past work point to several findings: (1) a number of measures commonly used in other vertebrate taxa and in other mammals have not been fully deployed for bats – sometimes owing to methodological hurdles; (2) due to a lack of tools, and often small sample volumes, most bat studies have relied on too-few measures, such as BMI (which suffers from allometric problems and is often surprisingly uninformative), the ubiquitous neutrophil-to-lymphocyte (N/L) ratio, ectoparasite load, and highly variable immune metrics such as hemmaglutination assays; (3) newer molecular methods, such as transcriptomic approaches hold promise for improving our understanding of bat health, especially when integrated with other measures such as infection status. We will present preliminary data from our recent field studies of African fruit bats in which we have deployed 20+ field diagnostic measures in combination with infection status and a transcriptomic approach. **Conclusions:** We recommend the development of integrative health metric(s), which will allow for the determination of the most informative measures for future studies. We also implore researchers to document normative physiological measures for more species of bats, analyzed with regards to life history, ecology, and phylogeny.

Host-pathogen interactions during white-nose syndrome

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Objectives: We have employed a dual RNA-Seq approach to study gene expression of both host and pathogen during the fungal infection that causes white-nose syndrome (WNS) in bats. **Results**: We have found that when *Pseudogymnoascus destructans* is causing WNS, the most significant differentially expressed genes in the pathogen were involved in heat shock responses, cell wall remodeling, and micronutrient acquisition. These results demonstrate that this fungal pathogen responds to host-pathogen interactions by regulating gene expression in ways that may contribute to evasion of host responses. We have also found that host responses vary between susceptible and resistant species of bats in ways that may indicate that host responses contribute more to pathogenesis than to protection. This may be because, during hibernation, host immune responses are too costly and lead to premature depletion of energy reserves. We have also determined which host transcriptomic responses to fungal infection can occur during torpor and which require arousal to euthermy. We found relatively few host transcripts that showed significant changes in expression levels due to fungal infection in torpid bats compared to euthermic bats. **Conclusions**: These results support the view that torpor is a period of relative dormancy and suggest that periodic euthermic arousals exist to provide an opportunity for host responses to pathogens.

Resistance or Tolerance – How do European bats cope with *Pseudogymnoascus destructans*?
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Objectives: *Pseudogymnoascus destructans* (*Pd*), the causing agent of the White-nose disease, colonizes bats during hibernation. The cold-loving fungus affects the snout and all the hairless skin membranes of torpid bats where it causes lesions. The spreading epidemic in North America (so called White-nose syndrome) is characterized by mass mortalities and regional extinctions of certain bat populations. In Europe, *Pd* has been recorded since several decades as a widespread pathogen, yet it does not cause mass mortalities. Several studies confirm that *Pd* is native to Europe and appeared as a new pathogen in North America in 2006. If and how European bats adapted to the disease and why North American bats cannot cope with the fungus remains unclear. **Methods**: We analysed data from over 300 hibernacula across Europe to test for factors influencing mortality, including *Pd* infections on bats. **Results**: Our results show an overall low mortality rate of bats in Europe with no evidence of *Pd*-associated mortalities. Physiological data and blood samples from infected and non-infected European bats were analysed to investigate, if bats suffer from White-nose disease and how the immune systems reacts to fungal infections during hibernation. **Conclusions**: Our ecological, physiological and immunological results suggest resistance and tolerance of European bats towards *Pd*.

Modeling the impact of White-nose syndrome on two western bat species
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Objectives: The rapid westward spread of white nose-syndrome (WNS) through North America has become a critical conservation issue for endemic hibernating bat species with many Eastern populations experiencing steep declines over the last ~10 years. The continued spread of the psychrophilic fungus *Pseudogymnoascus destructans* into Western states over the last two years has the potential to impact many hibernating species. Disease outcome varies widely between species, with infection of some species (namely European and Asian species) being largely benign. The identification of species that may be threatened is paramount to development of effective conservation strategies. **Methods:** Using field obtained morphometric data in conjunction with experimentally obtained estimations of key metabolic parameters we applied a modified hibernation model that includes fungal growth dynamics for two currently unaffected North American bat species: *Myotis californicus* and *Myotis yumanensis*. **Results:** Infection of *P. destructans* would likely reduce the maximal time spent in hibernation for both Western *Myotis* species. Reductions of maximal time spent in torpor were predicted to be the most drastic in microclimates with relative humidity approaching saturation and temperatures between ~5 °C and 10 °C. Despite the increased rate of overwinter energy consumption, fat reserves were still predicted to be sufficient to overwinter throughout the majority of their distribution. **Conclusions:** *M. californicus* and *M. yumanensis* are predicted not to experience distribution wide population declines like those witnessed for *M. lucifugus* and *M. septentrionalis* in eastern North America. Continuing field studies will provide data on important model parameter estimations, more species, realized hibernacula microclimate selection, and providing data to empirically validate model predictions.

Variable behaviors influence species susceptibility to disease – surviving white-nose syndrome.
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White-nose syndrome (WNS) continues to spread through populations of hibernating bats in North America, causing unprecedented mortality in several species occurring in eastern parts of the continent. Despite this devastation, other bat species that come into contact with the causative fungus, *Pseudogymnoascus destructans*, somehow survive. We still do not understand factors influencing species and continental differences in bat

susceptibility to WNS, but variability of innate behaviors among taxa and regions may help explain disease survival. This talk focuses on evidence suggesting infected bats can exploit 'survival habitats' (e.g., hibernacula with palliative microclimates) and 'survival behaviors' (e.g., palliative ways of regulating body temperature during winter). Our search for survival habitats and behaviors in WNS bats illustrates the challenges of understanding how microorganisms influence their cryptic hosts, how unknown host behaviors can obscure understanding of disease, and how new bat research methods may help overcome some of these challenges.

Emerging Insights into the Geographic Distribution, Genetic Diversity and Evolutionary Origin of Bat-borne Hantaviruses

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Objective: The recent discovery of genetically distinct hantaviruses in multiple species of shrews and moles (order Eulipotyphla) prompted a further exploration of their geographic distribution, genetic diversity and evolutionary relationships by analyzing tissues and feces from bats (order Chiroptera). **Methods:** Total RNA, extracted from frozen, ethanol-fixed or RNAlater®-preserved archival tissues (lung, liver, kidney, intestine, intercostal muscle) and rectal swab/feces of 1,890 bats, representing 10 families (Emballonuridae, Molossidae, Mormoopidae, Nycteridae, Phyllostomidae, Vespertilionidae in the Yangochiroptera suborder, and Pteropodidae, Hipposideridae, Megadermatidae, Rhinopholidae in the Yinpterochiroptera suborder), collected in Asia (China, Korea, Malaysia, Mongolia, Myanmar, Philippines, Republic of Georgia, Vietnam), Africa (Côte d'Ivoire, Guinea, Liberia) and the Americas (Bolivia, Brazil, Guyana, USA) during 1981–2015, were analyzed for hantavirus RNA by nested RT-PCR. Phylogenetic analysis was performed using maximum likelihood and Bayesian methods. **Results**: Hantavirus RNAs were detected in 2 of 12 *Neoromicia nanus* from Côte d'Ivoire (Mouyassué virus, MOYV), 6 of 49 *Hipposideros pomona* and 1 of 5 *Hipposideros cineraceus* from Vietnam (Xuan Son virus, XSV), 1 of 12 *Aselliscus stoliczkanus* from Vietnam (Dakrong virus, DKGV), 2 of 13 *Taphozous melanopogon* from Myanmar (Laibin virus, LBV), and 1 of 15 *Rousettus amplexicaudatus* from the Philippines (Quezon virus, QZN). Multiple attempts to acquire whole genomes of the newfound hantaviruses were unsuccessful, except for DKGV and QZNV. Phylogenetic analyses indicated incongruent topologies for each genomic segment, presumably because of the limited sequences available for most of the hantaviruses harbored by bats, shrews and moles. However, in both the S- and L-segment trees, QZNV appeared to share a common ancestry with XSV and LBV. Based on the host cytochrome *b* sequences, the phylogenetic positions of bats in the Yinpterochiroptera and Yangochiroptera suborders were consistent with the phylogenetic relationships among the bat-borne hantaviruses. **Conclusions:** Other research teams have reported Magboi virus in *Nycteris hispida* from Sierra Leone, Makokou virus in *Hipposideros ruber* from Gabon, Huangpi virus in *Pipistrellus abramus* from China, Longquan virus in *Rhinolophus affinis, Rhinolophus monoceros* and *Rhinolophus sinica* from China, Laibin virus in *Taphozous melanopogon* from China, and Brno virus in *Nyctalus noctula* from the Czech Republic, bringing to 11 the number of bat-borne hantaviruses to date. As in shrews, moles and rodents, the same hantavirus species was occasionally found in more than one bat species, and the same bat host species occasionally harbored more than one hantavirus species, suggesting that the formerly held conventional view of one hantavirus species and one host species is no longer tenable. Moreover, the basal position of the chiropteran-borne hantaviruses in phylogenetic trees and the demonstration that bat species in both suborders harbor hantaviruses suggest that primordial hantaviruses may have emerged in an early common ancestor of bats or other members of the Laurasiatheria superorder, that includes shrews and moles.

Neotropical Bats that Co-habit with Humans Function as Dead-End Hosts for Dengue Virus

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Objective: Several studies have shown Dengue Virus (DENV) nucleic acids and/or antibodies present in Neotropical wildlife including bats, suggesting that some bat species may be susceptible to DENV infection. Here we aim to elucidate the role of house-roosting bats in the DENV transmission cycle. **Methods**: Bats were sampled in households located in high and low dengue incidence regions during rainy and dry seasons in Costa Rica. We captured 318 bats from 12 different species in 29 households. Necropsies were performed in 205 bats to analyze virus presence in heart, lung, spleen, liver, intestine, kidney, and brain tissue. **Results**: Histopathology studies from all organs showed no significant findings of disease or infection. Sera were analyzed by $PRNT_{90}$ for a seroprevalence of 21.2% (51/241), and by PCR for 8.8% (28/318) positive bats for DENV RNA. From these 28 bats, 11 intestine samples were analyzed by RT-PCR. Two intestines were DENV RNA positive for the same dengue serotype detected in blood. Viral isolation from all positive organs or blood was unsuccessful. Additionally, viral load analyses in positive blood samples by qRT-PCR showed virus concentrations under the minimal dose required for mosquito infection. Simultaneously, 651 mosquitoes were collected using EVS-CO_2 traps and analyzed for DENV and feeding preferences (bat cytochrome b). Only three mosquitoes were found DENV positive and none was positive for bat cytochrome b. Our results suggest an accidental presence of DENV in bats probably caused from oral ingestion of infected mosquitoes. Phylogenetic analyses suggest also a spillover event from humans to bats. **Conclusion**: Therefore, we conclude that bats in these urban environments do not sustain DENV amplification, they do not have a role as reservoirs, but function as epidemiological dead end hosts for this virus.

Novel Gammaherpesvirus in Bats: discerning the secrets of these oncogenic viruses

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Objectives: *Gammaherpesvirinae* is a subfamily of herpesviruses which often cause lymphoproliferative diseases and have been linked to two human lymphoid cancers – Burkitt's lymphoma and Kaposi's sarcoma. Anecdotal evidence suggests that bats have lower rates of cancer than other mammalian species. This phenomenon may be because bats have evolved efficient mechanisms for detecting and repairing damaged DNA as a by-product of flight. How such a mechanism affects the interaction of Gammaherpesviruses (which cause cancer) with their bat, hosts is largely unknown. **Methods and Results:** We have isolated a novel Gammaherpesvirus (*Eptesicus fuscus* herpesvirus – EfHV) from a North-American Big Brown bat (*Eptesicus fuscus*). We have used a big brown bat cell line to study the growth kinetics of the virus. We have also performed electron microscopy and PCR to confirm that the virus belongs to the herpesvirus family. To determine the sequence of the herpesvirus, we have performed next generation sequencing (NGS) using Illumina mi-seq. Using the sequence obtained, we have performed phylogenetic analysis from which we found that although the EfHV belongs to the sub-family of Gammaherpesvirus, it forms a distinct branch within the sub-family. In addition to that we have identified the different proteins present in the virion by performing mass spectroscopy and have found that the virion components are similar to other herpesviruses. We have also infected cells of different species with the EfHV to understand the spectrum of different species that this virus is capable of infecting and we have found that it is able to infect human, monkey, porcine and feline cell lines apart from the bat cell line. **Conclusions:** The phylogenetic analysis shows that EfHV is a distant relative of all other gammaherpesviruses known so far. It might have evolved together with the big brown bat. Further studies looking at the interaction of EfHV and big brown bat might help us understand more about the persistent infection in bats and their unique was of resisting cancer.
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Experimental Infection of Jamaican Fruit Bats (*Artibeus jamaicensis)* with Zika Virus

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Objectives: Zika virus (ZIKV) emerged in the New World with the 2014 outbreak in Brazil. It has spread to much of South America, Central America, Mexico and the Caribbean, with hundreds of thousands of cases. While disease presentation may be subclinical to mild and include symptoms of maculopapular rash, conjunctivitis, and arthralgia, infection of pregnant women can lead to fetal microcephaly. Additionally ZIKV infection can induce Guillain-Barre syndrome. In the 1950s and 1960s bat species were investigated as possible reservoirs for ZIKV. In total, five different species of bats were found to be susceptible to the virus. Bats seroconverted, had viremia,

and, in one experimental infection study bats developed fatal neurological disease. This warranted further investigation of ZIKV in bats to determine their use as an animal-model, and to better understand the potential role of bats in viral ecology. **Methods:** Nine Jamaican fruit bats (*Artibeus jamaicensis*) were subcutaneously inoculated with $7.5x10^5$ pfu of ZIKV strain PRVABC59 and monitored over the course of 28 days, during which there were no conspicuous signs of disease. Bats were euthanized at 2, 5, 10 and 28 days post-inoculation to assess the course of infection and antibody responses. **Results:** Bats seroconverted by day 28 by ELISA with ZIKV-infected, fixed Vero E6 cells. Low levels of viral RNA were detected in one brain and one urine sample. IHC detected ZIKV antigen in lung and testes of one bat, and brains and salivary gland of two others. Pathology was consistently observed in the lungs, heart, testes and brain. Pneumonia was observed in four bats, cardiomyocyte necrosis in three bats, degeneration and lymphocyte infiltration in the testes of two bats, and neuronal degeneration in the hypothalamus and cerebellum in three bats. **Conclusions:** These results provide evidence that Jamaican fruit bats are susceptible to ZIKV and may serve as an animal model to study neurological components and sexual transmission of the virus. Low viral load in urine and tissues suggests the role of bats in viral ecology may be minimal.

Long-term monitoring of *Bartonella* bacteria in a captive colony of fruit bats and experimental evidence of bat flies as vectors of bartonella

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Objectives: Few experimental studies have monitored long-term infection dynamics in bat populations. This is especially true for vector-borne bacteria, where there can be significant challenges in maintaining both host and vector populations in controlled settings. In order to understand the importance of vector populations in the long-term maintenance of infection prevalence and bacterial diversity, we advocate for the use of semi-natural, long-term experiments capable of detecting changes in infection dynamics linked to the force of infection by vectors. **Methods:** Using blood samples taken from a captive colony of ~100 fruit bats (*Eidolon helvum*) in Accra, Ghana from July 2009 - March 2012, we monitored the dynamics of *Bartonella* spp. infection in the bat population using molecular techniques. Over this period, the bat fly population (*Cyclopodia greefi*) infesting the captive bats declined, but was then supplemented with additional flies from wild *E. helvum* in January 2012. We hypothesized that prevalence and species diversity of *Bartonella* infections in the colony will vary with changes in the bat fly population. **Results:** *Bartonella* prevalence and diversity peaked in March 2010 with 77% of bats infected and 8 *Bartonella* spp. present, then began to decline until July 2011 with only 15% of bats infected and 4 *Bartonella* spp. present. After the reintroduction of flies in January 2012, prevalence increased to 43% in March 2012 with 6 species present. Bats that received flies were equally likely to become positive after January 2012 as bats that did not receive flies, which may be attributable to dispersal of flies among bats after reintroduction. Additionally, changes in relative *Bartonella* spp. abundances showed that the species lost over time were uncommon in bats, but some of these uncommon species became more abundant after the reintroduction of flies. **Conclusions:** This experiment indicates that *C. greefi* bat flies are likely vectors of bartonella in *E. helvum* and play an important role in the maintenance of bacterial diversity in bats. Ongoing occupancy modeling work will explore the influence of within-host processes (including bacterial interactions and host resistance to infection) and alternative transmission routes on the long-term infection dynamics in individual bats.

Posters

1. Predicting the epizootiology of temperate bat disease: Is it all about the bats?James N. Aegerter[1], Ashley C. Banyard[2], Anthony R. Fooks[2], Graham C. Smith[1]

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Predicting the dynamics of disease in wild bats, their epizootiology, and the risks these pose to people, the economy or other biodiversity is complicated. Bats may be the evolved hosts for disease, effective maintenance hosts, or accidental spill-over hosts (we cannot always distinguish which), whilst their unique life-style permits the exceptional natural movement of disease, as well as an exceptional potential to vector disease into homes, farms or other sensitive sites. These diseases may pose social or economic concerns (i.e. to public or livestock health), or produce conservation concerns. Further, diseases may well also be endemic, exotic or newly emerging, and importantly their dynamics today occur in the contexts of rapid land-use change and climate change. With decision-makers relying on the quality of epizootiological predictions, and substantial uncertainty about the pathogen, its pathology in wild bats, a changing environment, and the abstraction of these into mathematical form, it is surprising that little effort has been made to construct and validate mechanistically realistic models of bat populations to act as the solid foundation for higher-level disease modelling. Here we aim to produce a generic tool to provide some evidence based predictions of bat disease epizootiology, founded on a coherent representation of bat ecology and behaviour deployed through an IBM (Individual Bat Model). Importantly, this is founded on an independently validated understanding of their ecology and population dynamics, both of which need to emerge as model behaviour before disease is added. We recognise at least two divergent life-history strategies and lifestyles; ‘slow’ bats, typified by cave hibernators, include a seasonal hierarchical spatial and population structure; ‘fast’ bats show larger but less structured communities. Both accommodate the emerging understanding of bats as social animals as well as assuming that spatial heterogeneity drives some form of meta-population process. Early work has illustrated the surprising variation/instability in demographic structure driven by environmental variation close to range edges (many British bats are at their cold edge in the UK), as well as highlighting basic gaps in knowledge which are pivotal in robust predictions of disease dynamics (males in summer – Where? When? And how much?).

2. **Comparative loss of function screens highlight common cellular pathways required by mumps virus for replication in bats and humans**
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Objectives: Bats have been implicated as an important source of new and emerging paramyxoviruses. The identification of bat-borne paramyxoviruses closely related to mammalian paramyxoviruses suggests a possible risk of zoonotic transmission of these paramyxoviruses. Mumps virus (MuV) a contagious virus of the genus *Rubulavirus*, was thought to be an exclusive human pathogen with no animal reservoir. Recently, the complete genomic sequence of a mumps-like rubulavirus was obtained from an African bat. In order to ascertain if bat and human cells are capable of supporting the replication of MuV, and to identify cellular proteins involved in the viral life cycle, we performed comparative genome scale siRNA screens using a human and novel bat siRNA library. **Methods**: Comparative genome scale siRNA screens with MuV were performed. The human MuV siRNA screen (Qiagen) was previously performed in our lab using A549 cells, a human lung adenocarcinoma cell line. A custom bat siRNA library was designed to target 18,328 genes of the *Pteropus alecto* genome. The bat siRNA screen was performed in PaKi cells, a *Pteropus alecto* kidney cell line. **Results**: The coatomer complex I, a known dependency factor was identified as required for MuV replication in both human and bat cells. Eukaryotic initiation factor 3 (eIF3) is a multiprotein complex that functions during the initiation phase of eukaryotic translation was also identified as a host factor. Interestingly, ABCE1, identified as a pan-paramyxovirus host factor, was not required for MuV replication in bat cells. **Conclusions**: This study is the first to utilize a bat genome scale siRNA screen and provides a novel overview of cellular proteins and pathways that impact this important pathogen.

3. **Implementation of a RT-PCR Assay to Detect Henipaviruses in Trinidad Bats**
Victoria Avanzato[1], Neeltje van Doremalen[1], Christine Carrington[2], Janine Seetahal[2], Tony Schountz[3], Vincent Munster[1]

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Objectives: Since the emergence of Hendra in Australia, and Nipah in Malaysia and Bangladesh, evidence of henipaviruses in bats has been reported in Thailand, Cambodia, India, Papau New Guinea, China, and Madagascar. Cedar virus, a novel henipavirus, has been isolated from bats in Australia. There has been evidence of seropositivity among humans and *Eidolon helvum* (Straw-coloured fruit bat) bats in Cameroon, as well the publishing of the genome sequence of a henipa-like virus from a bat sample in Ghana. More recently, sequences related to henipaviruses were identified in New World bats, and Brazilian bats were found to have antibodies against henipa-like viruses, though no viral isolate has yet been obtained. This suggests that henipaviruses are likely to exist in other regions, including the Western hemisphere, presenting a need to investigate host populations. The goal of this study is to design a PCR assay to screen bat samples from Trinidad to detect novel henipa or henipa-like viruses.
Methods: Using published primer sets from Tong, et al, and van Boheemen, et al, PCR assays were developed to screen various tissue samples collected from bats in Trinidad. Both primer sets will be evaluated for their ability to detect henipaviruses using viral RNA standards for Hendra, Nipah Bangladesh, and Nipah Malaysia. The 132 samples are from 30 bats, including the species *Saccopteryx bilineata* (greater sac-winged bat), *Carollia perspicillata* (Seba's short-tailed bat), and *Artibeus planirostris* (Flat-faced fruit-eating bat) (sensu Larsen, 2007). Tissues harvested include brain, kidney, liver, spleen, lung, and fetal tissue.
Results: The PCR assay is able to detect viral RNA standards of Hendra, Nipah Bangladesh, and Nipah Malaysia. The assay will be further optimized to screen tissue samples. Samples that screen positive by this assay will be sequencinged.
Conclusions: To our knowledge, no henipaviruses have yet been detected or isolated from New world bats, though studies suggest their presence. Thus, screening for novel henipaviruses in Trinidad bats will help elucidate the full geographic range of these viruses, allowing a better understanding of risks of emergence and outbreaks in humans.

4. **Genomic characterization and pathogenic potential of a novel evolutionarily-divergent alphacoronavirus isolated from *M. lucifigus* bats in Alaska.**
Jonathan C. Rupp[1], Maegan Lange[1], Megan Howard[2], Anitha Sundarajan[3], Jonny Sena[3], Faye D. Schilkey[3], Molly Murphy[4], Douglas Causey[1], Eric Bortz[1].

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3- National Center for Genome Resources, Santa Fe NM
4- Dept. of Veterinary Medicine, University of Alaska Fairbanks

Objectives: Coronaviruses (CoV) are zoonotic pathogens with the potential to cross species barriers from bats into other mammals, including marine mammals, swine and humans. Novel bat-origin coronaviruses have been responsible respiratory disease in humans, notably betacoronaviruses (OC43, HKU-1, SARS and MERS) and alphacoronaviruses (229E and NL63). Thus, it is important to identify the reservoirs of CoV in bats and their potential for transmission, and pathogenicity, in other mammalian species. We sought to analyze the virome of the most common bat species in Alaska, *Myotis lucifugus,* the little brown bat.

Methods: Swabs, tissue, and fecal samples were collected from habitats in close proximity to barns, farm buildings, and human habitations in southcentral Alaska. Total RNA extracts were screened by RT-PCR with coronavirus primers matching CoV ORF1a, and amplicon sequencing. Complete genomes of novel viruses were sequenced by next-generation sequencing (NGS) RNA-seq.

Results: Sanger sequencing of amplicons confirmed the presence of an alphacoronavirus phylogentically related to persistent alphacoronaviruses detected in bats in Colorado and the Rocky Mountains. Primary RNA samples were used in library preparation for short-read, paired-end next generation sequencing on an Illumina HiSeq platform. Aligning to a reference *M. lucifigus* virus from Colorado, bat alphacoronavirus CDPHE15/USA/2006, we assembled a full-length genome (28,515nt) identifying the novel alphacoronavirus/bat/Alaska/s7/2014. A high

degree of thermodynamically stable stem-loop RNA structures are predicted by Mfold within 700nt of 5' and 3' termini of genome**.** While nucleotide conservation to the Colorado virus was 96%, notable amino acid differences were identified in coronavirus proteins. The major CoV surface spike (S) protein exhibited 26 amino acid changes, including 14 in the globular head containing the putative receptor-binding domain, suggesting divergence based on immune evasion or receptor-specificity. Another 6 amino acids were altered in the fusion hinge. Protease cleavage sites were not conserved. Nucleoprotein (N) and ORF3 also exhibited amino acid differences.

Conclusions: Understanding the evolution and pathogenicity of this novel evolutionarily-divergent alphacoronavirus provides insight into the role of bats in virus transmission, and ecological assessment of bat-borne virus reservoirs in North American ecosystems.

5. Preliminary Evidence of Secondary Acquisition of Tymoviridae and Partitiviridae in Little Brown Bats (*Myotis lucifugus*) in Southcentral Alaska.

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We sought to analyze the virome of the most common bat species in Alaska, *Myotis lucifugus,* the little brown bat. Swabs, tissue, and fecal samples were collected from habitats in close proximity to barns, farm buildings, and human habitations in southcentral Alaska. Total RNA extracts were screened by RT-PCR and CoV ORF1a, and primary RNA samples were used in library preparation for short-read, paired-end next generation sequencing on an Illumina HiSeq platform. Sanger sequencing of amplicons confirmed the presence of an alphacoronavirus phylogenetically related to persistent alphacoronaviruses detected in bats in Colorado and the Rocky Mountains. In two distinct bat samples, preliminary results indicate the likely presence of tymovirus (eg. Dulcama mottle virus) probably acquired through ingestion of insects feeding on infected plants. In addition, initial results indicate presence of β-partitivirus closely aligned to *Rosellina*-type associated with spruce/alder and other partitivirus-like sequences. Secondary acquisition of virus obtained by feeding or incidental infection by fungi (eg. γ-partitivirus associated with *P. destructans*) has been previously described for bats collected from similar ecological settings (eg. Thapa *et al.* 2016). We continue to further refine these initial for better resolution of the virome of Alaska bats.

6. Molecular Screening of Zika and Dengue Viruses in Bats (*Artibeus jamaicensis, Glossophaga longirostris* and *Molossus molossus*) from Grenada, West Indies.

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Background: In recent years Zika virus (ZikV) has changed from an uncommon and poorly documented infection to a global public health concern. Dengue virus (DenV) has long-standing human health concerns worldwide, including Grenada, and has been detected in bats from other tropical countries. **Objective**: To determine if Grenada bats are infected with ZikV and DenV and thus possible reservoir hosts for these viruses. **Methods**: Forty-nine bats from 3 different genera and feeding behaviours (frugivorous, nectivorous and insectivorous) were trapped and humanly euthanized. ZikV RT-PCR was performed on serum, testes, spleen and brain samples, and a DenV RT-PCR multiplex was performed on serum. Amplicons of the expected sizes were sequenced for confirmation. **Results**: Physical exams prior to euthanasia and sample collection indicated all bats were clinically healthy. All 3 bat species collected tested positive for both viruses. Sera from 27 bats out of 41 tested were positive for ZikV (65.9%) and sera from 12 bats out of 19 tested were positive for DenV (63.2%). All DenV positive bats were infected with serotype 2, with one of these bats testing positive for both DenV serotype 2 and 4. Brains from 22 bats out of 48 tested were positive for ZikV (45.9%). Testes from 2 bats out of 12 tested were ZikV positive (16.7%) and a spleen from one bat out of 22 tested was ZikV positive (4.5%). **Conclusions**: The results demonstrate that frugivorous, nectivorous and insectivorous bats in Grenada are infected with both ZikV and DenV. Of interest is that despite many bats testing positive for ZikV in the brain, all bats appeared clinically healthy with no signs of neurologic dysfunction. Histopathology and immunohistochemistry are pending to

determine if infection is associated with lesions. Virus quantification is currently underway to determine if the level of viremia for either ZikV or DenV is high enough to consider the different bat species as potential reservoir hosts.

7. Serologic evaluation of Alphavirus and Flavivirus exposure in bats in Grenada

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Objective: Determine exposure to Alphaviruses and Flaviviruses in bats in Grenada. **Methods:** Fifty bats were trapped in August, 2015 in Grenada. Sera from all bats were tested for antibodies to flaviviruses: West Nile virus, Japanese Encephalitis virus, St. Louis Encephalitis virus, Bussuquara virus and dengue virus serotypes 1-4 (DENV-1,2,3,4) using the plaque reduction neutralization test (PRNT). Forty three of the 50 samples were tested for antibody to alphaviruses: Western Equine Encephalitis virus, Venezuelan Equine Encephalitis virus and Eastern Equine Encephalitis virus using epitope-blocking ELISA and 42 samples were tested for antibody to the alphavirus Chikungunya (CHIKV) using PRNT. **Results and Conclusions:** Two species of fruit bats were sampled, *Artibeus jamaicensis*, (48), and *A. lituratus*, (2). Fifteen of the 42 tested positive for neutralizing antibodies to CHIKV at $PRNT_{50}$ with titers 1:10 to 1:640. All 43 bats tested negative for epitope blocking antibody to the other alphaviruses except one positive for Venezuelan Equine Encephalitis virus. All 50 bats tested negative for neutralizing antibody to flaviviruses except one which had a Bussuquara virus $PRNT_{80}$ titer of 20. **Discussion:** Historically, DENV has been endemic in Grenada. CHIKV was introduced to the island in 2014. Bats for this study were trapped a year after the peak human CHIKV epidemic. Of interest is that in a separate study molecular detection confirmed the presence of both DENV and CHIKV RNA in bats serologically tested in this study. Of the 15 CHIKV seropositive bats, one was positive for CHIKV RNA. Of the 50 DENV seronegative bats, 6 showed detection of flavivirus RNA with a band compatible with DEN3. Thus, the negative DENV serology is unanticipated, but may reflect lack of neutralizing antibody responses developed for DENV. Future studies will characterize the humoral immune response to DENV in naturally exposed Grenada bats and determine whether non-neutralizing antibody responses are present. The type of immune response to DENV in bats may promote persistent infection and high-titer viremia and thus contribute to viral maintenance. Our results and those of the molecular study confirm that Grenada fruit bats are exposed to CHIKV and DENV, but their role in the epidemiology of these viruses is currently unknown.

8. **Isolation and molecular characterization of Bukakata orbivirus, a novel virus from a Ugandan bat, and associated pathology in experimentally infected Jamaican fruit bats (*Artibeus jamaicensis*)**

Fagre AC, Kityo R, Lee J, Mossel E, Crabtree, M, Nalikka B, Nakayiki T, Kerbis J, Gilbert, A, Bergren, N, Nyakarahuka L, Lutwama J, Stenglein M, Byas A, Malmlov A, Bergren N, Rice L, Miller B, Schountz T & Kading, RC.

Objectives: In 2013, a novel orbivirus (*Reoviridae: Orbivirus*) was isolated from an Egyptian fruit bat (*Rousettus aegyptiacus*) in Uganda. Preliminarily named "Bukatata orbivirus" after the region where the infected bat was captured, this virus is the fourth identified orbivirus of bats. The genomes of all four bat orbiviruses (Bukakata, Ife, Fomede, and Japanaut viruses) were sequenced to assess their phylogenetic placement within the genus *Orbivirus*, and develop hypotheses regarding virus-vector associations. **Methods:** Whole genomes of all four viruses were sequenced using an Illumina platform and assembled *de novo*. To begin studying the effect of infection with Bukakata orbivirus on a bat host, three male Jamaican fruit bats (*Artibeus jamaicensis*) were inoculated intraperitoneally with 5.3 $\log_{10}$ pfu Bukakata orbivirus and monitored daily for signs of clinical disease. **Results:** Phylogenetic analysis placed Fomede and Bukakata orbiviruses in the tick-borne clade, and Japanaut and Ife in the mosquito/*Culicoides* clade. On day 12, all three bats were diffusely hyperemic and tachypneic and, thus, were humanely euthanized. Histopathologic lesions of perivascular inflammation, hemorrhage and edema were present in varying degree of severity in the liver, lung and kidney of all three bats. Additional lesions included meningeal hemorrhage in two of the bats and evidence suggestive of early hepatic vasculitis in the other. Eosinophilic and suppurative gastroenteritis affected all bats with one containing intraluminal bacilli, suggesting secondary bacterial infection. **Conclusions:** Immunohistochemistry and qPCR will be performed to assess

relative abundance of virus in various organ systems to optimize future analyses. Future experimental infections will be performed to monitor temperature, physiological and immune parameters, virus shedding and viremia throughout the course of infection. These preliminary data are critical in the assessment of the potential role of bats as reservoirs for arboviruses.

9. **Using GIS to Guide Ebola Virus Disease Ecology Field Investigations**

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Objectives: In the health field GIS is being used to track epidemics in real time and to create predictive models of outbreak potential. We have investigated the feasibility of using a maximum entropy model (Maxent) to assist in determining the target species and optimum locations and times to direct field sampling efforts. **Methods:** We developed an ecological niche model of Ebola virus (EBOV) using the location of Ebola virus disease (EVD) outbreak index cases as presence points we developed an ecological niche model to predict geographic locations that had environmental conditions similar to those of known outbreaks. To determine which environmental parameters were important in constructing the model, a correlation matrix was constructed using ArcGIS and highly correlative parameters were eliminated and the model reconstructed. Additionally, home ranges of African mammals were overlaid on a map and compared to the model to determine which species inhabit the geographical regions predicted to be suitable for a spillover event. **Results:** The model was used to highlight environmental factors common to the location of the EVD index cases from 19 environmental parameters and altitude that were used to construct the model. A list of 66 mammals including 26 bat species with home ranges that overlap the modeled range of EBOV was produced. **Conclusions:** While there is no conclusive evidence that bats serve as the reservoir for Ebola virus (EBOV) i.e. there is no wild EBOV bat isolate, there is evidence that they may play a role in maintaining the virus in nature. Combining what is known about the natural histories of bat species and animal species known to be susceptible to EVD such as great apes, duikers and forest hogs coupled with environmental factors predicted to be important, we can further prediction when and where spillover events may occur and tailor our sampling efforts to target these conditions. Additionally, as there is a dearth of knowledge on the natural history of deep forest fruit bats we are planning to monitor the short term daily movements of *Hypsignathus monstrosus* with the aim of being able to predict where the movements of the bats and susceptible species may commonly intersect.

10. **Bat - infection interactions: Signals of evolution, ecology, immunity and deforestation**

Hannah Frank[1], David Enard[1], Chase Mendenhall[1,2,3], Ji-Yeun Lee[4], Ellie Armstrong[1], Stefan Prost[1], Seth Judson[5], Jamieson O'Marr[1], Gretchen Daily[1,3,6], Dmitri Petrov[1], Scott Boyd[4] and Elizabeth Hadly[1,6,7]

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Objectives: Bats are ecologically diverse and these ecological differences may lead to differences in infection prevalence and identity. We sought to discover the evolutionary and ecological signatures of differences in bat behavior and environment on bat-infection patterns, as well as to understand how these patterns are impacted by human activity. Regions where a high diversity of hosts occur with prevalent deforestation, human habitation and livestock rearing are of great concern for potential spillover. Accordingly, we aimed to characterize infections of potential spillover importance in an altered landscape. **Methods**: Using a combination of genomics, targeted sequence capture and tests of positive selection, we screened 60 species of bats distributed globally for evidence of selection in response to viruses. Additionally, we screened the speciose and ecologically diverse bat fauna of an agricultural landscape in Costa Rica for eight viral groups (Herpesviridae, Astroviridae, Adenoviridae, Paramyxoviridae, Coronaviridae, *Lyssavirus*, Filoviridae, Influenza A), *Bartonella* bacteria and ectoparasites to detect pathogen sharing, immunological and behavioral patterns of infection and the impact of humans on these relationships. **Results**: Evolutionarily, viral sharing has been important for shaping bat immune evolution. However, ecologically most infections are host specific and regulated by host immunity with species that are more frequently exposed less likely to yield detectable pathogen nucleic acids. In deforested areas, these patterns shift in a sex-specific manner, disproportionately impacting females with potential for population stability. **Conclusions**: This study yields evolutionary insights into the unique relationship between bats and viruses, identifying the environmental factors that are driving adaptation. Additionally, it represents one of the broadest infection screening studies in the Neotropics, which has the highest density of bat diversity but is less frequently screened than the Old World. Our data suggest that there are few pathogens of spillover concern circulating in this landscape, but that humans may be having a detrimental impact on bat health.

Daytime behavior of *Pteropus vampyrus* and *Acerodon jubatus* in the natural habitats: a cue of viral transmission

11. Yupadee Hengjan[1], Didik Pramono[2], Hitoshi Takemae[1], Ryosuke Kobayashi[1], Karla Cristine Doysabas[1], Keisuke Iida[1], Takeshi Ando[5], Supratikno[2], Chaerul Basri[2], Yuli Sulistya Fitriana[4], Eko M.Z. Arifin[6], Yasushige Ohmori[1], Ken Maeda[3], Srihadi Agungpriyono[2] and Eiichi Hondo[1]

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Objectives: The large flying fox (*Pteropus vampyrus*) are well-recognized host of Nipah virus. Base on serologic studies, the golden-crowned flying fox (*Acerodon jubatus*) are infected with Ebola Reston virus. To estimate the risk of disease emergence, it is important to understand the behavior of flying foxes. This study aimed to clarify diurnal behavior of *P. vampyrus* in Leuweung Sancang conservation area, Indonesia (7º 43′ 45.12″ S, 107º 54′ 10.08″ E), and *A. jubatus* in the Subic Bay Freeport, the Philippines (14º 46′ 31.54″ N, 120º 19′ 14.90″ E). **Methods:** Quantitative behavioral data were collected using instantaneous scan sampling and all occurrence focal sampling methods. **Results:** Unexpectedly, many flying foxes were awake during daytime (*P. vampyrus*: 46.9 ± 10.6%, *A. jubatus*: 23.7 ± 3.1% of scanned bats), and showed various activities. The commonly observed behavior were wing flapping and self-grooming behaviors. Males engaged in sexual activity more than females (*P. vampyrus*: 6.5 ± 1.6 % in males and 0.2 ± 0.1 in females, *A. jubatus*: 1.6 ± 0.5 % in males, 0% in females), sometimes accompanying with aggression behaviors between males and females. There was no significant difference in negative social behaviors (fighting and wing spreading) between males and females of *P. vampyrus*, whereas, the difference was found in *A. jubatus* (2.6 ± 0.7 % in males, 0.1 ± 0.04 % in females). The positive social behaviors (maternal care, mutual grooming and playing) were rarely found in *P. vampyrus*, but never in *A. jubatus*. Physical communications, not only among flying foxes, but also direct and/or indirect contacts between *P. vampyrus* and non-human primate (*Trachypithecus auratus*) were observed (3.3 ± 0.5 times per day). Specifically, periodic disturbance by tourists and unidentified aerial predators like raptors was observed at the roosting site of *A. jubatus*. *A. jubatus* shared the same roosting site with *P. vampyrus*, this enables the contacts between the two species of flying foxes, an average 25.4 ± 6.3 times per day. **Conclusions:** These observations would provide a cue to know how viral transmissions among flying foxes, other wildlife and humans in South-East Asia.

12. The study of whole spike gene of bat coronavirus from Thailand using Next Generation Sequencing

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Objectives Bats have been recognized as the natural reservoirs of a vast variety of viruses, including as host to Coronaviruses – a viral family of public health importance. Bat coronaviruses have been intensively studied since the discovery of Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) and have expanded even more after the emergence of Middle East Respiratory Syndrome Coronavirus (MERS-CoV), both of which are purposed to have originated from bats. Since spike protein is correlated with host cell receptor binding and membrane fusion, a better understanding of sequence diversity for this gene will help determine the potential for host-switching and zoonotic potential of CoVs. The aim of our study was to characterize the spike gene of bat coronaviruses from Thailand. **Methods** we PCR amplify about 4 kb of whole spike gene from seven PCR positive coronavirus of *M. magneter* and *R. shameli* bats from northern part of Thailand and sequencing using Next Generation Sequencing (NGS). Phylogenetic tree of the full alignment of whole spike gene sequences was estimated by maximum likelihood method. **Results** The average of 1,306,845 sequences of spike gene per sample was obtained from NGS. Phylogenetic tree of all seven spike sequences are grouped into the same clade in the alpha Coronavirus (α CoV) and mostly related to the Bat Coronavirus-1A (BatCoV-1A). **Conclusions** Even though seven spike genes of coronaviruses in this study showed sequence different from emerging disease beta coronavirus group B and C (β CoV B and β CoV C); nevertheless, more positive bat coronaviruses should be investigated including whole genome sequencing of bat coronaviruses that may useful for more understanding host-viral evolution and potential for host switching or spillover.

13. **Assessment of the cross-species potential of two emerging coronaviruses, SARS-CoV and MERS-CoV, by Protein-Protein Molecular Docking analyses**
Jun Li & Vincent Munster

Laboratory of Virology, Division of Intramural Research, National Institute of Allergy and Infectious Diseases, National Institutes of Health

Objectives: Coronaviruses are a virus family with broad host range, and have spilled over from their natural reservoirs into various mammalian species, including humans. For humans, four of them cause common cold and circulate exclusively in the human population. In addition, SARS-CoV and MERS-CoV, recently emerged in the human population and are associated with severe respiratory illness. Where do these zoonotic viruses come from, and how did they cross the species barrier? These questions are generally difficult to address. The critical residues at interaction interface of host receptors (DPP4 for MERS-CoV and ACE2 for SARS-CoV) are believed to impact the binding ability of the receptors with viruses' surface-located spike. The diversity of available protein sequences limits our understanding of the receptor-mediated pathogen-host interactions for bat coronaviruses. Computational molecular docking is a bioinformatics tool, which allows us to explore the potential receptor-spike interactions in silico. The aim of this study is to analyze the diversity of SARS-CoV and MERS-CoV receptors from different mammalian hosts, to predict the host range using modeling and molecular docking. **Methods:** Up to 109 DPP4 and 94 ACE2 sequences from mammalian hosts were downloaded from genbank or acquired by sequencing, covering 60 and 51 different families respectively. The putative crystal structures were homologically modeled, and protein-protein docking was performed using Autodock Vina on NIH HPC Biowulf cluster. **Results:** Both of DPP4 and ACE2 receptors sequences from the hosts have relative high diversity. The docking results point out wide but family specific of host range of MERS-CoV and SARS-CoV. Virtual mutagenesis studies explored the impact of each critical residue of DPP4 on binding interaction for *Homo sapiens*, *Mesocricetus auratus*, *Desmodus rotundus*, *Canis lupus familiaris* and *Felis catus*. **Conclusions:** Although currently in silico analysis of spike-receptor interactions utilizing molecular docking methods still are in its early stages of development, the generated results could be utilized to perform large screens of potential virus reservoir, and intermediate hosts associated with emerging coronaviruses, and could potentially be utilized to estimate the distribution of MERS-CoV and SARS-CoV in ecosystems.

14. **Hendra virus phylogeography in eastern Australia**
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Objectives: Hendra virus (HeV) is an emerging zoonotic paramyxovirus that causes sporadic fatal disease in horses and humans in mainland Australia. Australian flying foxes (*Pteropus* spp. fruit bats), the endemic host, are gregarious, semi-migratory species that occupy the tropical and subtropical forests of coastal Australia. Despite the vast range of flying foxes, current outbreaks of Hendra virus have been restricted to a narrow band in southeast Queensland and northern New South Wales. Transmission dynamics of HeV between flying foxes is poorly understood, which limits our ability to identify potential points for management and spillover prevention. We used a phylogeographic framework to explore the spatial structure of HeV over eastern Australia, and to investigate factors that contribute to maintenance and spread of HeV in flying foxes. **Methods:** A three-year surveillance field study was initiated to improve understanding of Hendra virus diversity and disease dynamics in wild flying foxes, generating partial sequences from 26 colonies across eastern Australia. We incorporated sequenced isolates from spillover events in horses, and applied discrete and continuous Bayesian phylogenetic approaches to explore patterns in the dynamics and spatial spread of Hendra virus. Analysis was performed on a 2015 bp intergenic region between the nucleoprotein and phosphoprotein genes. **Results**: Preliminary analysis indicates a broad spatial structure, with lineages clustering loosely in space and time. However, we also find that multiple variants co-circulate in one colony at any given time, and that identical variants may co-circulate in geographically disparate colonies. Our ongoing approach is to identify drivers in the spatial spread and diversity of Hendra virus by examining the role species composition, roost structure, and migratory behavior play in shaping the geneology of Hendra virus. **Conclusions**: These data suggest that host factors (e.g., species composition within roosts) and/or environmental factors may play a role in HeV circulation within and between bat colonies. This work represents a novel approach to understanding the transmission dynamics and evolution of Hendra virus, as well as the functional connectivity of flying fox populations in eastern Australia.

15. **Viral Zoonosis in Georgian Bats**

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Objectives: Bats are reservoir-hosts of viral agents (lyssaviruses, paramyxoviruses, coronaviruses, and filoviruses), which are transmittable to humans and other animals. There are few bat virus detection studies linked to the Caucasus region. In Georgia, bat *Lyssavirus* (Rabies virus) is listed as a priority pathogen, and West Caucasian Bat Virus (WCBV) is the most genetically different member of the *Lyssavirus* genus. The goal of our study was to find WCBV and the newly discovered bat Coronavirus (bat-CoV) in Georgian bats. **Methods:** Bats that were used for sampling were collected in 2012 from four different regions in Georgia. Bat brains (n=236) were sampled and tested for the presence of lyssavirus antigen by the direct fluorescent antibody (DFA) test. A total of 186 bats of 11 different species were sampled for CoV confirmation. RT-PCR amplification assay targeting the 180 bp fragment within the RNA-dependent RNA polymerase RdRp gene and sequencing of the amplified product was used to confirm the presence of coronaviruses in bat specimens. The PCR product was sequenced on an ABI 3130 Automatic Sequencer. **Results:** None of the bats had detectable antigen consistent with an active infection of related *Lyssavirus* or WCBV. We found an outstanding diversity of CoV strains in Georgia; 54 bats tested positive for CoV. Sequence analysis demonstrated 97- 99% identity to five different types of CoV available at NCBI database. Most CoV positive bats were collected from Imereti, which is located in western Georgia. Bats with a higher prevalence of CoV were *Myotis blhytii* and *Rhinolophus ferrumequinum.* **Conclusions:** Our study revealed that we need additional research for excluding the existence of WCBV in Georgian bats. Future work will include determining the prevalence of rabies virus in these bat samples. To do this, we will perform rabies virus neutralization “Rabies Vaccine Response End-Point Titer (RFFIT)” assays. This was the first study addressing the genetic diversity of bat-CoV in this region. Further analyses and interpretation of the phylogenetic results for CoV will be a benefit for surveillance, system control, and response measures of emerging pathogens in Georgia.

16. Forestalling Future Outbreaks: Enhancing Capacity for Surveillance of Viral Hemorrhagic Fever Viruses in Sierra Leone

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Objectives: The first outbreak of Ebola virus disease in Sierra Leone exposed the limited in-country capacity for effective disease surveillance. Heavy reliance was placed on international support for human, technical and material resources. While the source of the outbreak has not been confirmed, human interactions with wildlife and their habitats continue unabated, raising fears of future outbreaks of zoonotic diseases. Building national level capacity, especially in research universities, would enhance Sierra Leone’s capability to forestall future outbreaks involving viral pathogens of public health concern. **Methods:** Through a collaborative agreement with the Viral Special Pathogens Branch at the Centers for Disease Control & Prevention, staff and students at Njala University have received field and laboratory training in ecological surveillance and molecular diagnosis of hemorrhagic fever viruses in bat populations. **Results:** Training in safe capture techniques, collection of blood/serum samples, necropsy techniques and the safe processing and storage of tissues specimens have been achieved over a period of 18 months for 12 Njala University staff and students. Further, three additional staff and students have been trained in molecular diagnostics using robotic nucleic acid extraction and qRT-PCR methods. These trainings, coupled with the acquisition of laboratory and field equipment and renovations of laboratory space on the Njala University campus and its field research station, are resulting in the inclusion of ecological surveillance and molecular diagnostics of viral pathogens in wildlife populations in the curriculum of Njala University in Sierra Leone. **Conclusions:** Strengthening technical and human capacity for disease surveillance in bats through long-term partnerships with research institutions could lay the foundation for preventing future outbreaks of global concerns.

17. Ecological aspects of bats in a cave frequented by members of the local community in Kaptum Cave in eastern Uganda.

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Few studies have addressed the ecology of cave bats in Uganda. This study assessed the diversity, roosting and feeding ecology, of micro bats (order *chiroptera*) as well as influence and frequency of human disturbance, in Kaptum cave of Eastern Uganda. Field observations were conducted between July/Augst 2016 and October/ November 2016 to document aspects of roost utilisation by the bats, their feeding choices and human influences on the cave in which 6 species of microchiropteran bats roosted. We used Mist nets and a Harp trap to capture individuals for examination and identification of species present. Infrared Trail trap Cameras were used to monitor roosting habits and activity patterns of the bats in the cave. A portable whether station was used to record the microclimatic conditions in the different sections of the cave in which the bats roosted to evaluate if there was any influence on choice roost. Kaptum cave has 6 species of insectivorous bats which seemed to prefer different sections of the cave. From evidence of insect remains in the roost, the diet of the bats in Kaptum cave consisted of eight insect orders (*Lepidoptera, Coleoptera, Orthoptera, Dictyoptera, Heymenoptera, Isopteran, Hemiptera, and Odonata*) with the order *Lepidoptera* constituting the bulk of insects preyed upon. At the moment we cannot separate the diet of the different species, since most insect remains were recovered in a section the cave we refer to as the Nycteris corner, because it was most used by these bats, but other species of Rhinolophids and Hipposiderids also frequented this corner in any 24hr period. We believe that the continued human presence in the cave could have implications for roost stability, but also could predispose the humans to potentially harmful aerosols associated with bats and bat guano.

18. **Middle East respiratory syndrome coronavirus spike plasticity in the context of the common vampire bat (*Desmodus rotundus*) DPP4 receptor.**

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Objectives: In 2012, a novel coronavirus, Middle East respiratory syndrome coronavirus (MERS-CoV), was discovered in humans and dromedary camels, although genetic evidence supports a bat ancestor. This range of animal hosts lead us to hypothesize that MERS-CoV can readily adapt to new hosts. The receptor for MERS-CoV, dipeptidyl peptidase 4 (DPP4) has previously been shown to act as a species barrier. By passing the virus over time on cells stably expressing the common vampire bat (*Desmodus rotundus*) DPP4 receptor, which MERS-CoV binds inefficiently, we will determine how potential adaptation in the spike glycoprotein may influence species tropism. **Methods:** We have compared the growth kinetics of MERS-CoV over 72hrs between different bat DPP4 receptors transfected on baby hamster kidney (BHK) cells, which are naturally unsusceptible to MERS-CoV. We then generated BHK cell lines stably expressing the *D. rotundus* DPP4 receptor. By passing MERS-CoV on these cells over time, we hope to observe adaptations in the viral spike protein that allow more efficient viral growth kinetics. Viral genomes containing the relevant mutations can be created through a reverse genetics system and tested for binding affinity and growth potential. **Results:** We show here that MERS-CoV can use DPP4 from different animal hosts, including a variety of bat species. Notably, MERS-CoV can bind and replicate using the *D. rotundus* DPP4 but very inefficiently compared to human DPP4, leading to delayed growth. We observed that MERS-CoV growth on cells stably expressing D. rotundus DPP4 displays a similar inefficient growth pattern as seen previously using a transfection method. **Conclusions:** Our data demonstrates that MERS-CoV can use a diverse set of host species receptors. Although we have successfully generated BHK cells stably expressing *D. rotundus* DPP4, sequencing of the MERS-CoV spike over many passages is needed to identify relevant mutations. The ability of the MERS-CoV spike to adapt to diverse host species receptors may play a significant role in cross-species transmission.

19. **Viral community dynamics of Australian Flying foxes**

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Objectives: Bats are reservoirs for a disproportionate number of zoonotic viruses, with spillover to people and domestic animals resulting in significant public health implications globally. In Australia, bat viral research has largely focused on Hendra virus, yet a diverse viral community has been detected in Australian Pteropid fruit bats (flying-foxes)[1,2]. Additionally, while the four Australian flying fox are capable of being infected with Hendra virus, not all species appear to be equally competent hosts[3,4]. In this context, interactions among co-infecting viruses and the dynamical consequences of these interactions are under- studied. We aimed to gain further insight into bat viral transmission dynamics by exploring dynamics within a multi-host-multi-pathogen framework. **Methods:** To characterise existing knowledge of the bat viral-host community in Australian flying foxes, a systematic literature review of published studies was undertaken and then complimented with additional unpublished data. Using urine samples collected from three of the four Australian flying-fox species in a related field study[6], we utilised a novel high-throughput multiplex PCR[5] to simultaneously detect up to 11 known bat paramyxoviruses. Within a Bayesian framework, we then modelled the monthly presence of different virus species at the roost level in relation to environmental drivers and the co-occurrence of other virus species. **Results:** Results support synchronous shedding pulses of multiple viruses, with significant co-circulation associations between certain virus species. **Conclusions:** Natural host-virus systems comprise complex communities, and our study explores how moving beyond single-pathogen-single host studies of bat pathogen dynamics towards broader consideration of the biotic interactions within viral and reservoir communities could progress our understanding of transmission and spillover of bat pathogens.

20. **The glycoprotein of Nipah virus in Thai bats associated with Nipah virus in Bangladesh**

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Objectives Bats have been recognised as a natural reservoirs of a large number of viruses including Nipah virus (NiV) and are associated with human activities which plays important role in the transmission of pathogens from bats to human. Study the glycoprotein NiV protein which plays important role in virus entry into host cells is a crucial in order to know the virus transmission. **Methods** Bat urine were collected from Luang Phrommawat temple, Chonburi province and screened for NiV nucleocapsid by using hemi-nested RT-PCR. The NiV positive urine samples were amplified the whole glycoprotein gene (1.8 kb). The whole sequences of nucleotide and amino acid of NiV glycoprotein were compared with sequences from both Malaysian and Bangladeshi strains from bats and humans. The phylogenetic tree was constructed by comparing amino acid sequence between NiV from Thai bat and NiV Bangladeshi patient. **Results** NiV glycoprotein sequence from Thai bats were homologous with Bangladeshi strain compared to the Malaysian strain. Furthermore, it shared 99.2-100% and 99.2-99.5% identity with nucleotide sequence of NiV glycoprotein from Bangladeshi bats and Bangladeshi patients, respectively. Amino acid sequence of NiV glycoprotein from Thai bats shared 99.8-100% and 99.5-99.7% identity with Bangladeshi bats and Bangladeshi patients, respectively. While, nucleotide sequence of NiV glycoprotein in Thai bats shared only 93.0-93.3% and 93.2% identity with Malaysian bats and Malaysian patients, respectively. Like nucleotide sequence, the amino acid sequence of NiV Thai bats shared only 95.7-96.0% and 95.7% identity with Malaysian bats and Malaysian patients. Phylogenetic analysis of NiV glycoprotein amino acid revealed that the NiV glycoprotein in Thai bats belonged to Bangladeshi patients. **Conclusions** This is the first step to understand the mechanism of NiV entry to the host. The results may indicates that NiV Thai bat strain has the potential to cause infection in humans. NiV glycoprotein and host receptors should be further investigated in order to understand the viral entry mechanism, host range, including intra- and cross-species transmission. Understanding the transmission of NiV from bats to humans is crucial in order to predict and prevent NiV outbreaks.

21. **Genomic characterization and pathogenic potential of a novel evolutionarily-divergent alphacoronavirus isolated from *M. lucifigus* bats in Alaska.**

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Coronaviruses (CoV) are zoonotic pathogens with the potential to cross species barriers from bats into other mammals, including marine mammals, swine and humans. Novel bat-origin coronaviruses have been responsible respiratory disease in humans, notably betacoronaviruses (OC43, HKU-1, SARS and MERS) and alphacoronaviruses (229E and NL63). Thus, it is important to identify the reservoirs of CoV in bats and their potential for transmission, and pathogenicity, in other mammalian species. We sought to analyze the virome of the most common bat species in Alaska, *Myotis lucifugus,* the little brown bat. Swabs, tissue, and fecal samples were collected from habitats in close proximity to barns, farm buildings, and human habitations in southcentral Alaska. Total RNA extracts were screened by RT-PCR with coronavirus primers matching CoV ORF1a, and Sanger sequencing of amplicons confirmed the presence of an alphacoronavirus phylogentically related to persistent alphacoronaviruses detected in bats in Colorado and the Rocky Mountains. Primary RNA samples were used in library preparation for short-read, paired-end next generation sequencing on an Illumina HiSeq platform. Aligning to a reference *M. lucifigus* virus from Colorado, bat alphacoronavirus CDPHE15/USA/2006, we assembled a full-length genome (28,515nt) identifying the novel alphacoronavirus/bat/Alaska/s7/2014. A high degree of thermodynamically stable stem-loop RNA structures are predicted by Mfold within 700nt of 5' and 3' termini of genome**.** While nucleotide conservation to the Colorado virus was 96%, notable amino acid differences were identified in coronavirus proteins. The major CoV surface spike (S) protein exhibited 26 amino acid changes, including 14 in the globular head containing the putative receptor-binding domain, suggesting divergence based on immune evasion or receptor-specificity. Another 6 amino acids were altered in the fusion hinge. Protease cleavage sites were not conserved. Nucleoprotein (N) and ORF3 also exhibited amino acid differences. Understanding the evolution and pathogenicity of this novel alphacoronavirus provides insight into the role of bats in virus transmission, and ecological assessment of bat-borne virus reservoirs in North American ecosystems.

22. **Spatial pattern of genetic diversity and selection in the MHC class II DRB of three Neotropical bat species**

Salmier A., de Thoisy B., Crouau-Roy B., Lacoste V. and Lavergne A.

Host–pathogen interactions—greatly influenced by environmental characteristics—are a major determinant of the extensive polymorphism of the Major histocompatibility complex (MHC) genes that play an important role in both resistance and susceptibility to diseases. Amazonia encompasses the greatest bat richness, as well as great landscape diversity. However, there are few studies regarding adaptation to infectious diseases of bats and even less in contrasting environmental conditions. We analyzed the genetic variability and positive selection signatures of the expressed MHC class II *DRB* exon 2 in three sympatric Amazonian bat species, *Carollia perspicillata*, *Desmodus rotundus*, and *Molossus molossus* inhabiting different environments (*e.g.*, forests, edge habitats, and urban areas). The role of the environment on the allelic composition and distribution of the *DRB* gene, as well as the effects of pathogen-mediated selection, recombination, gene conversion, demographic history and population structure on the MHC diversity were investigated. Overall, we identified 23 *DRB* alleles in 19 *C. perspicillata*, 30 *DRB* alleles in 35 *D. rotundus* and 20 *DRB* alleles in 28 *M. molossus*. We found clear evidence of at least two functional *DRB* loci as well as a trans-species mode of evolution within the Phyllostomidae family. Bats inhabiting forest environments presented higher number of alleles, revealing a heterozygote advantage likely associated with higher diversity of microorganisms in forest environments due to greater host species richness and better transmission-promoting parameters compared to disturbed environments. The *DRB* polymorphism was high in all sampling sites and for all species but different signatures of positive selection were detected depending on the environment, suggesting a local adaptation characteristic driven by an area-limited pathogen-mediated selection. The patterns of *DRB* diversity were similar to those of neutral markers for *C. perspicillata* and *M. molossus* while these patterns were different for *D. rotundus* for which a geographical structure was highlighted. These results supported that demographic process acts as an additional force in shaping *DRB* diversity. However, in structured populations, environmental constraints associated with characteristic pathogen pressures are the main drivers of MHC diversity.

23. Establishing a field collection scheme to investigate the role of African fruit bats as the natural reservoir of ebolaviruses

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Objectives: Filoviruses are among the most well-known and well-studied zoonotic pathogens, yet we know little about filovirus populations in their natural reservoirs. Phylogeographic and population genetic studies of filoviruses isolated from their natural reservoirs would shed light on the population structure and evolutionary history of these important zoonotic pathogens. African fruit bats including *Hypsignathus monstrosus* and *Epomops franqueti*, are the candidate natural reservoirs for filoviruses in the *Ebolavirus* genus; however, there have been no successful attempts to sequence or isolate *Ebolavirus sp.* from PCR-positive bats due to low viral copy numbers in the bats and difficulty associated with sampling from wild bat populations. We sought to increase the likelihood of acquiring live virus and viral whole genome sequences through extensive sampling from wild bat species in the Odzala-Kokoua National Park, Republic of Congo, within the geographical area of previous Zaire ebolavirus outbreaks. **Methods:** Multiple capture-release studies were performed to sample fruit bats over a period of four years. Bats were captured by mist netting near an *H. monstrosus* lekking tree and sampled for whole blood in addition to collecting nasal, urogenital, and rectal swabs. **Results:** In total, samples were taken from 456 *H. monstrosus* bats and 43 *E. franqueti* bats across four years of sampling. An additional 57 samples were taken from other bat species. Preliminary serological work shows 4.9% seroprevalence against Zaire ebolavirus in a subset of the *H. monstrosus* bats. **Conclusions:** The field collection efforts have yielded a large number of bats sampled which show a history of Zaire ebolavirus exposure. Future work will focus on detecting active infection with ebolavirus and isolation of live ebolavirus for whole genome sequencing.

24. **Co-infection in Georgian Bats**

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Objectives: Bats have been recognized as natural reservoirs for a variety of zoonotic pathogens. The prevalence of different pathogens in bats could be associated with colony size and migration patterns. In this study, bats were collected from four different Georgian regions (Kakheti, Imereti-Tskhaltubo, Samegrelo, Kvemo Kartli) and were tested for different pathogens that are endemic to Georgia. **Methods**: In total, 218 bats (*Eptesicus serotinus*-20, *Miniopterus shrebersii*-27, *Myotis blythii*-67, *Myotis emarginatus*-38, *Pipistrellus pygmaeus*-12, *Rhinolopus Euriale*-26, and *Rhinolopus ferrumequinum*-22) were tested for four bacterial agents (*Bartonella, Brucella, Leptospira,* and *Yersinia*). Bat kidneys were dissected, and their DNA was tested for *Bartonella*, and *Leptospira*. Spleen DNA was tested for *Brucella* and *Yersinia*, and the intestine DNA was tested for *Yersinia*. Triplex Real-Time PCR (rtPCR) Assay was performed to detect *Brucella* (IS711), *Bartonella* (tmRNA), and *Yersinia* (pal). Singleplex rtPCR was used to identify *Leptospira* (LipL32). Targeting the 16S rRNA gene, conventional PCR was performed to detect multiple bacterial strains. Cultured *Bartonella* isolates of the *gltA* gene were sequenced. **Results:** A total of 113 (51%) were positive for at least one of the four pathogens. Co-infection was detected in different bat species from Tskhaltubo and Kakheti. One Tskhaltubo bat was positive for *Bartonella*, *Brucella*, and *Leptospira*. Two bats from Kakheti were co-infected with *Bartonella* and *Brucella*: (*Myotisblythii* (n=1), and *Miniopterusschreibersii* (n=1). Eighteen bats were co-infected with *Bartonella* and *Leptospira*: *Myotisblythii* (n=15), and *Miniopterusschreibersii* (n=3). Sequencing analysis confirmed a co-infection with two different *Bartonella* sequences from 16 different bats: *Myotisblythii blythii* (n=3), *Miniopterusschreibersii schreibersii* (n=7), *Myotisblythii emarginatus* (n=1), *Rhinolophus euryale* (n=2), and *Rhinolophus ferrumequinum* (n=3). All bats were negative for *Yersinia*. **Conclusions:** Our results indicate that bat colonies in Tskhaltubo have the highest prevalence of infection and co-infection; since these bats are in enclosed, small spaces such as caves, this may be a reason we see a mixture of pathogens and mutation. In the past couple of years', Georgian caves have become a popular tourist attraction; from a public health standpoint, it is important to know what types of pathogens exists in these local bats.

25. Caves of Myanmar: a high-risk human-wildlife interface for zoonotic disease
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The Southeast Asian country of Myanmar has been deemed a “hotspot,” both in terms of its biodiversity and disease emergence potential. Despite this recognition, there is a paucity of data and limited surveillance on emerging infectious diseases in Myanmar, due in part to almost five decades of political isolation. Recent changes in the government have expanded economic development, strengthening trade with neighboring countries and opening border access to tourists and investors, further contributing to potential underlying drivers of disease emergence. Of particular import and concern are zoonotic diseases arising from human-animal contact. The vast cave and karst system of Myanmar presents an understudied interface between humans and wildlife, such as bats, rodents, and non-human primates. Caves, particularly where intricate Buddhist shrines have been installed, are popular destinations for local, national, and international visitors despite high-contact potential with animals and their excrement. This poster underscores the growing risk of bat-borne pathogen exposure in relation to cave utilization in Myanmar, exemplified by the popular tourist destination town, Hpa-An.

26. **Prevalence Patterns of Coronaviruses in Lyle's flying fox (*Pteropus lylei*) in Thailand**
Supaporn Wacharapluesadee[1], Prateep Duengkae[2], Aingorn Chaiyes[2], Sangchai Yinsakmongkon[3], Pattarapol Maneeorn[4], Patcharakiti Phengsakul[2], Wachirapon Khumbucha[2], Thongchai Kaewpom[1], Apaporn Rodpan[1], Thiravat Hemachudha[1]

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Objectives Coronavirus (CoV) surveillance in Lyle’s flying fox (*Pteropus lylei*); a medium-sized flying fox which forms large colonies high up in trees in areas close to humans and other animals, was conducted to characterize strain of CoV and determine prevalence patterns in Chonburi province, Thailand. **Methods** *P. lylei* bats were captured monthly during January - December 2012 for detection of CoV at three closed areas in Chonburi province, two human dwellings which were 0.6 (S1) and 5.5 km (S2) away from the bat roost, and a bat roosting site (S3). Two nested RT-PCR of RNA-dependent RNA polymerase (RdRp) from rectal swabs were used for CoV detection. The strain of CoV was confirmed by sequencing and phylogenetic analysis. **Results** From 390 *P. lylei* bats, 239 were male and 151 were female, while 101 were juvenile (forearm length ≤136 mm) and 289 were adult. CoVs were detected in 68 bats, 17.4% using family-wide CoV PCR but not by group C betacoronavirus assay. The positive samples were found in eight months in the year that the study was conducted, the highest in June 2012. Ten mother–pup pairs were captured. Samples from 10 mothers were negative. Rectal swabs from 9 unweaned pups were available for CoV PCR assays and three of them were positive. PCR positive pup was identified with a PCR negative mother. Phylogenetic analysis of conserved RdRp gene revealed that the detected CoVs belonged to group D betacoronavirus (n=64) and alphacoronavirus (n=4). **Conclusions** Younger bats appeared to play a more significant epidemiological role in harbouring CoV. Young age but not sex or gravidity, correlated significantly with CoV detection. CoV was found in unweaned pups whose mothers tested negative for CoV. One possible conclusion is transient shedding from mother during peri-partum to the young, may maintain the virus transmission within the population. The immune status of young and adult bats against CoV, in terms of susceptibility to infection, needs to be studied to explore this. Further study into the association of CoVs with natural hosts is necessary to understand their prevalence and maintenance patterns, to evaluate its zoonotic potential.

27. Genetically Diverse Filoviruses in *Rousettus* and *Eonycteris* spp. Bats, China, 2009 and 2015
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Bats have been implicated as natural reservoirs for filoviruses based on serological or nucleotide evidence from 19 bat species in 8 countries across Asia, Africa, and Europe. Previously, we discovered filovirus antibodies in several bat species in China. Here we report genetically divergent novel filoviruses are circulating in the *Rousettus* and *Eonycteris* bats from China. The 310-bp L-gene sequences exhibited 65–99% nucleotide (nt) identity among themselves and 61–78% nt identity with known filoviruses. Phylogenetic analysis of these sequences suggests that at least 3 distinct groups of filovirus are circulating in these bats. Q-PCR results showed these filoviruses were mainly located in the lung, with genome copy number varying from 29 to 523,582/mg of tissue. Thus, these filoviruses may have the potential to be transmitted through the respiratory tract. Co-infection with four different filoviruses was found in a single bat. ELISA and Western Blot showed the antibodies reacting more strongly to EBOV NP than RESTV NP in some filovirus RNA negative bats. One of the viruses named BtFilo9447 were tried to amplify the whole genome. The GP gene of BtFilo9447 shared 34-39% similarity on aa level and 35-53% similarity on nt level with known filoviruses. Our results demonstrate that fruit bats may are important reservoirs of filoviruses. Considering their feeding habitats, fruit bats are often in close contact with domestic animals and human populations. It is therefore necessary to establish long-term and proactive surveillance of these viruses and related diseases.

28. **Development of a monoclonal antibody to Jamaican fruit bat CD3γ**
Miles Eckley, Ann Hawkinson, Tyler Sherman, Tony Schountz, Corey L Campbell

[1]Arthropod-borne and Infectious Diseases Laboratory, Colorado State University and [2]Department of Biology, University of Northern Colorado.

Objective: T cells have critical immunomodulatory roles in the innate immune response to infection. The CD3 cell-surface protein complex is required for T cell activation, and thus treating bats with therapeutic Aj-anti-CD3 IgG antibodies may have immunosuppressive effects. Monoclonal antibodies are of particular interest for this application because of their ability to bind to the Fc receptor of phagocytic and cytotoxic cells and label a pathogen for destruction. Our goal is to investigate the biological mechanisms by which T cells may induce immunopathology in response to viral infection. **Methods**: BALB/c mice were immunized and boosted with a KLH-conjugated 30mer peptide from Jamaican fruit bat CD3γ. Hybridoma cells were produced from the fusion of splenocytes with Sp2/0-Ag14 myeloma cells. Hybridoma cells were selected and cloned on methylcellulose plates, transferred to 24 well plates and supernatants screened. Candidates were identified by ELISA to 30mer peptide conjugated to BSA first, followed by flow cytometry of bat splenocytes. Antibodies were purified from supernatants by affinity chromatography using a protein A/G agarose resin bed. Isotype determination was done by ELISA using HRP labeled mouse anti-IgM, IgG2a, IgG1 and biotin labeled rat anti- IGg2b, IgA and IgG3 primary antibodies. **Results**: Three hybridoma clones for Aj-anti-CD3 IgG were purified from the cell culture supernatants and stored for later use. Each of the three hybridoma clones are expected to have produced a different isotype based on flow cytometry data. **Conclusions**: In future work, we will use Aj-anti-CD3 antibody labelling of T cells in vivo to deplete T cells and determine whether immunopathology to Tacaribe virus, which normally causes fatal infection, will be ameliorated.

29. **Bats and Immunity: Anti-Viral IFNγ Responses Differ Among Hosts**
C. Cotter, T. Schountz, C.L. Campbell

Arthropod-borne and Infectious Diseases Laboratory, Colorado State University

Anti-viral responses in bats (order Chiroptera) is largely unknown to researchers. Although bats account for 20% of all mammal species, they are relatively understudied in the scientific community (Baker et al., 2013). Bats are reservoir hosts for zoonotic diseases such as severe acute respiratory syndrome (SARs), rabies virus, and Ebola virus (Mandl et al., 2015). Reservoir hosts, generally, do not show pathogenic signs or succumb to disease when infected with such viruses. Current efforts by Kuzmin et al to better understand anti-viral responses in Egyptian rousette bat (*Rousettus aegyptiacus*) and human cells include a comparative study of host innate immune response to infection with Ebola virus or Marburg virus. They focused on the interferon (IFN) response. Kuzmin et al. demonstrated that bat IFNγ (type II IFN response) decreased viral replication in cell culture, whereas the human IFNγ produced by the human cells did not. Additionally, IFNγ stimulated the type I IFN (IFNα/β) response Kuzmin et al., 2017). My research focuses on Jamaican fruit bat (*Artibeus jamaicensis*—Aj) IFNg and its role in an anti-viral response to New World mammarenavirus Tacaribe (TCRV). *A. jamaicensis*, when infected with

TCRV, suffer fatal infections (Cogswell-Hawkinson, 2012). Most arenaviruses, TCRV excluded, produce a nuclear protein (NP) that blocks the type I IFN response at interferon response factor-3 (IRF-3) (Martinez-Sobrido et al., 2007). Pathogenesis of TCRV is still unknown; however I hypothesize that it interferes with the IFN response pathway by a different mechanism. Therefore, introduction of therapeutic Aj IFNγ to TCRV infected A. jamaicensis should be able to stimulate an appropriate, anti-viral innate immune response to rescue them from death. My project focuses on cloning, expressing, and purifying Aj IFNγ in order to synthesize a recombinant antibody for Aj IFNγ.

30. **Virome analysis of neotropical bats on the Caribbean island of Trinidad**

Janine F.R. Seetahal[1], Orchid M. Allicock[1,2], Stephen C. Sameroff[2], Christopher Oura[3], Vernie Ramkissoon[1], W. Ian Lipkin[2], Christine V.F. Carrington[1]

[1] Department of Preclinical Sciences, Faculty of Medical Sciences, The University of the West Indies, St Augustine, Trinidad and Tobago; [2] Center for Infection and Immunity, Mailman School of Public Health, Columbia University, New York, USA; [3] School of Veterinary Medicine, Faculty of Medical Sciences, The University of the West Indies, St. Augustine, Trinidad and Tobago

Objectives: Bats are recognized as reservoirs for a number of important zoonotic viruses. The Caribbean island of Trinidad is richly diverse in bat fauna with 68 species recognized. Viruses detected in Trinidad bats include Rabies virus, Tacaribe virus, Rio Bravo virus, Tamana bat virus and more recently a bat coronavirus. The objective of this study was to identify and characterize known and novel viruses in Trinidad bat species. **Methods:** During the period 2012- 2016, bats were sampled from 19 locations in Trinidad. The novel virome capture sequencing platform for vertebrate viruses (VirCapSeq-VERT) was employed to sequence faecal swab samples from 73 bats belonging to seven neotropical species (*Desmodus rotundus, Carollia perspicillita, Uroderma bilobatum, Molossus molossus, Molossus rufus, Pteronotus parnellii* and *Artibeus spp*). Sequence reads were processed using the bioinformatics pipeline at Center for Infection and Immunity to remove host background and assemble contigs that were then subjected to homology search using MegaBlast against the GenBank nucleotide database. Sequences that showed poor or no homology at the nucleotide level were searched against the GenBank viral protein database using BLASTx. The bat fecal samples were also screened by consensus PCR for 8 viral families (*Arenaviridae*, *Herpesviridae*, *Coronaviridae*, *Orthomyxoviridae*, *Alphaviridae*, *Flaviviridae*, *Rhabdoviridae*, *Picornaviridae*) using broadly reactive degenerate primers as outlined in the laboratory protocol for the PREDICT II surveillance project. All PCR products were confirmed by sequencing. **Results:** Consensus PCR detected sequences of Herpesviridae (bat herpesviruses) and Coronaviridae (bat coronaviruses). Preliminary analysis of VirCapSeq-VERT data provided evidence of both known and potentially novel viruses, the majority of which belonged to the families *Anelloviridae*, *Herpesviridae*, *Coronaviridae*, *Orthomyxoviridae*, *Parvoviridae*, *Rhabdoviridae* and *Retroviridae*. The *Anelloviridae* and *Herpesviridae* were detected primarily in fruit bats. The *Orthomyxoviridae* family included Influenza A viruses and were identified in *Desmodus* and *Molossus* species. *Parvoviridae* were overwhelmingly from *Desmodus* and *Artibeus* bats from one trapping site within the same year. *Rhaboviridae* viruses were detected in Desmodus bats sampled from various locations throughout the sampling period. The Retroviridae were primarily previously described bat endogenous retroviruses. **Conclusions:** Our results indicate the presence of a wide range of both known and novel viruses in faeces from Trinidad bats. The limited identification of viruses by consensus PCR as compared to the deep sequencing technique implies that viral detection is more efficient by targeted deep sequencing. Further analysis including targeted PCR and sequencing to assemble full genomes is required to further characterise the viruses detected. Analysis of other tissues will be required to distinguish between bat viral infections and viruses associated with animal prey.

31. **Delineating the phenotype and function of major lymphocyte populations in the fruit-eating bat, Pteropus Alecto.**

Periasamy P.[1,2], Martínez Gómez J.M.[1,2], Wang LF[3] , and Alonso S.[1,2]

[1]Department of Microbiology and Immunology, [2]Immunology Programme, Yong Loo Lin School of Medicine, Life Sciences Institute, National University of Singapore, Singapore. [3]DUKE-NUS, Singapore.

Objective: The unique ability of bats to act as reservoir for viruses that are highly pathogenic to humans suggests unique properties and functional characteristics of their immune system. However, the lack of bat specific reagents, in particular antibodies, has limited our knowledge of bat's immunity. **Methods and Results**: Here, using cross-reactive antibodies, we report the phenotypic and functional characterization of CD3+ T cell subsets, CD19+ B and NK1.1+ NK cells in the fruit-eating bat Pteropus alecto. Our findings indicate the predominance of CD8+ T cells in the spleen from wild-caught bats that may reflect either the presence of viruses in this organ or predominance of these cells at steady state. In addition, bone marrow of the bat contains over 30% T lymphocytes. This is significantly greater when compared to the T cell percentages in human and mouse bone marrow which ranges between 4% and 8%. Uniquely, a significant proportion of CD3+ T cells in bat spleen constitutively express IL-17A, IL-22 and TGF- at the mRNA level. Hence, the spleen may contain a substantial population of naïve T cells that are programmed to readily differentiate into TH17 cells or Tregs. Furthermore, mitogenic stimulation induced proliferation of bat immune cells and production of cytolytic molecules granzyme and perforin, and cytokines IL-2, IL-10, TNF and IFN. Additionally, we also demonstrate B cell function via calcium flux assay. **Conclusions**: This work paves the way towards a better understanding of bat's immunity that may offer new perspectives of therapeutic interventions for humans.

32. **Seasonal serological signals in viral infections for Madagascar fruit bats**

Cara E. Brook[1], Hafaliana C. Ranaivoson[2], Christopher C. Broder[3], Andrew A. Cunningham[4], Andrea L. Graham[1], Jean-Michel Héraud[2], Louise Wong[4], James L.N. Wood[5], Andrew P. Dobson[1*], C. Jessica E. Metcalf[1*]

[1]Department of Ecology and Evolutionary Biology, Princeton University; [2]Virology Unit, Institut Pasteur of Madagascar; [3]Department of Microbiology and Immunology, Uniformed Services University; [4]Institute of Zoology; Zoological Society of London; [5]Department of Veterinary Medicine; University of Cambridge;
*These senior authors contributed equally to this work.

Objectives: Considerable evidence supports a seasonal driver of bat-borne zoonoses, with most spillover events aligned with the synchronous reproductive season of the bat host in question. Previous modeling work proposes three possible mechanisms which could underpin such seasonality: classic Susceptible-Infectious-Recovered (SIR) dynamics with a seasonal influx of naïve juveniles, Susceptible-Infected-Recovered-Susceptible (SIRS) dynamics with periodic, waning immunity, and Susceptible-Infectious-Latent-Infectious (SILI) dynamics, by which hosts maintain virus persistently but shed seasonally. We fit variations on these contrasting dynamic models to age-seroprevalence data for henipavirus infections in Madagascar fruit bats in order to test these hypotheses. **Methods:** We live-captured, serum-sampled, and extracted lower premolar teeth (under anesthesia) from 340 Madagascan fruit bats (Eidolon dupreanum) over an eighteen-month seasonal trajectory. Serum samples were subjected to Luminex assay for henipavirus antibodies, and teeth underwent histological processing to quantify bat age, resulting in the construction of age-serprevalence curves for heniapivrus exposure in E. dupreanum. We fit variations on SI, SIR, SIS, and SIRS compartmental models to these data and used generalized additive models (GAMs) to investigate seasonal variation in antibody titers for both sexes, including several individuals recaptured across our time series. **Results:** Seroprevalence to henipavirus increased with age across the early years of life in our dataset, then declined to zero in later life. Field data were best fit by either frequency-dependent transmission models incorporating infection-induced mortality or by density-dependent transmission models, allowing for rapid waning of immunity. GAM analysis of seasonal trends showed significant seasonality in an animal's serostatus, corresponding to the nutritional calendar for male bats and the reproductive calendar for female bats. Recaptured individuals demonstrated considerable dynamism in antibody titers, changing serostatus in both directions across our time series. **Conclusions:** Our analyses suggest that henipavirus infections in E. dupreanum fruit bats are governed by highly dynamic transmission mechanisms, involving rapidly waning immunity and seasonal peaks and troughs in infection status. We reject a classic SIR model in favor of a more flexible SIRS or SILI model underpinning viral transmission among bat hosts in our system. More fine-scale field data will be needed to further parse remaining hypotheses.

Acknowledgements

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Thanks to Ashley Malmlov for the symposium logo.

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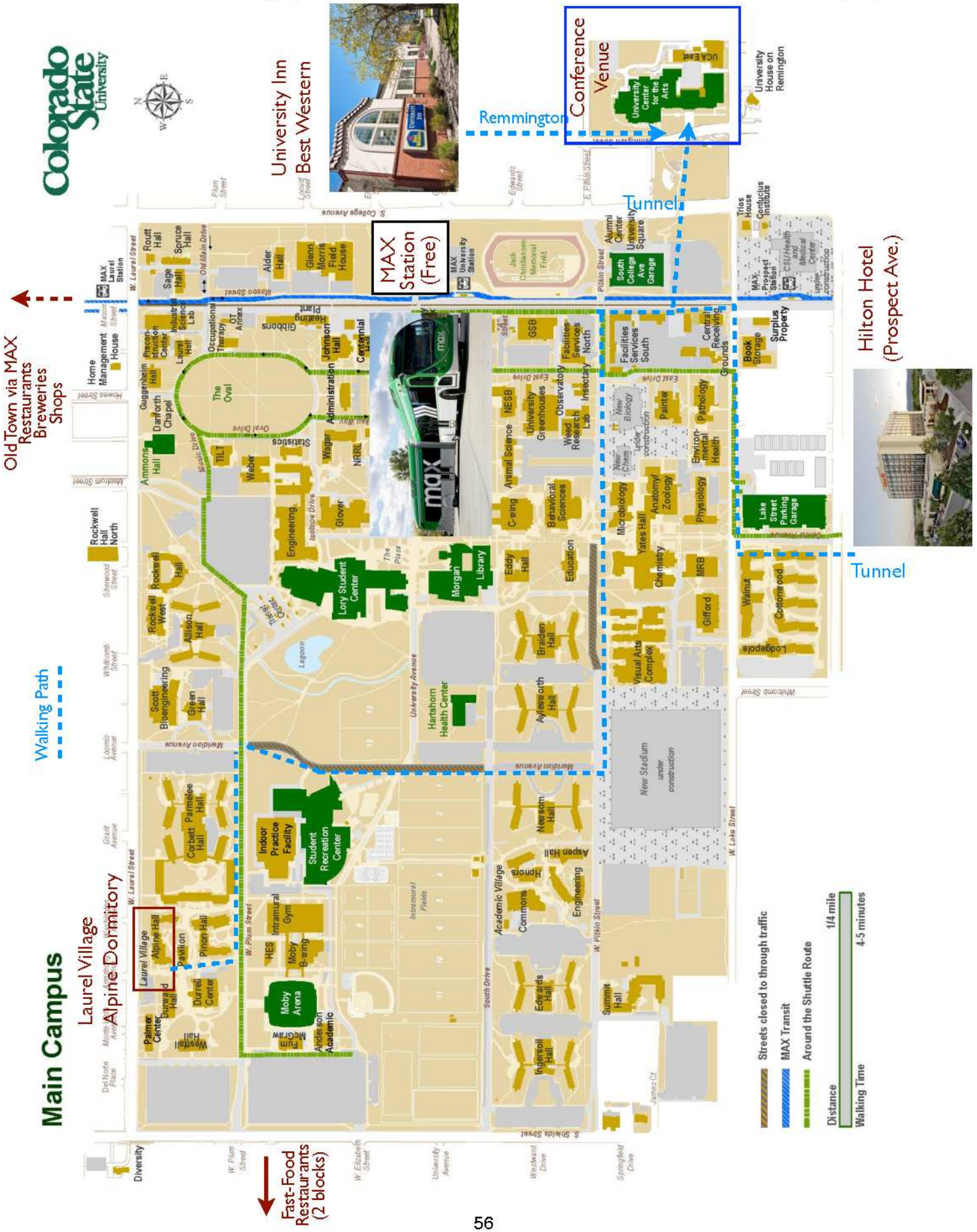
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MAX Transit
Around the Shuttle Route
Distance
1/4 mile
Walking Time
4-5 minutes

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From: Schountz,Tony on behalf of Schountz,Tony
Sent: Wednesday, May 27, 2020 12:56 PM EDT
To: epstein @ecohealthalliance.org>
Subject: Call?

Jon, do you have time for a call later today? only need about 10 minutes.

Thanks,

T.

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Tony Schountz on behalf of Schountz,Tony < >
Sent: Tuesday, March 17, 2020 3:44 PM EDT
To: Schountz,Tony
BCC:

Subject: Cancelation of the 3rd International Symposium on Infectious Diseases of Bats

Dear Colleagues,

As you may have expected, due to the COVID-19 outbreak, the*3rd International Symposium on Infectious Diseases of Bats* has been canceled. We are considering hosting the meeting in the summer of 2021 if the resources are available to do so. If so, I will send another email this fall altering you.

For those of you who have already paid your registration, you will receive a full refund from the Colorado State University Conference Services. I have been told this can take about a month, so if you have not received a refund by April 20, please email me and I will contact Conference Services.

Thank you for your understanding.

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Feb 19, 2020, at 4:09 PM, Schountz,Tony wrote:

Dear Colleagues,

Registration is now open for the 3rd International Symposium on Infectious Diseases of Bats. With the emergence of yet another pathogenic coronavirus, we are planning to have an extended session to learn from one another about this new virus and I hope some of you can foster collaborative interactions while you are here. The URL for the meeting is:

http://www.batid.org

Please note a few important dates. **Abstract submission closes on April 17, 2020**. The format of the abstract is indicated on the web site and we ask that you follow it for purposes of continuity in the program. In addition, please send MS Word, Apple Pages or Rich Text files so that we can rapidly build the program. Please DO NOT send a PDF because they are much more difficult to integrate into the program. After you submit your abstract, you should receive a confirmation email. If you do not, please let me know and I'll resolve the issue.

Registration will close on May 1, 2020. Registration will be handled by the Colorado State University Conference Services with a direct link on the Bat ID web site. You can select registration only, or registration with dormitory housing on campus near the conference venue (Lory Student Center). Registration included breakfast for the two days, and the dormitory includes breakfast, too. If you prefer to stay in a hotel, the Fort Collins Hilton (on Prospect Avenue) and the Best Western University Inn are walking distance to campus. Links to these hotels are provided on the Registration page.

We also have the pleasure of hosting**This Week in Virology**. Vincent and crew will record an episode from the meeting.

Please let me know if you have questions or comments.

Thanks very much, and we are looking forward to seeing you again in Fort Collins.

Tony

From: Tony Schountz on behalf of Schountz,Tony <
Sent: Thursday, July 30, 2020 5:44 PM EDT
To: epstein ecohealthalliance.org>
Subject: Email

Jon, I have been told to contact Alan Rudolph, so I just sent him an email to see if he will be interested in providing funds to renovate the bull barn. I'll let you know as soon as I hear anything.

T.

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Tony Schountz > on behalf of Schountz,Tony >
Sent: Wednesday, October 21, 2020 3:33 PM EDT
To: epstein ecohealthalliance.org>
Subject: Genome paper

Jon, I suspect you've seen this?

https://www.frontiersin.org/articles/10.3389/fmicb.2020.01807/full

Should be quite helpful for the grant.

T.
—
Tony Schountz, PhD
Associate Professor
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College of Veterinary Medicine
Colorado State University

From: Schountz,Tony
Sent: Wednesday, July 12, 2017 8:19 PM EDT
To: peng.zhou <peng.zhou
Subject: Greetings

Hi Peng,

Thanks again for attending the symposium. I really appreciate your comments during the discussion as well as the questions. I hope to make the conference at your institution next year if I can manage to get travel funds.

Thanks,

Tony

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony on behalf of Schountz,Tony
Sent: Monday, April 10, 2017 12:52 PM EDT
To: Schountz,Tony
BCC:

Subject: Infectious Diseases of Bats Symposium, June 29-July 1, 2017, Fort Collins, Colorado

Dear Colleagues,

This email is the final reminder that the abstract submission deadline for the symposium is this **Friday, April 14**. The web page has been updated with the confirmed speaker list on the **Topics** page. After the abstract deadline, abstracts from those who requested talks will be evaluated by the selection committee for oral presentations. We plan to have the final selection for talks soon after and notifications sent by email. All abstracts submitted for posters will be accepted, provided they are relevant.

Early registration closes May 1 and late registration closes May 15.

http://www.batid.org

If you have any questions, please do not hesitate to contact me.

Thank you,

Tony Schountz

> On Mar 20, 2017, at 10:49 AM, Schountz,Tony wrote:
>
> Dear Colleagues,
>
> We have had several requests for an abstract submission deadline extension, thus, it has been extended two weeks to **Friday, April 14**. This is probably a fixed deadline because we will still need to select abstracts for talks, which will take a couple of weeks for the external reviewers to complete. If this is still not enough time for you, please let me know. We can add poster abstracts for a few weeks after this deadline, but after April 14 we will be unable to consider abstracts for oral presentations.
>
> Please let me know if you have any question.
>
> Thanks,
>
> Tony
>
> > On Jul 20, 2016, at 4:39 PM, Schountz,Tony wrote:
> >
> > Dear Colleagues,
> >
> > At the conclusion of the bat ID symposium in 2014, there was unanimous support for having another meeting in three years. This email is to inform you that we have begun the process of setting up the symposium for next summer. Because we nearly exceeded the capacity of the conference hall in 2014, we have secured a larger room that can accommodate up to 300 attendees, and which has better viewing and acoustics for presentations.
> >
> > We have set the dates to coincide with the end of the American Society for Virology meeting (which will be held in Madison, Wisconsin and which ends on Wednesday, June 28) to reduce the travel burden of our international colleagues who will also attend the ASV meeting. There are several non-stop flights between Madison and Denver, thus it should be relatively quick flight (about 1.5 hours).
> >
> > We will have oral and poster presentation sessions. Our tentative schedule is:
> >
> > Thursday, June 29: Social mixer with snacks and drinks, 18:00-21:00
> > Friday, June 30: Conference day 1
> > Saturday, July 1: Conference day 2
> >
> > The web page is: http://batid.org
> >
> > As with the previous meeting, we will arrange for campus housing to keep costs as low as possible. In addition, there are hotels near the venue.

Please forward this email to those who you think may be interested. A follow-up email will be sent in the fall, probably in November, with additional information. In the meanwhile, it would be helpful if you could let me know if you plan to attend (or not).

Thanks,

Tony Schountz

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony on behalf of Schountz,Tony
Sent: Saturday, April 29, 2017 7:29 PM EDT
To: Schountz,Tony
BCC:

Subject: Infectious Diseases of Bats Symposium; Presentations and Registration Deadline

Colleagues,

A list of oral and poster presentations is now available on the web site (http://www.batid.org) under the Topics tab. This list is provisional; however, we expect the times of the talks will be as listed. If you have questions or if we have made an error on your presentation please let me know. The final program will include all author affiliations and we expect to have it completed in two to three weeks.

Please also note that the registration deadline is Monday. We will keep registration open for two weeks thereafter; however, there will be an additional charge of $50 per registration.

Thanks and we look forward to seeing you in Fort Collins.

Tony

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony on behalf of Schountz,Tony
Sent: Monday, March 27, 2017 5:19 PM EDT
To: Kevin Olival, PhD ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>
Subject: Invited talks

Hi Jon and Kevin,

I hope you're still planning to attend the symposium. I am just now getting around to sending out emails to invited speakers and would like to invite each of you to give talks. If so, could you email me your provisional titles?

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Tony Schountz on behalf of Schountz,Tony >
Sent: Monday, August 24, 2020 5:50 PM EDT
To: Kevin Olival ecohealthalliance.org>
Subject: Jon?

Hi Kevin, I've sent Jon a few emails over the last couple of weeks but have not heard back from him. Is he currently unavailable?

Thanks,

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Tony Schountz on behalf of Schountz,Tony
Sent: Monday, October 19, 2020 4:27 PM EDT
To: epstein ecohealthalliance.org>
Subject: Monoclonal antibodies

Jon, I think a really important part of the grant will be to make monoclonal antibodies to various proteins (e.g., CD antigens, cytokines) and cytokines as reagents. If you agree, I'd like to approach a colleague of my, Brian Geiss, to see if he is willing to be on the grant. Recombinant protein expression is his "thing" and he would be a great asset for the grant.

I also think we should get as many letters of support that we can get. I can probably get at least 10 from people we've helped over the years (provided tissues and cells, conducted experimental infections, etc.).

Let me know what you think.

Just moved into our new building. It is really sweet. :)

Thanks,

T.

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road, Bldg T

From: Tony Schountz > on behalf of Schountz,Tony
Sent: Tuesday, March 31, 2020 12:50 PM EDT
To: epstein ecohealthalliance.org>
Subject: Multimammate rats

RML imported the Lassa virus reservoir by having them born in captivity in Africa, then the offspring were imported directly to RML. Don't know if horseshoe bats can be born in captivity, but that could be an avenue to alleviate CDC concerns.

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Tony Schountz on behalf of Schountz,Tony >
Sent: Friday, March 13, 2020 6:58 PM EDT
To: Jon Epstein ecohealthalliance.org>; Ebel,Greg ; Rudolph,Alan

Subject: NIH R24 + C06

Alan and Greg, as you know I chatted with Jon Epstein yesterday. He has had discussions with NIH about interest in having a grant submission regarding bats and SARS-CoV-2 and other coronaviruses. I think the four of us ought to have a conference call next week to see if we can make something work.

Alan, we would need to have access to a room or building large enough to house large flying foxes as well as smaller horseshoe bats. I know the barn at ARBL was once available but I suspect it no longer is?

Thanks,

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Tony Schountz on behalf of Schountz,Tony >
Sent: Tuesday, April 14, 2020 6:48 PM EDT
To: Ken Field DeeAnn Reeder wfrick
Plowright, Raina ; Rynda-Apple, Agnieszka >; epstein
ecohealthalliance.org>; Richard Yanagihara >
Subject: NSF bat immunology interest

Hi everyone,

I hope you are all safe.

I wanted to let you know about two NSF programs that have urgent deadlines (first week of May) that has bat immunology as its principal interest. The first is a RAPID for 12 months/$200k (including direct costs) and EAGER for 2 years/$300k (including direct costs). The NSF contact is Dr. Joanna Shisler My understanding is they are interested in the biology of bat immune systems relevant to coronaviruses, but because of the potential spill back issues they will also consider nonviral diseases, including white nose syndrome. I don't have other information but I'm sure Dr. Shisler will be happy to chat with you if you are interested.

If you know of others who are interested in the biology of bat immunity, please pass this email along to them.

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony
Sent: Friday, August 28, 2020 1:45 PM EDT
To: Ebel,Greg epstein ecohealthalliance.org>
Subject: R24

Greg and Jon, I think we ought to schedule a conference call in a couple of weeks to hash out the R24 approach, namely to determine the goals and to identify people who need to be involved. How does the week of Sept 7 look? We're taking the kids hiking on Labor Day but otherwise my week is mostly open except for the morning of Thursday, September 10.

Tony

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony on behalf of Schountz,Tony
Sent: Friday, November 15, 2019 1:45 PM EST
To: Kevin Olival ecohealthalliance.org>
Subject: Re: 3rd International Symposium on Infectious Diseases of Bats, 17-19 June 2020, Fort Collins, Colorado, USA

Hi Kevin,

Thanks for the heads-up. We could only book the venue after ASV (instead of before) and to help the international people save on flights, we needed to schedule it next to ASV. Hopefully, some of you from EcoHealth can make it.

I mentioned you in my virology class on Tuesday. Only good things. 😊

I hope all is well with you and yours.

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Kevin Olival ecohealthalliance.org>
Date: Thursday, November 14, 2019 at 11:17 AM
To: "Schountz,Tony"
Subject: Re: 3rd International Symposium on Infectious Diseases of Bats, 17-19 June 2020, Fort Collins, Colorado, USA

Tony, just an FYI, this overlaps (at the tail end) with the World One Health Congresshttps://onehealthplatform.com/wohc/home. May not be a big deal for most, but I think some of us were going to do the other meeting also. I haven't figured out my travel yet, but nonetheless I'll plan to come to CO so long as I can and really looking forward to this!

Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

www.ecohealthalliance.org

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

> On Nov 14, 2019, at 12:52 PM, Schountz,Tony wrote:
>
> Dear colleagues,
>
> I am pleased to announce the **3rd International Symposium on Infectious Diseases of Bats** that will be held at Colorado State University in Fort Collins, Colorado, 17 June to 19 June, 2020. The previous meetings were quite successful and led to several new collaborations amongst participants. We hope we can continue to foster interactions and additional collaborations between groups. Please forward this email to colleagues and students that may be interested in the symposium.
>
> We are currently finalizing details of the symposium but I wanted to send this email so that you can add the dates to your calendar if you are interested in attending. The American Society for Virology Annual Conference will also be hosted at CSU in 2020 and it ends on Wednesday, June 17 at noon. Thus, the Bat ID Symposium will follow with a reception on the evening of June 17th and two days of talks and posters on the 18th and 19th. As with previous meetings, we will end each day with an open discussion about bats and their infectious agents.
>
> Should you have questions, please do not hesitate to contact me.

We look forward to hosting you next summer.

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Tony Schountz on behalf of Schountz,Tony
Sent: Wednesday, February 26, 2020 2:23 PM EST
To: zlshi
Subject: Re: 3rd International Symposium on Infectious Diseases of Bats, 17-19 June 2020, Fort Collins, Colorado, USA

Dear Zhengli,

I understand your frustration. There are a lot of crazy people that have no idea what they are talking about and who just want to cause trouble. We will be disappointed that you cannot make it to provide valuable insight into the virus; however, should you change your mind I will keep my offer open and ensure you can give a talk.

Thank you,

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Feb 24, 2020, at 10:38 PM, zlshi wrote:

Dear Tony,

I'm sorry to let you know that I'll not be able to particiapte in the ASV meeting and the bat meeting due to the safety issue. I need to calm down myself and get recovered from the rumors of the public.

Best regards,
Zhengli,

SHI Zhengli, Ph. D
Senior Scientist & Professor
Wuhan Institute of Virology, Chinese Academy of Sciences
44 Xiao Hong Shan
430071 Wuhan, Hubei
China

From: Schountz,Tony
Date: 2020-02-20 07:09
To: Schountz,Tony
Subject: 3rd International Symposium on Infectious Diseases of Bats, 17-19 June 2020, Fort Collins, Colorado, USA

Dear Colleagues,

Registration is now open for the 3rd International Symposium on Infectious Diseases of Bats. With the emergence of yet another pathogenic coronavirus, we are planning to have an extended session to learn from one another about this new virus and I hope some of you can foster collaborative interactions while you are here. The URL for the meeting is:

http://www.batid.org

Please note a few important dates. **Abstract submission closes on April 17, 2020**. The format of the abstract is indicated on the web site and we ask that you follow it for purposes of continuity in the program. In addition, please send MS Word, Apple Pages or Rich Text files so that we can rapidly build the program. Please DO NOT send a PDF because they are much more difficult to integrate into the program. After you submit your abstract, you should receive a confirmation email. If you do not, please let me know and I'll resolve the issue.

Registration will close on May 1, 2020. Registration will be handled by the Colorado State University Conference

Services with a direct link on the Bat ID web site. You can select registration only, or registration with dormitory housing on campus near the conference venue (Lory Student Center). Registration included breakfast for the two days, and the dormitory includes breakfast, too. If you prefer to stay in a hotel, the Fort Collins Hilton (on Prospect Avenue) and the Best Western University Inn are walking distance to campus. Links to these hotels are provided on the Registration page.

We also have the pleasure of hosting **This Week in Virology**. Vincent and crew will record an episode from the meeting.

Please let me know if you have questions or comments.

Thanks very much, and we are looking forward to seeing you again in Fort Collins.

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Nov 14, 2019, at 10:52 AM, Schountz,Tony wrote:

Dear colleagues,

I am pleased to announce the **3rd International Symposium on Infectious Diseases of Bats** that will be held at Colorado State University in Fort Collins, Colorado, 17 June to 19 June, 2020. The previous meetings were quite successful and led to several new collaborations amongst participants. We hope we can continue to foster interactions and additional collaborations between groups. Please forward this email to colleagues and students that may be interested in the symposium.

We are currently finalizing details of the symposium but I wanted to send this email so that you can add the dates to your calendar if you are interested in attending. The American Society for Virology Annual Conference will also be hosted at CSU in 2020 and it ends on Wednesday, June 17 at noon. Thus, the Bat ID Symposium will follow with a reception on the evening of June 17th and two days of talks and posters on the 18th and 19th. As with previous meetings, we will end each day with an open discussion about bats and their infectious agents.

Should you have questions, please do not hesitate to contact me.

We look forward to hosting you next summer.

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony
Sent: Friday, June 23, 2017 4:31 PM EDT
To: Kevin Olival, PhD ecohealthalliance.org>
Subject: Re: Abstracts

Got it, thanks Kevin.

T.

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Kevin Olival, PhD ecohealthalliance.org>
Sent: Friday, June 23, 2017 11:26 AM
To: Schountz,Tony
Subject: Re: Abstracts

Tony,

Abstract attached! Sorry for the delay.

From: Schountz,Tony on behalf of Schountz,Tony >
Sent: Wednesday, June 21, 2017 10:59 AM EDT
To: Kevin Olival, PhD ecohealthalliance.org>
CC: Jon Epstein ecohealthalliance.org>
BCC: Schountz,Tony >
Subject: Re: Abstracts

Yup tomorrow's fine. Program gets printed on Friday.

Thanks

Tony

Sent from my iPhone

On Jun 21, 2017, at 7:26 AM, Kevin Olival, PhD ecohealthalliance.org> wrote:

> Pretty sure I never wrote one! Just title. Can get it to you tomorrow if that's ok!
>
> On Jun 21, 2017, at 10:24 AM, Schountz,Tony wrote:
>
> > Hi Jon and Kevin,
> >
> > I don't seem to have abstracts for your bat ID talks. Could you (re)send them directly to me today or tomorrow?
> >
> > Thanks
> >
> > Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony < > on behalf of Schountz,Tony
Sent: Monday, October 01, 2018 7:18 PM EDT
To: 胡犇 <huben >
Subject: Re: Agenda of the 8th International Symposium of Emerging Viral Diseases

Hi Ben,

My arrival is flight NH 937 (Air Japan), Friday, Oct 19 at 10:00 PM.

My departure is flight NH 938, Tuesday, October 23 at 9:35 AM.

My CV is quite lengthy. Do you want me to send an abbreviated version?

Thank you,

Tony

> On Sep 28, 2018, at 9:17 PM, 胡犇 <huben > wrote:
>
> Dear speaker:
>
> We have made the program for our emerging virus symposium. Your presentation is scheduled in the afternoon of 21st October, in the session "emerging viral pathogens".
>
> I have attached the program for your information.
>
> We have reserved accommodation for you at the conference venue, Optic Valley Plaza hotel. Please provide me your flight information once it is available, and we will arrange pick-up service at the airport.
>
> Also, please send me your update CV by 7th October, as we would like to include the CV of our speakers together with the abstracts in the conference proceedings.
>
> Thank you!
>
> Best wishes
>
> Ben Hu Ph.D
>
> Wuhan Institute of Virology, CAS
> Secretary of the 8th ISEVD
> <Program of the 8th ISEVD.pdf>

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony on behalf of Schountz,Tony
Sent: Monday, October 01, 2018 7:45 PM EDT
To: 胡犇 <huben >
Subject: Re: Agenda of the 8th International Symposium of Emerging Viral Diseases
Attachment(s): "Schountz CV for Wuhan.docx"

OK, here's a 4 page version. Please feel free to cut it down as you see fit.

Thanks for all your help, Ben. It is greatly appreciated!

Tony

> On Oct 1, 2018, at 5:36 PM, 胡犇 <huben > wrote:
>
> Dear Dr. Schountz:
>
> I only need a short version.
>
> Thanks.
>
> Ben
>
> -----原始邮件-----
> **发件人:**"Schountz,Tony" >
> **发送时间:**2018-10-02 07:18:52 (星期二)
> **收件人:** "胡犇" <huben
> **抄送:**
> **主题:** Re: Agenda of the 8th International Symposium of Emerging Viral Diseases
>
> Hi Ben,
>
> My arrival is flight NH 937 (Air Japan), Friday, Oct 19 at 10:00 PM.
>
> My departure is flight NH 938, Tuesday, October 23 at 9:35 AM.
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> > On Sep 28, 2018, at 9:17 PM, 胡犇 <huben > wrote:
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> > We have made the program for our emerging virus symposium. Your presentation is scheduled in the afternoon of 21st October, in the session "emerging viral pathogens".
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> >
> > Thank you!
> >
> > Best wishes
> >
> > Ben Hu Ph.D

> Wuhan Institute of Virology, CAS
> Secretary of the 8th ISEVD
> <Program of the 8th ISEVD.pdf>

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

William A. "Tony" Schountz

EDUCATION

1996 Ph.D. Microbiology, Kansas State University
1992 M.S., Microbiology, Emporia State University (Kansas)
1986 B.S. Biology, Newman University (Kansas)

ACADEMIC POSITIONS

2013-Present	Associate Professor, Arthropod-borne and Infectious Diseases Laboratory, Department of Microbiology, Immunology and Pathology, Colorado State University
2008-2013	Associate Professor (Tenured 2009), Department of Biological Sciences, University of Northern Colorado, Greeley, CO
2005-2008	Assistant Professor, Department of Biological Sciences, University of Northern Colorado, Greeley, CO
2003-2005	Associate Professor (Tenured 2003), Department of Biology, Mesa State College, Grand Junction, CO
1998-2003	Assistant Professor, Department of Biology, Mesa State College, Grand Junction, CO
1996-1998	Post-Doctoral Fellow, Department of Biomedical Sciences, Oak Ridge National Laboratory/University of Tennessee, Oak Ridge, TN

PUBLISHED WORKS

Refereed Journal Articles:

1. Campbell CL, Phillips AT, Rico A, McGuire A, Aboellail TA, Quackenbush S, Olson KE, **Schountz T**. Involvement of Pro-Inflammatory Macrophages in Liver Pathology of Pirital Virus-Infected Syrian Hamsters. Viruses. 2018 May 2;10(5). pii: E232. doi: 10.3390/v10050232. PubMed PMID: 29724035.
2. Milholland MT, Castro-Arellano I, Arellano E, Nava-García E, Rangel-Altamirano G, Gonzalez-Cozatl FX, Suzán G, **Schountz T**, González-Padrón S, Vigueras A, Rubio AV, Maikis TJ, Westrich BJ, Martinez JA, Esteve-Gassent MD, Torres M, Rodriguez-Ruiz ER, Hahn D, Lacher TE. Species Identity Supersedes the Dilution Effect Concerning Hantavirus Prevalence at Sites across Texas and México. ILAR J. 2017 Dec 15;58(3):401-412. doi: 10.1093/ilar/ily001. PubMed PMID: 29635404.
3. Banerjee A, Misra V, **Schountz T**, Baker ML. Tools to study pathogen-host interactions in bats. Virus Res. 2018 Mar 15;248:5-12. doi: 10.1016/j.virusres.2018.02.013. Epub 2018 Feb 15. Review. PubMed PMID: 29454637.
4. Gerrard DL, Hawkinson A, Sherman T, Modahl CM, Hume G, Campbell CL, **Schountz T**, Frietze S. Transcriptomic Signatures of Tacaribe Virus-Infected Jamaican Fruit Bats. mSphere. 2017 Sep 27;2(5). pii: e00245-17. doi: 10.1128/mSphere.00245-17. eCollection 2017 Sep-Oct. PubMed PMID: 28959737; PubMed Central PMCID: PMC5615131.
5. **Schountz T**, Baker ML, Butler J, Munster V. Immunological Control of Viral Infections in Bats and the Emergence of Viruses Highly Pathogenic to Humans. Front Immunol. 2017 Sep 11;8:1098. doi: 10.3389/fimmu.2017.01098. eCollection 2017. PubMed PMID: 28959255; PubMed Central PMCID: PMC5604070.
6. Malmlov A, Seetahal J, Carrington C, Ramkisson V, Foster J, Miazgowicz KL, Quackenbush S, Rovnak J, Negrete O, Munster V, **Schountz T**. Serological evidence of arenavirus circulation among fruit bats in Trinidad. PLoS One. 2017 Sep 27;12(9):e0185308. doi:

10.1371/journal.pone.0185308. eCollection 2017. PubMed PMID: 28953976; PubMed Central PMCID: PMC5617188.
7. Woo PCY, Lau SKP, Teng JLL, Cao KY, Wernery U, **Schountz T**, Chiu TH, Tsang AKL, Wong PC, Wong, EYM, Yuen KY. A novel hepatitis E virus in Bactrian camels and seroepidemiology of hepatitis E virus in dromedary and Bactrian camels in the Middle East, USA, Australia and Xinjiang. Emerg Infec Dis. 2016. 22:2219. PubMed PMID: 27869607.
8. Rico AB, Phillips AT, **Schountz T**, Jarvis DL, Tjalkens RB, Powers AM, Olson KE. Venezuelan and western equine encephalitis virus E1 liposome antigen nucleic acid complexes protect mice from lethal challenge with multiple alphaviruses. Virology. 2016 Dec;499:30-39. doi: 10.1016/j.virol.2016.08.023. PubMed PMID: 27632563.
9. Kading RC, **Schountz T**. Flavivirus Infections of Bats: Potential Role in Zika Virus Ecology. Am J Trop Med Hyg. 2016 Nov 2;95(5):993-996. Review. PubMed PMID: 27645783; PubMed Central PMCID: PMC5094249.
10. McGuire A, Miedema K, Fauver JR, Rico A, Aboellail T, Quackenbush SL, Hawkinson A, **Schountz T**. Maporal Hantavirus Causes Mild Pathology in Deer Mice (*Peromyscus maniculatus*). Viruses. 2016 Oct 18;8(10). pii: E286. PubMed PMID: 27763552; PubMed Central PMCID: PMC5086618.
11. Miller MR, McMinn RJ, Misra V, **Schountz T**, Müller MA, Kurth A, Munster VJ. Broad and Temperature Independent Replication Potential of Filoviruses on Cells Derived from Old and New World Bat Species. J Infect Dis. 2016 Oct 15;214(suppl 3):S297-S302. PubMed PMID: 27354372; PubMed Central PMCID: PMC5050464.
12. Munster VJ, Adney DR, van Doremalen N, Brown VR, Miazgowicz KL, Milne-Price S, Bushmaker T, Rosenke R, Scott D, Hawkinson A, de Wit E, **Schountz T**, Bowen RA. Replication and shedding of MERS-CoV in Jamaican fruit bats (*Artibeus jamaicensis*). Sci Rep. 2016 Feb 22;6:21878. doi: 10.1038/srep21878. PubMed PMID: 26899616; PubMed Central PMCID: PMC4761889.
13. Rubio A, Vigueras-Galvána AL, **Schountz T**, Moreno-Torres K, List R, Sarmiento-Silva RE , Ávila-Flores R, Suzán G. Abundance of hantavirus hosts in a landscape with black-tailed prairie dog colonies in northwestern Mexico. Mammalian Biology. 2015. 80:491.
14. Campbell CL, Torres-Perez F, Acuna-Retamar M, **Schountz T**. Transcriptome markers of viral persistence in naturally-infected Andes virus (*Bunyaviridae*) seropositive long-tailed pygmy rice rats. PLoS One. 2015 Apr 9;10(4):e0122935. doi: 10.1371/journal.pone.0122935. eCollection 2015. PMID: 25856432.
15. **Schountz T**. Immunology of Bats and Their Viruses: Challenges and Opportunities. Viruses. 2014 Dec 8;6(12):4880-4901. PubMed PMID: 25494448.
16. **Schountz T**, Quackenbush S, Rovnak J, Haddock E, Black WC 4th, Feldmann H, Prescott J. Differential lymphocyte and antibody responses in deer mice infected with Sin Nombre hantavirus or Andes hantavirus. J Virol. 2014 Aug;88(15):8319-31. PubMed PMID: 24829335.
17. Cautivo K, **Schountz T**, Acuña-Retamar M, Ferrés M, Torres-Pérez F. Rapid enzyme-linked immunosorbent assay for the detection of hantavirus-specific antibodies in divergent small mammals. Viruses. 2014 May 6;6(5):2028-37. PubMed PMID: 24806874.
18. **Schountz T**, Prescott J. Hantavirus immunology of rodent reservoirs: current status and future directions. Viruses. 2014 Mar 14;6(3):1317-35.
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From: Schountz,Tony on behalf of Schountz,Tony
Sent: Thursday, February 07, 2019 2:03 PM EST
To: Jon Epstein ecohealthalliance.org>
Subject: Re: Bat conference advisory committee

Thanks, Jon, I appreciate your support.

I hope all is well, wherever you might be at the moment!

Tony

On Feb 4, 2019, at 2:00 PM, Jon Epstein ecohealthalliance.org> wrote:

Tony,
Glad to hear this is happening again. I'm happy to help out.
Cheers,
Jon

On Mon, Feb 4, 2019 at 3:57 PM Schountz,Tony wrote:

> Dear colleagues,
>
> We're planning to host the third international bat infectious disease symposium June 18-20, 2020 here in Fort Collins. This coincides with the end of the 2020 ASV meeting that will also be in Fort Collins and which ends on June 17. I will submit an R13 proposal (Conference Support) to NIH in April to get a few thousand dollars to help with student travel awards for the conference. I hope you don't mind, but I would like to list each of you as members of the advisory committee. Probably not too much for you to do, but it will be helpful for the submission. Is that OK? If you plan to attend the bat symposium, I will waive your registration fee.
>
> Thanks,
>
> Tony
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street, Ste. 1701

New York, NY 10001

)

web: ecohealthalliance.org

From: Schountz,Tony on behalf of Schountz,Tony >
Sent: Thursday, February 07, 2019 1:54 PM EST
To: 石正丽 <zlshi
Subject: Re: Bat conference advisory committee

Zhengli, thanks very much for helping us. I will keep you posted on any updates.

Tony

> On Feb 4, 2019, at 11:48 PM, 石正丽 <zlshi wrote:
>
> Dear Tony,
>
> Thank you very much for your planning the meeting. I'll be happy to be the committee member and help it out.
>
> Best regards,
> Zhengli,
>
> -----原始邮件-----
> **发件人:**"Schountz,Tony"
> **发送时间:**2019-02-05 04:57:32 (星期二)
> **收件人:** "Christian Drosten" "Wang Linfa" , "Michelle Baker" >, "Susanna Lau" < "Patrick Woo" , "Martin Schwemmle" >, "Richard Yanagihara" >, "Jon Epstein" ecohealthalliance.org>, "石正丽" <zlshi >
> **抄送:**
> **主题:** Bat conference advisory committee
>
> Dear colleagues,
>
> We're planning to host the third international bat infectious disease symposium June 18-20, 2020 here in Fort Collins. This coincides with the end of the 2020 ASV meeting that will also be in Fort Collins and which ends on June 17. I will submit an R13 proposal (Conference Support) to NIH in April to get a few thousand dollars to help with student travel awards for the conference. I hope you don't mind, but I would like to list each of you as members of the advisory committee. Probably not too much for you to do, but it will be helpful for the submission. Is that OK? If you plan to attend the bat symposium, I will waive your registration fee.
>
> Thanks,
>
> Tony
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony on behalf of Schountz,Tony >
Sent: Thursday, April 27, 2017 1:00 PM EDT
To: Schountz,Tony
CC: huben
Subject: Re: Bat ID Abstract Submission

Dear Ben,

Your abstract submission has been accepted for a **POSTER** presentation. The session is **Friday, April 30 from 12:00 to 2:00 PM** in the University Center for the Arts. The maximum size of your poster **should not exceed 122 cm/48 inches height and width**. We will provide push pins for mounting your poster on the easel. If you have questions, please feel free to contact me.

Thank you and we look forward to your presentation.

Tony Schountz

On Apr 1, 2017, at 7:20 PM, Tony Schountz wrote:

Thank you for submitting an abstract to the Bat ID Symposium. A decision on its disposition will be made in May.

Bat ID Abstract Submission

Presenting author email address *	
Presentation Type *	Poster Presentation
Please choose ONE or TWO categories for your abstract *	• Coronaviruses
Title *	Genomic characterization of diverse BatCoV HKU10 and three novel alphacoronaviruses
Authors *	Wang N, Luo CM, Yang XL, Liu HZ, Zhang W, Li B, Ge XY, Hu B, Zhu Y, Peng C, Shi ZL
Institutions *	Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan 430071, China.
Upload your abstract *	us_bat_conference_ben_hu_poster.docx 17.15 KB · DOCX

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony on behalf of Schountz,Tony
Sent: Wednesday, April 26, 2017 6:24 PM EDT
To: Schountz,Tony
CC: peng.zhou
Subject: Re: Bat ID Abstract Submission

Dear Peng,

We have you scheduled to give a 15 min talk (12 minutes plus 3 minutes for questions) at the bat infectious diseases symposium, probably Saturday afternoon, July 1. I should have the program draft up next week.

I look forward to finally meeting you in person!

Thanks,

Tony

On Mar 7, 2017, at 5:05 AM, Tony Schountz wrote:

Thank you for submitting an abstract to the Bat ID Symposium. A decision on its disposition will be made in May.

Bat ID Abstract Submission

Presenting author email address *	
*	Oral Presentation
Please choose ONE or TWO categories for your abstract *	• Immunology
Title *	Dampening of STING-dependent IFN production: an implication of virus tolerance in bats?
Authors *	Xie J, Ma C, Li Y, Cui J, Wang L-F, Shi Z, Zhou P*
Institutions *	Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan 430071, China; Emerging Infectious programme, Singapore Duke-NUD Medical School, Singapore 169857, Singapore
Upload your abstract *	us_bat_conference_peng_zhou_oral1.docx 14.40 KB · DOCX

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony > on behalf of Schountz,Tony >
Sent: Thursday, April 27, 2017 12:49 PM EDT
To: Schountz,Tony
CC: yangxl
Subject: Re: Bat ID Abstract Submission

Dear Xing-Lou,

Your abstract submission has been accepted for a **POSTER** presentation. The session is **Friday, April 30 from 12:00 to 2:00 PM** in the University Center for the Arts. The maximum size of your poster **should not exceed 122 cm/48 inches height and width**. We will provide push pins for mounting your poster on the easel. If you have questions, please feel free to contact me.

Thank you and we look forward to your presentation.

Tony Schountz

On Apr 1, 2017, at 1:51 AM, Tony Schountz > wrote:

Thank you for submitting an abstract to the Bat ID Symposium. A decision on its disposition will be made in May.

Bat ID Abstract Submission

Presenting author email address *	
Presentation Type *	Poster Presentation
Please choose ONE or TWO categories for your abstract *	• Filoviruses
Title *	Genetically Diverse Filoviruses in Rousettus and Eonycteris spp. Bats, China, 2009 and 2015
Authors *	Xing-Lou Yang, Yun-Zhi Zhang, Ren-Di Jiang, Hua Guo, Wei Zhang, Bei-Li, Ning Wang, Li-Wang, Cecilia Waruhiu, Ji-Hua Zhou, Shi-Yue Li, Peter Daszak, Lin-Fa Wang, Zheng-Li Shi
Institutions *	Wuhan Institute of Virology, Chinese Academy of Sciences
Upload your abstract *	abstract_for_bat_virus_meeting.docx 19.29 KB · DOCX

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony > on behalf of Schountz,Tony
Sent: Wednesday, April 26, 2017 6:05 PM EDT
To: Schountz,Tony
CC: zlshi
Subject: Re: Bat ID Abstract Submission

Dear Dr. Shi,

We have you scheduled to give a 15 min talk (12 minutes plus 3 minutes for questions) at the bat infectious diseases symposium, probably Friday morning, June 30. I should have the program draft up next week.

Thanks,

Tony

On Mar 29, 2017, at 7:37 AM, Tony Schountz wrote:

Thank you for submitting an abstract to the Bat ID Symposium. A decision on its disposition will be made in May.

Bat ID Abstract Submission

Presenting author email address *	
Presentation Type *	Oral Presentation
Please choose ONE or TWO categories for your abstract *	• Coronaviruses
Title *	SARS coronavirus may have originated from frequent recombination events between SARS-like coronaviruses in a single horseshoe bat habitat
Authors *	Hu B, Zeng L-P, Yang X-L, Ge X-Y, Zhang W, Li B, Luo D-S, Zhang Y-Z, Wang M-N, Daszak P, Wang L-F, Cui J, Shi Z-L.
Institutions *	CAS Key Laboratory of Special Pathogens and Biosafety, Center for Emerging Infectious Diseases of Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China; Yunnan Institute of Endemic Diseases Control and Prevention, Dali, China; EcoHealth Alliance, New York, New York, USA; Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore
Upload your abstract *	us_bat_conference_zhengli_shi_oral.docx 16.38 KB · DOCX

—
Tony Schountz, PhD
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College of Veterinary Medicine
Colorado State University

From: Tony Schountz < on behalf of Schountz,Tony
Sent: Saturday, February 01, 2020 1:04 PM EST
To: zlshi 周鹏 <peng.zhou
CC: Schountz,Tony
Subject: Re: Bat ID conference

Dear Zhengli,

If there is anything I can do to help you with your travels, please let me know. I can prepare a letter of invitation for you if you need it.

Peng, I'm sorry you cannot make it. I was looking forward to visiting with you about bat immunology. We have tried many ways of making bone marrow dendritic cells and macrophages but with little success. We have tried adapting mouse protocols with artibeus bat cytokine orthologs but the do not work as well with the bats as they do with mice. I am beginning to think the developmental pathways of bats and mice are substantially different.

I am sure all of you are overwhelmed with the coronavirus outbreak. I really hope it subsides soon because it has been really terrible for China.

Be safe.

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Jan 30, 2020, at 9:24 PM, zlshi wrote:

Dear Tony,

I plan to participate in the ASV meeting and the Bat meeting. In view the current situation, I'm not sure if I can get permission to travel and the Visa as well.

Best regards,
Zhengli,

SHI Zhengli, Ph. D
Senior Scientist & Professor
Wuhan Institute of Virology, Chinese Academy of Sciences
44 Xiao Hong Shan
430071 Wuhan, Hubei
China

From: Schountz,Tony
Date: 2020-01-31 04:46
To: 周鹏; 石正丽
Subject: Bat ID conference

Dear Zhengli and Peng,

I was wondering if you will be attending the bat meeting after ASV. (I realize some of you may be at the Paris meeting instead.) If so, I'd like to list you as confirmed speakers. I'm awaiting a small grant decision from my university that would be used to waive your registration fee if you are a confirmed speaker. The decision is supposed to be made in the next week or two, so I won't be able to let you know for sure until then. I understand you are quite busy with the new coronavirus and that there may be travel issues, but if it is possible for you to make it, I would be most grateful.

Thank you,

Tony

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Tony Schountz < on behalf of Schountz,Tony >
Sent: Thursday, January 30, 2020 4:25 PM EST
To: Kevin Olival ecohealthalliance.org>
CC: Schountz,Tony Peter Daszak ecohealthalliance.org>; Jon Epstein ecohealthalliance.org>
Subject: Re: Bat ID meeting

Right, Edinburgh. Somehow, I had in my mind it was the EEID meeting in Paris.

We will be sorry to miss your group here, it's always brought good science and information to the symposium.

Let me know if things change and we'll get you in.

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

> On Jan 30, 2020, at 2:03 PM, Kevin Olival ecohealthalliance.org> wrote:
>
> Tony, I'm in the same spot right now too. Likely need to go to the Edinburgh meeting, but still waiting on things to shake down a bit.
>
> Sorry couldn't be more positive. Will let you know early next week if anything changes.
>
> Cheers,
> Kevin
>
> > On Jan 30, 2020, at 3:52 PM, Jon Epstein ecohealthalliance.org> wrote:
> >
> > Tony,
> > I was really hoping to come, but we have the One Health meeting in Edinburgh at the same time, and there are some side meetings there associated with current projects we're on, which is a bummer.
> > I'll let you know if things change, but as of now, at least for me, I'm not going to be able to get to Colorado.
> >
> > Cheers,
> > Jon
> >
> > On Thu, Jan 30, 2020 at 3:36 PM Schountz,Tony > wrote:
> > > Hi Peter, Jon and Kevin,
> > >
> > > I was wondering if you will be at the bat meeting after ASV. (I realize some of you may be at the Paris meeting instead.) If so, I'd like to list you as confirmed speakers. I'm awaiting a small grant decision from my university that would be used to waive your registration fee if you are a confirmed speaker. The decision is supposed to be made in the next week or two, so I won't be able to let you know for sure until then.
> > >
> > > We also have a commitment from Vincent Racaniello to have a TWiV podcast from the meeting. □
> > > □
> > >
> > > Thanks,
> > >
> > > Tony
> > > —
> > > Tony Schountz, PhD
> > > Associate Professor
> > > Arthropod-borne and Infectious Disease Laboratory
> > > Department of Microbiology, Immunology and Pathology

From: Schountz,Tony on behalf of Schountz,Tony >
Sent: Wednesday, June 14, 2017 2:06 PM EDT
To: Jon Epstein ecohealthalliance.org>
BCC: Schountz,Tony
Subject: Re: bat meeting

Hi Jon

The Hilton on Prospect is only half a mile from the meeting. Theres also the University Inn Best Western on College Ave that is about a quarter of a mile.

See you in a couple of weeks.

Tony

Sent from my iPhone

On Jun 14, 2017, at 10:35 AM, Jon Epstein ecohealthalliance.org> wrote:

> Tony,
> Should I book in at the Hilton for the bat meeting? Or is there a more convenient hotel?
> -Jon
>
> --
>
> **Jonathan H. Epstein DVM, MPH, PhD**
>
> *Vice President for Science and Outreach*
>
> EcoHealth Alliance
> 460 West 34th Street – 17th floor
> New York, NY 10001
>
> web: ecohealthalliance.org
>
> -
>
>

From: Schountz,Tony > on behalf of Schountz,Tony >
Sent: Tuesday, December 04, 2018 2:53 PM EST
To: Kevin Olival ecohealthalliance.org>
CC: Schountz,Tony >; Munster, Vincent (NIH/NIAID) [E] Laing, Eric >; Chris Broder ; Luke Hamel

Subject: Re: Bat MERS-CoV sera for S protein luminex-based assay R&D

Hi Kevin,

How much serum (volume) do you need? We have just finished an infection experiment with our Aj bats but we have not done the serology, yet.

Tony

On Dec 4, 2018, at 12:25 PM, Kevin Olival ecohealthalliance.org> wrote:

Dear Tony and Vincent,

Hope this finds you both well! I know Vincent is in the Congo, so his responses are delayed.

I'm working on a grant proposal (GHERI) with Chris Border and Eric Laing to do some serological screening and assay development for MERS-CoV and other CoVs using a Luminex-based platform. This builds off the work Broder and crew have already done, but will provide support for additional R&D for the MERS-CoV Spike assay, and for in-country capacity building and testing. The idea is to then use the multiplex CoV assays to screen bat sera that we are currently collecting under a DTRA supported project across Western Asia/Middle East (which I'm PI on, and Vincent is involved with).

In order to validate the MERS-CoV assay during the R&D phase,**it would be super helpful to have some confirmed MERS-CoV positive bat sera to work with**. Given that you guys have run MERS-CoV bat infection trials (and may be doing more?), I'm wondering what the possibility of getting some positive bat sera over to Chris' lab for validation? Also, in reading your paper again I remembered that you observed limited seroconversion in bats at 28 dpi… so maybe this is a moot question? Any additional evidence that supports seroconversion in bats?

The grant is due in a couple of weeks, so at this stage I'm just really looking for a general response if you think this is feasible, so we can throw a line in the proposal. i.e. "In collaboration with Vincent Munster (NIH) and Tony Schountz (CSU) we will validate our MERS S protein assay using positive control bat sera from previous experimental infection studies".

Please let me know your thoughts or any additional ideas.

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

www.ecohealthalliance.org

From: Schountz,Tony
Sent: Saturday, August 12, 2017 10:39 AM EDT
To: Jon Epstein cohealthalliance.org>
Subject: Re: Bat proposal

Jon, did you hear back from either of them? Did Dick ever respond to you?

T.

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Jon Epstein ecohealthalliance.org>
Sent: Thursday, August 3, 2017 3:42 PM
To: Patricia (NIH/NIAID) Repik [E]; Park, Eun-Chung (NIH/NIAID) [E]
Cc: Schountz,Tony; Munster, Vincent; R. A. Bowen
Subject: Bat proposal

Dear Pat and Eun Chung,
It was wonderful to see you in Ft. Collins. I'm grateful that we had time to talk about this project and for your interest and support. Attached are two briefs which detail the scope of work and scientific rationale for setting up the Pteropus colony. Let's use this as a starting point for further discussion about a potential contract. I'd be happy to provide additional information as per your guidance.

Cheers,
Jon

--
Jonathan H. Epstein DVM, MPH, PhD
Vice President for Science and Outreach
EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

web: ecohealthalliance.org

From: Schountz,Tony
Sent: Friday, May 19, 2017 10:08 AM EDT
To: Jon Epstein ecohealthalliance.org>
CC: Munster, Vincent
Subject: Re: Bat tissue

No, I didn't get anything, Jon. Frozen tissues? Too bad we couldn't get live bone marrow and spleen.

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Jon Epstein ecohealthalliance.org>
Sent: Friday, May 19, 2017 7:48 AM
To: Schountz,Tony
Cc: Munster, Vincent
Subject: Bat tissue

Tony,
I just heard that Lubee's P. giganteus recently died and I think they've harvested tissue. Were you aware? Did you get any samples?
-Jon

From: Tony Schountz > on behalf of Schountz,Tony >
Sent: Wednesday, May 20, 2020 4:20 PM EDT
To: Ebel,Greg >
CC: epstein ecohealthalliance.org>; Schountz,Tony
Subject: Re: C06 check in

Yes, that works for me, too.

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On May 20, 2020, at 11:50 AM, Ebel,Greg > wrote:

Tony and Jon,

See below. I can do Thursday, May 28th at 4:00 EST (2:00 mountain). Can you please rearrange your schedules to accommodate this call? Let' hope for some good news.

Greg

From: Patterson, Jean (NIH/NIAID) [E] >
Sent: Wednesday, May 20, 2020 11:38 AM
To: Ebel,Greg >
Subject: RE: C06 check in

Morning, Greg. Why don't we try to get on a call with you all next week? Mark and I are available Wed. May 27th: 2-3:30pm, Thurs. May 28th: after 3pm, and Fri. May 29th: 10-11am or after 4pm – all EST. If you don't mind, please coordinate with related folks on your end, (especially Jon Epstein) and send us an invite. We will accept.
Thanks and look forward to talking with you again!
Jean

From: Ebel,Greg >
Sent: Thursday, May 14, 2020 2:29 PM
To: Patterson, Jean (NIH/NIAID) [E] >
Subject: RE: C06 check in

OK thanks a lot, Jean.

Hang in there!

Greg

From: Patterson, Jean (NIH/NIAID) [E]
Sent: Thursday, May 14, 2020 12:24 PM
To: Ebel,Greg
Subject: RE: C06 check in

Hi Greg,
We are all hanging in here, just working! Hope you are doing well too.
I don't have confirmation yet as to whether the C06 will get picked up. I will say that Mark and I have been thinking of a Plan B just in case and at some point soon plan to set up a call with you all to discuss further.
Sorry I don't have better news, but will explain when we get on a call.
Be in touch!
Jean

From: Ebel,Greg <
Sent: Thursday, May 14, 2020 1:25 PM
To: Patterson, Jean (NIH/NIAID) [E]

Subject: C06 check in

Hi Jean,

Just wanting to check in on the C06 progress.

Hope things are going well for you and that you’re staying safe.

Greg Ebel

From: Tony Schountz > on behalf of Schountz,Tony
Sent: Wednesday, May 27, 2020 1:20 PM EDT
To: epstein ecohealthalliance.org>
Subject: Re: Call?

OK, I'll give you a call after 6 PM your time.

Thanks,

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On May 27, 2020, at 10:59 AM, Jon Epstein cohealthalliance.org> wrote:

Yes, but after 6pm

Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
New York

On Wed, May 27, 2020, 12:56 PM Schountz,Tony wrote:

> Jon, do you have time for a call later today? only need about 10 minutes.
>
> Thanks,
>
> T.
>
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

From: Tony Schountz > on behalf of Schountz,Tony >
Sent: Tuesday, March 24, 2020 10:17 AM EDT
To: Kevin Olival ecohealthalliance.org>
Subject: Re: Cancelation of the 3rd International Symposium on Infectious Diseases of Bats

Yeah, we'll probably have 5 sessions on coronaviruses at the next symposium!

Good news on bat colony front, though.

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Mar 18, 2020, at 6:56 AM, Kevin Olival ecohealthalliance.org> wrote:

Damn emerging bat CoV messing everything up!

-Kevin

On Mar 17, 2020, at 3:44 PM, Schountz,Tony wrote:

Dear Colleagues,

As you may have expected, due to the COVID-19 outbreak, the*3rd International Symposium on Infectious Diseases of Bats* has been canceled. We are considering hosting the meeting in the summer of 2021 if the resources are available to do so. If so, I will send another email this fall altering you.

For those of you who have already paid your registration, you will receive a full refund from the Colorado State University Conference Services. I have been told this can take about a month, so if you have not received a refund by April 20, please email me and I will contact Conference Services.

Thank you for your understanding.

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Feb 19, 2020, at 4:09 PM, Schountz,Tony wrote:

Dear Colleagues,

Registration is now open for the 3rd International Symposium on Infectious Diseases of Bats. With the emergence of yet another pathogenic coronavirus, we are planning to have an extended session to learn from one another about this new virus and I hope some of you can foster collaborative interactions while you are here. The URL for the meeting is:

http://www.batid.org

Please note a few important dates. **Abstract submission closes on April 17, 2020**. The format of the abstract is indicated on the web site and we ask that you follow it for purposes of continuity in the program. In addition, please send MS Word, Apple Pages or Rich Text files so that we can rapidly build the program. Please DO NOT send a PDF because they are much more difficult to integrate into the program. After you submit your abstract, you should receive a confirmation email. If you do not, please let me know and I'll resolve the issue.

Registration will close on May 1, 2020. Registration will be handled by the Colorado State University Conference Services with a direct link on the Bat ID web site. You can select registration only, or registration with dormitory housing on campus near the conference venue (Lory Student Center). Registration included breakfast for the two days, and the dormitory includes breakfast, too. If you prefer to stay in a hotel, the Fort Collins Hilton (on Prospect Avenue) and the Best Western University Inn are walking distance to campus. Links to these hotels are provided on the Registration page.

We also have the pleasure of hosting**This Week in Virology**. Vincent and crew will record an episode from the meeting.

Please let me know if you have questions or comments.

Thanks very much, and we are looking forward to seeing you again in Fort Collins.

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony > on behalf of Schountz,Tony
Sent: Thursday, December 07, 2017 1:59 PM EST
To: Mattina Alonge
CC: Munster, Vincent (NIH/NIAID) [E] >; Olson, Sarah ; Schountz,Tony ; Theresa Laverty >; Nate Fuller Raina Plowright >; Liam Mcguire ; Kevin Olival ecohealthalliance.org>; Lausen, Cori >
Subject: Re: E-introduction

Hi Mattina,

I'm not sure who all needs to be on this reply so I cc'd everyone.

We can get these tissues for you from Jamaican fruit bats in our colony; however, they will have to be collected opportunistically. It may not be until January before we could collect them for you.

Regards,

Tony

> On Dec 7, 2017, at 11:33 AM, Mattina Alonge > wrote:
>
> Thanks a ton Vincent. I appreciate your help in spreading the word!
>
> Mattina
>
> On Thu, Dec 7, 2017 at 9:50 AM, Munster, Vincent (NIH/NIAID) [E]< wrote:
>
> > Hi Mattina,
> >
> > I'm looping in my friends Tony Schountz and Dick Bowen from CSU, Tony might have access to tissues from Carollia and Artibeus bats. And Dick my know people who once in a while get bats submitted for rabies testing.
> >
> > Cheers,
> >
> > Vincent Munster
> >
> > ---
> >
> > **From:** Mattina Alonge
> > **Date:** Tuesday, December 5, 2017 at 8:35 PM
> > **To:** Sarah Olson
> > **Cc:** Theresa Laverty >, Nate Fuller < >, Raina Plowright >, "vincent.munster " , Liam Mcguire <liam.mcguire , "Kevin Olival," ecohealthalliance.org>, "Lausen, Cori" < >
> > **Subject:** Re: E-introduction
> >
> > Hi Sarah, Thanks! As for gaining field experience within the next year I think I am limited to North America purely to minimize cost of gaining a foundation of skills/training...but for research questions I am able to develop and field studies I may want to propose for funding, a wider (global) range of locations can certainly be relevant and beneficial!
> >
> > For all that are curious or may be interested, here's a nutshell explanation of what my science interests are:
> >
> > Right now I'd like to characterize the localization and expression of gonadotropin inhibitory hormone (GnIH) in bats; it's a neuropeptide that inhibits the downstream signals involved in the hypothalamic-pituitary-gonadal

axis in vertebrates, but has yet to be described in any bat species. This fits into my broad interest of how environmental and social cues modulate reproductive physiology at a molecular level. For this basic early work, I'm looking to find people who are willing to donate existing, or collect, some tissue samples for me to work on in the lab (IHC, qPCR, westerns...). I'm looking for brains and gonads from any species of bat (male and female) either isolated and flash frozen, or fixed in formaldehyde of some kind. If any of you have insight into this that'd be awesome!

After this initial step, I'd also like to do my own field studies (shooting for 2018-2019) to wild-catch some bats across seasons within a region where species exhibit hibernation or torpor, and examine how GnIH and GnRH fluctuate seasonally across reproductive life history stages and suppression. This connects to ideas within the context of energy partitioning and tradeoff, within which I think those of you working in disease dynamics and immunology could be cool collaborators if interested. If I am able to terminally collect samples for myself perhaps others can collect data on immune aspects of the individuals across seasons as well. Just some early thoughts.

Looking forward to any feedback, potential field work training I can get, and maybe even ideas about where I can get tissues to start.

Mattina

On Tue, Dec 5, 2017 at 10:26 AM, Olson, Sarah > wrote:

> Hi Mattina!
>
> I'm at a remote field camp so I'll cut to the chase. I'm copying in a few folks and members of my WNS team to see if something might work or if someone might be interested in collaborating. I'm not sure if your project is limited to NA so I've also looped in some additional friends.
>
> Hopefully something works out,
>
> Sarah
>
> ---------- Forwarded message ----------
> From: **Mattina Alonge** >
> Date: Mon, Dec 4, 2017 at 10:59 AM
> Subject: [wbwg] Berkeley PhD Student - Looking to help you with field work / Bat Tissues
> To: wbwglist
>
> Hello all!
>
> My name is Mattina and I'm a first year PhD student at UC Berkeley within the Integrative Biology Dept. I'm working under the supervision of Dr. George Bentley, developing projects that broadly encompass the ways animals translate environmental cues via neuroendocrinology to support (or inhibit) reproductive physiology. I have a few different project ideas surrounding bat reproductive neuroendocrine regulation that I'd be happy to chat about if anyone is interested, but I'm reaching out to this group to also offer my help, and ask for some help.
>
> - **I'm really interested in gaining some bat field experience and training in wild-capture (handling, mist netting, harp traps, etc.)** as this is something I'd like to do as part of my dissertation but have no experience. If you are planning to do field work of any capacity over the upcoming Spring/Summer and

would like a responsible set of eyes and hands to help, please let me know!

- I'm attempting to get some preliminary data this year regarding localization and expression of a neurohormone that inhibits the HPG axis in vertebrates. I'd like to characterize it in bats as a starting point and build funding proposals off of that for future field studies. This is where I need help - I am hoping to get some donated **brain, ovary, and testes** tissues from a few different bat species for me to do some IHC/gene expression work on. **If anyone has bat tissues of this type that they do not need for their own research programs, I'd love to talk further!** Flash frozen is ideal, and RNAlater or PFA fixed is also okay.

Thanks so much!

Mattina

--

Mattina Alonge

PhD Student, University of California, Berkeley

Bentley Lab (Reproductive Neuroendocrinology)

--

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PhD Student, University of California, Berkeley

Bentley Lab (Reproductive Neuroendocrinology)

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Mattina Alonge
PhD Student, University of California, Berkeley
Bentley Lab (Reproductive Neuroendocrinology)

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony on behalf of Schountz,Tony
Sent: Thursday, August 13, 2020 8:38 AM EDT
To: epstein ecohealthalliance.org>
Subject: Re: Email

Jon, I have a meeting with Alan this morning. I'll let you know how it goes.

Get Outlook for iOS

From: Jon Epstein ecohealthalliance.org>
Sent: Wednesday, August 12, 2020 11:30:06 PM
To: Schountz,Tony
Subject: Re: Email

Tony,
any progress?

On Mon, Aug 3, 2020 at 10:03 AM Schountz,Tony wrote:

> Jon, I think thinks are moving forward with Alan Rudolf. I'm getting on a conference call right now but hope to hear more from him later today.
>
> Good news, for sure.
>
> T.
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

> On Jul 30, 2020, at 3:48 PM, Jon Epstein ecohealthalliance.org> wrote:
>
> That's great news. Please let me know if you need any info before then.
> Fingers crossed....
> -Jon
>
> On Thu, Jul 30, 2020 at 5:44 PM Schountz,Tony wrote:
>
> > Jon, I have been told to contact Alan Rudolph, so I just sent him an email to see if he will be interested in providing funds to renovate the bull barn. I'll let you know as soon as I hear anything.
> >
> > T.
> > —
> > Tony Schountz, PhD
> > Associate Professor
> > Arthropod-borne and Infectious Disease Laboratory
> > Department of Microbiology, Immunology and Pathology
> > College of Veterinary Medicine
> > Colorado State University
>
> --
>
> **Jonathan H. Epstein DVM, MPH, PhD**
>
> *Vice President for Science and Outreach*

From: Tony Schountz > on behalf of Schountz,Tony >
Sent: Monday, August 03, 2020 10:04 AM EDT
To: Schountz,Tony <>
CC: epstein ecohealthalliance.org>
Subject: Re: Email

"Think things…" LOL.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

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> Colorado State University

--

Jonathan H. Epstein DVM, MPH, PhD

From: Tony Schountz > on behalf of Schountz,Tony >
Sent: Monday, August 03, 2020 12:29 PM EDT
To: epstein ecohealthalliance.org>
CC: Schountz,Tony
Subject: Re: Email

Jon, any chance you could get *Rousettus leschenaultii* bats? The Ace2 receptor of this species has 16 of the 20 critical spike protein binding residues.

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
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> Colorado State University

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

web: ecohealthalliance.org

From: Tony Schountz on behalf of Schountz,Tony
Sent: Monday, August 24, 2020 11:48 AM EDT
To: epstein ecohealthalliance.org>
CC: Schountz,Tony
Subject: Re: Email

Jon, I'm having a meeting with Alan's team tomorrow morning and need to prepare a couple of paragraphs for them. Initial cost estimate isn't very good - something on the order of $1 million to renovate it. Apparently, it does not have any HVAC system, which is probably the plurality of the cost.

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Aug 13, 2020, at 11:06 AM, Schountz,Tony > wrote:

Jon, good news, Alan wants to move forward on this. He's willing to pony up the renovation funds, but he wants a one-page description for why it will be beneficial for the long-term. I suspect you have something already that could be edited? If so, send it to me and I'll get it to him.

Thanks,

T.
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Tony Schountz, PhD
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Arthropod-borne and Infectious Disease Laboratory
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--

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)

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--

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T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony on behalf of Schountz,Tony
Sent: Wednesday, October 17, 2018 11:40 AM EDT
To: 胡犇 <huben@
Subject: Re: Final Program of the 8th International Symposium on Emerging Viral Diseases

Hi Ben,

I just want to verify a driver will pick me up at the airport upon my arrival and take me to the hotel.

Thank you,

Tony

> On Oct 15, 2018, at 7:14 AM, 胡犇 <huben wrote:
>
> Dear speaker:
>
> We will have the 8th International Symposium on Emerging Viral Diseases in Wuhan soon this weekend.
>
> Please find enclosed the final program of the meeting, as minor changes have been made compared with the version that I previously sent to you.
>
> You will be accommodated in the venue hotel of the symposium, the Optics Valley Kingdom Plaza. Our student volunteers or myself will pick you up at Wuhan airport or Wuhan railway station when you arrive.
>
> We look forward to meeting you soon.
>
> Sincerely
>
> Ben Hu Ph.D
> Wuhan Institute of Virology, CAS
> Secretary of the 8th ISEVD
> <Program of the 8th ISEVD_Final.pdf>

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony
Sent: Sunday, October 21, 2018 11:44 PM EDT
To: 胡犇 <huben >
BCC: Schountz,Tony >
Subject: Re: Final Program of the 8th International Symposium on Emerging Viral Diseases

Hi Ben

Do I need to schedule a ride to the airport tomorrow? Also do you know if I can print my boarding passes here at the hotel?

Thanks

Tony

Sent from my iPhone

On Oct 18, 2018, at 10:16 PM, 胡犇 <huben wrote:

> Dear Dr.Schountz:
>
> I have an app via which I can follow the status of any flight.
>
> So I can arrange with flexibility.
>
> But hope everything will be fine.
>
> Sincerely
>
> Ben
>
> -----原始邮件-----
> **发件人:**"Schountz,Tony" >
> **发送时间:**2018-10-18 21:59:58 (星期四)
> **收件人:** "胡犇" <huben >
> **抄送:**
> **主题:** Re: Re:Re: Final Program of the 8th International Symposium on Emerging Viral Diseases
>
> Hi Ben,
>
> It looks like heavy thunderstorms for my arrival in Tokyo. Hopefully, they will not delay my connection to Wuhan. If I miss the flight to Wuhan, I will email you so that you can let the driver know. Otherwise, I should see him/her in about 24 hours!
>
> Thanks,
>
> Tony
>
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University
>
> ---
>
> **From:** 胡犇 <huben >
> **Sent:** Wednesday, October 17, 2018 9:54 AM
> **To:** Schountz,Tony
> **Subject:** Re:Re: Final Program of the 8th International Symposium on Emerging Viral Diseases

Yes Dr.Schountz.

The pick-up from the airport to the hotel will be arranged.

Safe journey and see you soon.

Best

Ben

在 2018-10-17 23:41:10，"Schountz,Tony" 写道：

>Hi Ben,
>
>
>I just want to verify a driver will pick me up at the airport upon my arrival and take me to the hotel.
>
>
>Thank you,
>
>
>Tony

From: Schountz,Tony on behalf of Schountz,Tony
Sent: Wednesday, October 17, 2018 11:54 AM EDT
To: 胡犇 <huben
Subject: Re: Final Program of the 8th International Symposium on Emerging Viral Diseases

Great, thank you, Ben.

Tony

> On Oct 17, 2018, at 9:54 AM, 胡犇 <huben > wrote:
>
> Yes Dr.Schountz.
>
> The pick-up from the airport to the hotel will be arranged.
>
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>
> Best
>
> Ben
>
> 在 2018-10-17 23:41:10，"Schountz,Tony" 写道：
>
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> >
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> > We will have the 8th International Symposium on Emerging Viral Diseases in Wuhan soon this weekend.
> >
> > Please find enclosed the final program of the meeting, as minor changes have been made compared with the version that I previously sent to you.
> >
> > You will be accommodated in the venue hotel of the symposium, the Optics Valley Kingdom Plaza. Our student volunteers or myself will pick you up at Wuhan airport or Wuhan railway station when you arrive.
> >
> > We look forward to meeting you soon.
> >
> > Sincerely
> >
> > Ben Hu Ph.D
> > Wuhan Institute of Virology, CAS

Secretary of the 8th ISEVD
<Program of the 8th ISEVD_Final.pdf>

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Tony Schountz on behalf of Schountz,Tony >
Sent: Wednesday, October 21, 2020 4:28 PM EDT
To: epstein ecohealthalliance.org>
Subject: Re: Genome paper

Yes, I'd like to start on it next week. I have some grading to do this week plus interviews for DVM/PhD candidates for our program, so calendar is quite full. Next week is pretty good for me except (MST) Monday 2-3, Tues 12-2, Wed 3-5. Any of those work for you?

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Oct 21, 2020, at 2:05 PM, Jon Epstein ecohealthalliance.org> wrote:

Yes! I agree.

Should we schedule a time to talk? So we can start to organize for writing this thing?

On Wed, Oct 21, 2020 at 3:33 PM Schountz,Tony > wrote:

> Jon, I suspect you've seen this?
>
> https://www.frontiersin.org/articles/10.3389/fmicb.2020.01807/full
>
> Should be quite helpful for the grant.
>
> T.
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

web: ecohealthalliance.org

From: Schountz,Tony > on behalf of Schountz,Tony >
Sent: Wednesday, January 25, 2017 5:32 PM EST
To: Jon Epstein ecohealthalliance.org>
Subject: Re: Infectious Diseases of Bats Symposium, June 29-July 1, 2017, Fort Collins, Colorado

Jon, I am really, really, terribly sorry I missed your email. I only found it because I was going through the replies to locate an errant email and yours was in the midst of them.

I think if you can do it with a focus on the bat viruses that would be great. Just to let you know, we are also hosting the INKY meeting this year, where other viruses would be relevant.

http://www.zonnosis.org

Still a work in progress, though.

The bats are doing well since the move from Greeley to FC. It took 2 years get through all the hoops to move them here. Anyway, we've done a few more infection experiments and have one more virus that kills them. We need the colony to expand quite a bit, so we're sort of pausing on infection studies for a few months.

Tony

> On Dec 15, 2016, at 11:48 AM, Jon Epstein ecohealthalliance.org> wrote:
>
> Thanks Tony.
> Looking forward to it.
> We haven't spoke for a while, but should catch up about immunology work, the colony, etc..
>
> Also, in thinking about keynote talks, if of interest, we're working on a new international initiative that's very relevant, called the Global Virome project, which aims to characterize the complete viral diversity in key wildlife species, including bats, over a 10 year period. It might be of interest to this audience. Happy to chat more about it.
>
> Cheers,
> Jon
>
> On Thu, Dec 15, 2016 at 1:18 PM, Schountz,Tony > wrote:
>> Dear Colleagues,
>>
>> (Please forward this email to colleagues who may be interested.)
>>
>> We have made arrangements for the upcoming symposium and this email is to update you on a few items.
>>
>> 1. Registration will open January 15 and will close May 1.
>> 2. Abstract submission will open January 15 and will close April 1. Authors will be notified of acceptance for talk or poster by April 21.
>> 3. We will offer campus housing in university dormitories, which can be reserved at the time of registration. However, there are also hotels near the conference venue, including a Hilton Hotel and a Best Western Hotel. Links to these hotels are on the conference web page.
>> 4. We have received a very good score on an NIH conference support proposal and are optimistic that we will be able to subsidize registration fees and dormitory costs for some students and post-docs. However, we have not received a letter of award yet so we cannot guarantee these funds will be available, nor how much subsidies may be. I will send another email when we know if these funds are awarded.
>>
>> As a reminder, the symposium web site is http://www.batid.org
>>
>> If you have questions, please do not hesitate to contact me.
>>
>> Thank you,
>>
>> Tony Schountz
>>
>> ---
>> **From:** Schountz,Tony
>> **Sent:** Wednesday, July 20, 2016 4:39 PM
>> **To:** Schountz,Tony
>> **Subject:** Infectious Diseases of Bats Symposium, June 29-July 1, 2017, Fort Collins, Colorado
>>
>> Dear Colleagues,
>>
>> At the conclusion of the bat ID symposium in 2014, there was unanimous support for having another meeting in three years. This email is to inform you that we have begun the process of setting up the symposium for next summer. Because we nearly exceeded the capacity of the conference hall in 2014, we have secured a larger room that can accommodate up to 300 attendees, and which has better viewing and acoustics for presentations.
>>
>> We have set the dates to coincide with the conclusion of the American Society for Virology meeting (which will be held in Madison, Wisconsin and which ends on Wednesday, June 28) to reduce the travel burden of our international colleagues who will also attend the ASV meeting. There are several non-stop flights between Madison and Denver, thus it should be relatively quick flight (about 1.5 hours).
>>
>> We will have oral and poster presentation sessions. Our tentative schedule is:
>>
>> Thursday, June 29: Social mixer with snacks and drinks, 18:00-21:00
>> Friday, June 30: Conference day 1
>> Saturday, July 1: Conference day 2
>>
>> The web page is: http://batid.org
>>
>> As with the previous meeting, we will arrange for campus housing to keep costs as low as possible. In addition, there are hotels near the venue.
>>
>> Please forward this email to those who you think may be interested. A follow-up email will be sent in the fall, probably in November, with additional information. In the meanwhile, it would be helpful if you could let me know if you plan to attend (or not).

Thanks,

Tony Schountz

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

--

Jonathan H. Epstein DVM, MPH

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

web: ecohealthalliance.org

-

EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony < on behalf of Schountz,Tony
Sent: Monday, March 20, 2017 12:49 PM EDT
To: Schountz,Tony <
BCC:

.

Subject: Re: Infectious Diseases of Bats Symposium, June 29-July 1, 2017, Fort Collins, Colorado

Dear Colleagues,

We have had several requests for an abstract submission deadline extension, thus, it has been extended two weeks to **Friday, April 14**. This is probably a fixed deadline because we will still need to select abstracts for talks, which will take a couple of weeks for the external reviewers to complete. If this is still not enough time for you, please let me know. We can add poster abstracts for a few weeks after this deadline, but after April 14 we will be unable to consider abstracts for oral presentations.

Please let me know if you have any question.

Thanks,

Tony

> On Jul 20, 2016, at 4:39 PM, Schountz,Tony > wrote:
>
> Dear Colleagues,
>
> At the conclusion of the bat ID symposium in 2014, there was unanimous support for having another meeting in three years. This email is to inform you that we have begun the process of setting up the symposium for next summer. Because we nearly exceeded the capacity of the conference hall in 2014, we have secured a larger room that can accommodate up to 300 attendees, and which has better viewing and acoustics for presentations.
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> We have set the dates to coincide with the end of the American Society for Virology meeting (which will be held in Madison, Wisconsin and which ends on Wednesday, June 28) to reduce the travel burden of our international colleagues who will also attend the ASV meeting. There are several non-stop flights between Madison and Denver, thus it should be relatively quick flight (about 1.5 hours).
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> As with the previous meeting, we will arrange for campus housing to keep costs as low as possible. In addition, there are hotels near the venue.
>
> Please forward this email to those who you think may be interested. A follow-up email will be sent in the fall, probably in November, with additional information. In the meanwhile, it would be helpful if you could let me know if you plan to attend (or not).
>
> Thanks,
>
> Tony Schountz
>
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory

From: Schountz,Tony > on behalf of Schountz,Tony >
Sent: Monday, April 17, 2017 5:48 PM EDT
To: Schountz,Tony <
BCC:

Subject: Re: Infectious Diseases of Bats Symposium, June 29-July 1, 2017, Fort Collins, Colorado

Colleagues,

Please note that abstract submission for the symposium is now closed. We received 66 abstracts (compared to about 45 for the first meeting). For those of you who requested oral presentations, the abstracts will go to the members of the selection committee tomorrow and you will be notified next week if yours was selected for a talk or a poster. We will do our best to accommodate as many speakers as possible.

As a reminder, symposium registration closes in about 2 weeks, on**May 1, 2017**.

If you have questions, please feel free to contact me.

Thank you,

Tony

> On Apr 10, 2017, at 10:52 AM, Schountz,Tony > wrote:
>
> Dear Colleagues,
>
> This email is the final reminder that the abstract submission deadline for the symposium is this**Friday, April 14**. The web page has been updated with the confirmed speaker list on the **Topics** page. After the abstract deadline, abstracts from those who requested talks will be evaluated by the selection committee for oral presentations. We plan to have the final selection for talks soon after and notifications sent by email. All abstracts submitted for posters will be accepted, provided they are relevant.
>
> **Early registration closes May 1** and late registration closes May 15.
>
> http://www.batid.org
>
> If you have any questions, please do not hesitate to contact me.
>
> Thank you,
>
> Tony Schountz
>
> > On Mar 20, 2017, at 10:49 AM, Schountz,Tony > wrote:
> >
> > Dear Colleagues,
> >
> > We have had several requests for an abstract submission deadline extension, thus, it has been extended two weeks to **Friday, April 14**. This is probably a fixed deadline because we will still need to select abstracts for talks, which will take a couple of weeks for the external reviewers to complete. If this is still not enough time for you, please let me know. We can add poster abstracts for a few weeks after this deadline, but after April 14 we will be unable to consider abstracts for oral presentations.
> >
> > Please let me know if you have any question.
> >
> > Thanks,
> >
> > Tony
> >
> > > On Jul 20, 2016, at 4:39 PM, Schountz,Tony > wrote:
> > >
> > > Dear Colleagues,
> > >
> > > At the conclusion of the bat ID symposium in 2014, there was unanimous support for having another meeting in three years. This email is to inform you that we have begun the process of setting up the symposium for next summer. Because we nearly exceeded the capacity of the conference hall in 2014, we have secured a larger room that can

accommodate up to 300 attendees, and which has better viewing and acoustics for presentations.

We have set the dates to coincide with the end of the American Society for Virology meeting (which will be held in Madison, Wisconsin and which ends on Wednesday, June 28) to reduce the travel burden of our international colleagues who will also attend the ASV meeting. There are several non-stop flights between Madison and Denver, thus it should be relatively quick flight (about 1.5 hours).

We will have oral and poster presentation sessions. Our tentative schedule is:

Thursday, June 29: Social mixer with snacks and drinks, 18:00-21:00
Friday, June 30: Conference day 1
Saturday, July 1: Conference day 2

The web page is: http://batid.org

As with the previous meeting, we will arrange for campus housing to keep costs as low as possible. In addition, there are hotels near the venue.

Please forward this email to those who you think may be interested. A follow-up email will be sent in the fall, probably in November, with additional information. In the meanwhile, it would be helpful if you could let me know if you plan to attend (or not).

Thanks,

Tony Schountz

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony on behalf of Schountz,Tony <
Sent: Friday, May 11, 2018 12:01 PM EDT
To: 胡犇 <huben
CC: Schountz,Tony >; 石正丽 <zlshi >; 周鹏 <peng.zhou
Subject: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Hi Ben,

I have my flight booked and will arrive in Wuhan at 10:00 PM on October 19 (All Nippon Airways **NH 937**). Can you tell me the name and address of the hotel? I will need it for my visa and for my university administrators.

Thank you,

Tony

> On Apr 9, 2018, at 8:06 AM, 胡犇 <huben > wrote:
>
> Dear Dr.Schountz:
>
> The 8th International Symposium on Emerging Viral Diseases will be held in October 20-22, 2018, in Wuhan, China. The biennial symposium is organized by Wuhan Institute of Virology, Chinese Academy of Sciences and has become an important event for leading Chinese and international virologists to discuss cutting-edge science on emerging viruses as well as to foster global collaborations.
>
> Prof Zhengli Shi and Dr.Peng Zhou had a nice experience last year in Colorado when attending the symposium on bat-borne infectious diseases, and we know you have made great contributions to bat virus researches. We sincerely hope that you can attend the symposium. Please find enthe formal invitation letter for the meeting.
>
> If you have any question regarding the conference, please contact me.
>
> Thank you!
>
> Best regards
>
> Ben Hu Ph.D
>
> Research Assistant
>
> Secretary of the 8th International Symposium on Emerging Viral Diseases
>
> Wuhan Institute of Virology, Chinese Academy of Sciences
> Wuhan 430071, P.R. China
>
> <Invitation letter Tony Schountz.pdf>

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony > on behalf of Schountz,Tony
Sent: Wednesday, August 08, 2018 2:12 PM EDT
To: 胡犇 <huben >
CC: 石正丽 <zlshi >
Subject: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Hi Ben,

I'm having trouble getting my visa for my visit. Apparently, I need the letter from you that has some kind of seal stamped on it, and this letter requires my passport number is listed on it. That number is 546272602. My legal name is **William A Schountz** and this is the name on my passport so the letter should be addressed with that name. Can you mail the letter directly to me at:

William Schountz

It would be helpful to get the letter by the end of next week because I need my passport back by September 14 for upcoming travel. I cannot get the passport back until I have the visa approved.

Thanks,

Tony

> On Aug 6, 2018, at 5:27 PM, 胡犇 <huben > wrote:
>
> Thanks a lot for the abstract, Dr.Schountz.
>
> Best
>
> Ben
>
> 在 2018-08-07 04:36:28，"Schountz,Tony" > 写道：
>
> > Hi Ben,
> >
> > Attached is my abstract. I should have quite a bit more information for the talk as we have many bats infected with the virus and are getting some very interesting results.
> >
> > Thanks,
> > Tony
> >
> > On Apr 9, 2018, at 8:06 AM, 胡犇 <huben > wrote:
> >
> > Dear Dr.Schountz:
> >
> > The 8th International Symposium on Emerging Viral Diseases will be held in October 20-22, 2018, in Wuhan, China. The biennial symposium is organized by Wuhan Institute of Virology, Chinese Academy of Sciences and has become an important event for leading Chinese and international virologists to discuss cutting-edge science on emerging viruses as well as to foster global collaborations.
> >
> > Prof Zhengli Shi and Dr.Peng Zhou had a nice experience last year in Colorado when attending the symposium on bat-borne infectious diseases, and we know you have made great contributions to bat virus researches. We sincerely hope that you can attend the symposium. Please find enthe formal invitation letter for the meeting.

If you have any question regarding the conference, please contact me.

Thank you!

Best regards

Ben Hu Ph.D

Research Assistant

Secretary of the 8th International Symposium on Emerging Viral Diseases

Wuhan Institute of Virology, Chinese Academy of Sciences
Wuhan 430071, P.R. China

<Invitation letter Tony Schountz.pdf>

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony > on behalf of Schountz,Tony u>
Sent: Saturday, May 12, 2018 2:36 PM EDT
To: 胡犇 <huben >
Subject: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Great, thank you Ben.

Tony

> On May 12, 2018, at 9:37 AM, 胡犇 <huben wrote:
>
> No need, Dr.Schountz. For invited speakers the rooms will be reserved by the conference.
>
> Ben
>
> 在 2018-05-12 23:15:20，"Schountz,Tony" > 写道：
>
> > Thank you, Ben. Should I make my own reservation?
> >
> > Tony
> >
> > —
> > Tony Schountz, PhD
> > Associate Professor
> > Arthropod-borne and Infectious Disease Laboratory
> > Department of Microbiology, Immunology and Pathology
> > College of Veterinary Medicine
> > Colorado State University
> >
> > From: 胡犇 <huben
> > Sent: Friday, May 11, 2018 6:47 PM
> > To: Schountz,Tony
> > Cc: 石正丽; 周鹏
> > Subject: Re: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases
> >
> > Dear Dr.Schountz:
> >
> > Here is the hotel information:
> >
> > name: Optics Valley Kingdom Plaza Hotel Wuhan,
> >
> > address: No.1 Wu Jia Wan, Hongshan District, Wuhan, Hubei Province, China.
> >
> > Best
> >
> > Ben

-----原始邮件-----
发件人:"Schountz,Tony"
发送时间:2018-05-12 00:01:20 (星期六)
收件人: "胡犇" <huben
抄送: "Schountz,Tony" >, "石正丽" <zlshi >, "周鹏" <peng.zhou >
主题: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Hi Ben,

I have my flight booked and will arrive in Wuhan at 10:00 PM on October 19 (All Nippon Airways NH 937). Can you tell me the name and address of the hotel? I will need it for my visa and for my university administrators.

Thank you,

Tony

On Apr 9, 2018, at 8:06 AM, 胡犇 <huben > wrote:

Dear Dr.Schountz:

The 8th International Symposium on Emerging Viral Diseases will be held in October 20-22, 2018, in Wuhan, China. The biennial symposium is organized by Wuhan Institute of Virology, Chinese Academy of Sciences and has become an important event for leading Chinese and international virologists to discuss cutting-edge science on emerging viruses as well as to foster global collaborations.

Prof Zhengli Shi and Dr.Peng Zhou had a nice experience last year in Colorado when attending the symposium on bat-borne infectious diseases, and we know you have made great contributions to bat virus researches. We sincerely hope that you can attend the symposium. Please find enthe formal invitation letter for the meeting.

If you have any question regarding the conference, please contact me.

Thank you!

Best regards

Ben Hu Ph.D

Research Assistant

Secretary of the 8th International Symposium on Emerging Viral Diseases

Wuhan Institute of Virology, Chinese Academy of Sciences
Wuhan 430071, P.R. China

From: Schountz,Tony > on behalf of Schountz,Tony
Sent: Monday, April 09, 2018 12:50 PM EDT
To: 胡犇 <huben >
CC: Schountz,Tony >; 石正丽 <zlshi >; 周鹏 <peng.zhou
Subject: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Dear Ben,

Thank you for the invitation. I plan to attend!

See you then,

Tony

> On Apr 9, 2018, at 8:06 AM, 胡犇 <huben > wrote:
>
> Dear Dr.Schountz:
>
> The 8th International Symposium on Emerging Viral Diseases will be held in October 20-22, 2018, in Wuhan, China. The biennial symposium is organized by Wuhan Institute of Virology, Chinese Academy of Sciences and has become an important event for leading Chinese and international virologists to discuss cutting-edge science on emerging viruses as well as to foster global collaborations.
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> Thank you!
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> Best regards
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> Ben Hu Ph.D
>
> Research Assistant
>
> Secretary of the 8th International Symposium on Emerging Viral Diseases
>
> Wuhan Institute of Virology, Chinese Academy of Sciences
> Wuhan 430071, P.R. China
>
> <Invitation letter Tony Schountz.pdf>

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony > on behalf of Schountz,Tony >
Sent: Monday, August 06, 2018 4:33 PM EDT
To: 胡犇 <huben
BCC: Tony Schountz
Subject: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases
Attachment(s): "Wuhan Bat Flu abstract.docx"

Hi Ben,

Attached is my abstract. I should have quite a bit more information for the talk as we have many bats infected with the virus and are getting some very interesting results.

Thanks,
Tony

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> Dear Dr.Schountz:
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> <Invitation letter Tony Schountz.pdf>

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

Infection and Immune Responses of Jamaican Fruit Bats (*Artibeus jamaicensis*) Experimentally Challenged with a Bat HL18NL11 Influenza A Virus

Tony Schountz, PhD

Arthropod-borne and Infectious Diseases Laboratory, Department of Microbiology, Immunology and Pathology, College of Veterinary Medicine and Biomedical Sciences, Colorado State University

Nucleotide sequences of two novel influenza A-like viruses, HL17NL10 and HL18NL11, were recently discovered in New World little yellow shouldered fruit bats (*Sturnira lilium*) and flat-faced fruit bats (*Artibeus planirostris*), respectively. Serological studies indicated high prevalence to these viruses among many species of Phyllostomidae leaf-nosed fruit bats of Central and South America, including Jamaican fruit bats (*Artibeus jamaicensis*). Infectious viruses have not been isolated from bats, therefore an infectious clone of HL18NL11 was generated by reverse genetics technologies and inoculated into Jamaican fruit bats. During a 28 day challenge experiment with intranasal inoculation, the bats exhibited no clinical signs of disease. However, rectal swabs had up to 10^5 $TCID_{50}$ equivalents of HL18NL11 vRNA by real-time PCR in each bat on days 2, 4 and 7 post inoculation, and in the lungs of one of the bats on day 28 when they were euthanized. Inclusion of contact bats two days after inoculation resulted in virus transmission. Histopathology revealed minimal evidence of disease except for the one bat with detectable vRNA in its lung. This bat's lungs had aggregates of macrophages and lymphoplasmacytes intermixed with fewer neutrophils that expanded into the interstitium, especially around the adventitia. RNAscope probes identified vRNA in the jejunal Peyer's patch of acutely-infected bats and nuclear localization of viral antigen. Bats held to 28 day each had low titer neutralizing antibodies. In a second study, inoculation of bats with a mutant HL18NL11 virus with a premature stop codon in the neuraminidase replicated poorly; however, the virus transmitted to contact bats and with each bat passage resulted in greater abundance of vRNA in rectal swabs, suggesting the virus may have reverted back to wildtype. This work is the first in vivo study of bat influenza viruses and supports the hypothesis that Jamaican fruit bats may be a natural reservoir host of the HL18NL11 virus.

From: Schountz,Tony > on behalf of Schountz,Tony
Sent: Monday, March 27, 2017 5:30 PM EDT
To: Kevin Olival, PhD ecohealthalliance.org>
Subject: Re: Invited talks

Kevin, also, do you have Jane Greenhalgh and Michaeleen Doucleff's email addresses? I want to let them know about the meeting in case they're interested.

Thanks,

T.

On Mar 27, 2017, at 3:24 PM, Kevin Olival, PhD ecohealthalliance.org> wrote:

Hey Tony,

Was just thinking about this and about putting together a talk abstract… When do you need a title by? Definitely planning on this, I think I'm going to present some new modeling we've done with global data on bat virus associations; network models; etc; some of it still in the works - but will be done by June!

Cheers,
Kevin

Kevin J. Olival, PhD

Associate Vice President for Research

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

www.ecohealthalliance.org

On Mar 27, 2017, at 5:19 PM, Schountz,Tony wrote:

Hi Jon and Kevin,

I hope you're still planning to attend the symposium. I am just now getting around to sending out emails to invited speakers and would like to invite each of you to give talks. If so, could you email me your provisional titles?

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony > on behalf of Schountz,Tony >
Sent: Monday, April 10, 2017 11:18 AM EDT
To: Kevin Olival, PhD @ecohealthalliance.org>
Subject: Re: Invited talks

No, just the title for now. I'll need an abstract in a few weeks for the program. I already have you listed on the web site with your title.

I've received quite a few abstracts - more than the last time, it seems, so I think it will shape up to be another good meeting.

Thanks,

T.

> On Apr 10, 2017, at 8:08 AM, Kevin Olival, PhD ecohealthalliance.org> wrote:
>
> Hi Tony,
>
> Just wondering if you need a full abstract submitted by the end of this week for my talk?
>
> Cheers,
> Kevin

> On Mar 29, 2017, at 4:48 PM, Kevin Olival, PhD ecohealthalliance.org> wrote:
>
> Tony, gave a thought to what I'd like to present, and we've done a bunch of new stuff to build models to estimate viral richness in bats and further examine patterns in viral sharing. Thoughts this would be of general interest to the group. This builds on analyses using previously published data (literature reviews) from our own group and others (e.g. Luis et al.); but will also include some analysis of recent field data from PREDICT and other EHA projects.
>
> **Title: "Estimating viral richness and viral sharing in bats: integrating previously-published and newly-aquired field data".**
>
> Cheers,
> Kevin
>
> **Kevin J. Olival, PhD**
>
> *Associate Vice President for Research*
>
> EcoHealth Alliance
> 460 West 34th Street – 17th floor
> New York, NY 10001
>
> www.ecohealthalliance.org
>
> *EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that promote conservation and prevent pandemics.*

> On Mar 27, 2017, at 5:28 PM, Schountz,Tony > wrote:
>
> It would be great if I could have titles by Wednesday. I want to get the web page updated with the invited speaker list.

Thanks,

Tony

> On Mar 27, 2017, at 3:24 PM, Kevin Olival, PhD
> ecohealthalliance.org> wrote:
>
> Hey Tony,
>
> Was just thinking about this and about putting together a talk abstract… When do you need a title by? Definitely planning on this, I think I'm going to present some new modeling we've done with global data on bat virus associations; network models; etc; some of it still in the works - but will be done by June!
>
> Cheers,
> Kevin
>
> **Kevin J. Olival, PhD**
>
> *Associate Vice President for Research*
>
> EcoHealth Alliance
> 460 West 34th Street – 17th floor
> New York, NY 10001
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> www.ecohealthalliance.org
>
>
>
> > On Mar 27, 2017, at 5:19 PM, Schountz,Tony
> > > wrote:
> >
> > Hi Jon and Kevin,
> >
> > I hope you're still planning to attend the symposium. I am just now getting around to sending out emails to invited speakers and would like to invite each of you to give talks. If so, could you email me your provisional titles?
> >
> > Thanks,
> >
> > Tony
> > —
> > Tony Schountz, PhD
> > Associate Professor
> > Arthropod-borne and Infectious Disease Laboratory
> > Department of Microbiology, Immunology and Pathology
> > College of Veterinary Medicine
> > Colorado State University

From: Schountz,Tony > on behalf of Schountz,Tony
Sent: Monday, March 27, 2017 5:28 PM EDT
To: Kevin Olival, PhD @ecohealthalliance.org>
CC: Schountz,Tony Jon Epstein ecohealthalliance.org>
Subject: Re: Invited talks

It would be great if I could have titles by Wednesday. I want to get the web page updated with the invited speaker list.

Thanks,

Tony

> On Mar 27, 2017, at 3:24 PM, Kevin Olival, PhD ecohealthalliance.org> wrote:
>
> Hey Tony,
>
> Was just thinking about this and about putting together a talk abstract… When do you need a title by? Definitely planning on this, I think I'm going to present some new modeling we've done with global data on bat virus associations; network models; etc; some of it still in the works - but will be done by June!
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> Cheers,
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> **Kevin J. Olival, PhD**
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>
> > On Mar 27, 2017, at 5:19 PM, Schountz,Tony > wrote:
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> > Hi Jon and Kevin,
> >
> > I hope you're still planning to attend the symposium. I am just now getting around to sending out emails to invited speakers and would like to invite each of you to give talks. If so, could you email me your provisional titles?
> >
> > Thanks,
> >
> > Tony
> > —
> > Tony Schountz, PhD
> > Associate Professor
> > Arthropod-borne and Infectious Disease Laboratory
> > Department of Microbiology, Immunology and Pathology
> > College of Veterinary Medicine
> > Colorado State University

From: Tony Schountz > on behalf of Schountz,Tony >
Sent: Friday, July 10, 2020 5:46 PM EDT
To: Kevin Olival ecohealthalliance.org>
Subject: Re: Just opening my CSU alumni mail

Yeah, it's kind of embarrassing. I'd rather not have notoriety of any kind. :)

I hope you're doing well. This coronavirus business is something else.

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Jul 9, 2020, at 6:25 AM, Kevin Olival ecohealthalliance.org> wrote:

Nice one!

Kevin

<IMG_3666.jpg>

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
New York, NY 10018

)
www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

From: Tony Schountz > on behalf of Schountz,Tony
Sent: Monday, March 30, 2020 11:50 AM EDT
To: Kendall,Lon
CC: Bowen,Richard >; Bosco-Lauth,Angela >; Schountz,Tony ; epstein ecohealthalliance.org>; Ebel,Greg ; Dean,Gregg >; Szalai,Edit
Subject: Re: Meeting agenda

Looks good to me.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

> On Mar 30, 2020, at 9:31 AM, Kendall,Lon > wrote:
>
> All,
>
> Here is a proposed agenda for tomorrows meeting. Please edit freely.
>
> Introduction
> Lon- why meeting was initially organized, then turf to Jon (I won't be long)
> Jon- provide background about program discussions with CSU and NIAID and why we are here (Jon really sparked this discussion, and is probably best to lead)
> Jean- Discuss NIAID possibilities and expectations and what's needed from CSU (Thought Jean should go sooner to help frame discussion below. I will send her agenda once we get it finalized)
> Ebel- Discuss CVID abilities, and possibilities related to emerging disease, prior C06
> Tony- Discuss current research and potential needs
> Bowen/Angela- Discuss current research and potential needs
> Determine next steps
>
> Lon
>
> Lon V. Kendall, DVM, PhD, DACLAM
> Director, Laboratory Animal Resources and
> Attending Veterinarian, Colorado State University
>
> Colorado State University
> Fort Collins, CO 80523

From: Tony Schountz > on behalf of Schountz,Tony >
Sent: Monday, October 19, 2020 4:40 PM EDT
To: epstein ecohealthalliance.org>
Subject: Re: Monoclonal antibodies

It would be a great idea to have another building in-country for housing and staging bats for quarantine before shipping to USA.

Getting on a call with DARPA in a few minutes, so won't be responsive for an hour or so.

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Oct 19, 2020, at 2:38 PM, Jon Epstein ecohealthalliance.org> wrote:

Awesome - and agree.
I would like to brainstorm together for the letters before we approach anyone. I'll start a google doc and we can live edit it.
Let's think about who the 'dream team' will be for this.
It also occurred to me - what do you think about building in a facility in Bangladesh where we keep a captive breeding colony, that would serve as a feeder if we need more bats along the way? We could develop and fund a closed colony there, like what Cambridge did in Ghana, and we'd know the status of each bat. Brian Pope would be great at helping set this up. And it would allow the colony at CSU to fluctuate a bit in size, and we could pull in new bats as needed. I think it's a nice insurance policy to support the colony in CO as we develop it. This could be something I would manage - but I think we could convince the govt and if we provide all the funding for construction and upkeep, it could really happen.

Thoughts?

On Mon, Oct 19, 2020 at 4:27 PM Schountz,Tony > wrote:

> Jon, I think a really important part of the grant will be to make monoclonal antibodies to various proteins (e.g., CD antigens, cytokines) and cytokines as reagents. If you agree, I'd like to approach a colleague of my, Brian Geiss, to see if he is willing to be on the grant. Recombinant protein expression is his "thing" and he would be a great asset for the grant.
>
> I also think we should get as many letters of support that we can get. I can probably get at least 10 from people we've helped over the years (provided tissues and cells, conducted experimental infections, etc.).
>
> Let me know what you think.
>
> Just moved into our new building. It is really sweet. :)
>
> Thanks,
>
> T.
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

--

From: Tony Schountz > on behalf of Schountz,Tony >
Sent: Tuesday, March 31, 2020 1:24 PM EDT
To: epstein ecohealthalliance.org>
Subject: Re: Multimammate rats

We might know that soon. One of the bats we euthanized yesterday was pregnant.

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Mar 31, 2020, at 11:22 AM, Jon Epstein ecohealthalliance.org> wrote:

I don't know either. We could try to catch them while pregnant. I also don't know if there's vertical transmission.
This will be challenging, but I'm confident we can get to a point where we can safely ship. Maybe if they go straight into a BL3 facility, CDC will have less concern.
-Jon

On Tue, Mar 31, 2020 at 12:50 PM Schountz,Tony wrote:

> RML imported the Lassa virus reservoir by having them born in captivity in Africa, then the offspring were imported directly to RML. Don't know if horseshoe bats can be born in captivity, but that could be an avenue to alleviate CDC concerns.
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street, Ste. 1701

New York, NY 10001

web: ecohealthalliance.org

From: Tony Schountz > on behalf of Schountz,Tony >
Sent: Tuesday, March 31, 2020 5:35 PM EDT
To: epstein ecohealthalliance.org>
Subject: Re: Multimammate rats

Jon, I've gotten tied up with some unanticipated things so I probably can't get you anything before you start working on it. Please send to me and I'll get on it tonight and have it to you tomorrow morning.

Thanks,

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Mar 31, 2020, at 11:57 AM, Jon Epstein ecohealthalliance.org> wrote:

Wow. You're doing some great stuff. I'm always amazing at how quickly you can spin up these experimental infections. I think we should include a US species in our proposal so we can help address questions of US relevance in terms of spillback. I can find out which ones NWHC is using.
-Jon

On Tue, Mar 31, 2020 at 1:24 PM Schountz,Tony > wrote:

> We might know that soon. One of the bats we euthanized yesterday was pregnant.
>
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

> On Mar 31, 2020, at 11:22 AM, Jon Epstein ecohealthalliance.org> wrote:
>
> I don't know either. We could try to catch them while pregnant. I also don't know if there's vertical transmission.
> This will be challenging, but I'm confident we can get to a point where we can safely ship. Maybe if they go straight into a BL3 facility, CDC will have less concern.
> -Jon
>
> On Tue, Mar 31, 2020 at 12:50 PM Schountz,Tony wrote:
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> > RML imported the Lassa virus reservoir by having them born in captivity in Africa, then the offspring were imported directly to RML. Don't know if horseshoe bats can be born in captivity, but that could be an avenue to alleviate CDC concerns.
> > —
> > Tony Schountz, PhD
> > Associate Professor
> > Arthropod-borne and Infectious Disease Laboratory
> > Department of Microbiology, Immunology and Pathology
> > College of Veterinary Medicine
> > Colorado State University

From: Tony Schountz on behalf of Schountz,Tony
Sent: Monday, March 16, 2020 11:22 AM EDT
To: Schountz,Tony
CC: Jon Epstein ecohealthalliance.org>; Ebel,Greg >; Rudolph,Alan ; Kendall,Lon ; Richard Bowen
Subject: Re: NIH R24 + C06

All, just adding Lon Kendall to the email string. He has assured me there is space for the horseshoe bats and probably for the pteropid bats, but he would like to be on the conference call for this discussion.

Alan, can you help arrange the call through your office?

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

> On Mar 13, 2020, at 4:58 PM, Schountz,Tony wrote:
>
> Alan and Greg, as you know I chatted with Jon Epstein yesterday. He has had discussions with NIH about interest in having a grant submission regarding bats and SARS-CoV-2 and other coronaviruses. I think the four of us ought to have a conference call next week to see if we can make something work.
>
> Alan, we would need to have access to a room or building large enough to house large flying foxes as well as smaller horseshoe bats. I know the barn at ARBL was once available but I suspect it no longer is?
>
> Thanks,
>
> T.
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University
>

>

From: Schountz,Tony on behalf of Schountz,Tony
Sent: Wednesday, April 15, 2020 9:13 AM EDT
To: epstein ecohealthalliance.org>
Subject: Re: NSF bat immunology interest

Yes, we're going to target T cells and the innate response in Jamaican fruit bats to see how it impacts viral shedding, tissue tropism and disease (if any).

T.

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Jon Epstein ecohealthalliance.org>
Sent: Wednesday, April 15, 2020 12:06 AM
To: Schountz,Tony < >
Subject: Re: NSF bat immunology interest

Tony,
Are you planning to apply?
-Jon

On Tue, Apr 14, 2020 at 6:48 PM Schountz,Tony wrote:

> Hi everyone,
>
> I hope you are all safe.
>
> I wanted to let you know about two NSF programs that have urgent deadlines (first week of May) that has bat immunology as its principal interest. The first is a RAPID for 12 months/$200k (including direct costs) and EAGER for 2 years/$300k (including direct costs). The NSF contact is Dr. Joanna Shisler . My understanding is they are interested in the biology of bat immune systems relevant to coronaviruses, but because of the potential spill back issues they will also consider nonviral diseases, including white nose syndrome. I don't have other information but I'm sure Dr. Shisler will be happy to chat with you if you are interested.
>
> If you know of others who are interested in the biology of bat immunity, please pass this email along to them.
>
> Thanks,
>
> Tony
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

--
Jonathan H. Epstein DVM, MPH, PhD
Vice President for Science and Outreach
EcoHealth Alliance
460 West 34th Street, Ste. 1701
New York, NY 10001

From: Tony Schountz > on behalf of Schountz,Tony
Sent: Tuesday, June 23, 2020 3:36 PM EDT
To: epstein ecohealthalliance.org>
CC: bpope >; Ebel,Greg ; Schountz,Tony

Subject: Re: Pteropus space requirements

Hi Jon,

We'd like to move this forward, but we will have to get support from a few levels above us. Give us a week or so to see what progress we can make.

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Jun 18, 2020, at 8:40 AM, Jon Epstein ecohealthalliance.org> wrote:

Thanks so much Brian.
It sounds like the space might be too small for the size colony we were thinking of founding (as you noted, Greg). We should discuss whether a smaller founder colony might still make sense given the opportunity we have. I think the consideration is whether the colony could produce a sufficient birth cohort each year to allow for meaningful research. For example, if we reduced the planned size from 40 to 20, with 3 males and 17 females, with 15 expected to produce pups each year, we'd have 35 bats in Y1 - still within capacity. And we could plan to use most if not all of F1. Long term, we would just have to manage the colony to keep it within size. We could selectively breed a subgroup of females in alternate years, as well.

Just brainstorming here. Tony and Greg, please weigh in. Meanwhile, I'm also going to speak with Jean to push back on the need for construction money to build a bigger facility.

Cheers,
Jon

On Mon, Jun 8, 2020 at 2:57 PM Brian Pope > wrote:

> Jon,
>
> Based on Association of Zoos and Aquariums Bat Taxon Advisory Group space requirements, you can fit approximately 38 bats in a 2500 sq. ft. building. Keep in mind these are AZA requirements and wouldn't affect your holding or operation. That being said, you want the bats to be in an environment that limits stress, provides for natural behaviors, and is ultimately conducive to proper research. Please provide specifics on the building - images, dimensions (including ceiling height), existing facilities, etc?
>
> Food storage wouldn't take up much (ours is 160 sq. ft. and that holds diet for 200 bats with plenty of room to spare). Where would the diet be prepared?
>
> An appropriate exam room should be sufficient to not only perform procedures but also hold bats that may be injured. 300-400 sq. ft. should suffice.
>
> Brian Pope
>
> Director
>
> Lubee Bat Conservancy

http://www.lubee.org

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WATCH OUR BATS LIVE 24/7/365 THROUGH EXPLORE.ORG!

GIANT FLYING FOX CAM

MIXED SPECIES FLYING FOX CAM

From: Jon Epstein [mailto ecohealthalliance.org]
Sent: Wednesday, June 3, 2020 10:57 AM
To: Brian Pope
Cc: Ebel,Greg >; Tony Schountz
Subject: Pteropus space requirements

Hi Brian,

I wanted to introduce you to Professor Greg Ebel, who's the Director of the Arthropod-Borne and Infectious Disease Lab at Colorado State and who's recently become a partner in our efforts, with Tony Shountz, to establish a Pteropus breeding colony there. We're trying to get an accurate understanding of the physical space required for the proposed colony, which if you recall we had discussed starting with 40 bats (4 male, 36 female) which would then become about 60-70 bats post breeding.

Could you help give us a sense of what physical space you think would be necessary in terms of a holding / flight cage, plus support rooms like food storage and a handling / exam area? We've got an existing building on campus that's abou 2500 sq ft that could be gutted & equipped as needed, but the concern is that it's just not big enough for the planned number of bats.

Thanks for your help in thinking through this.

Cheers,

Jon

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
460 West 34th Street, Ste. 1701

New York, NY 10001

From: Tony Schountz > on behalf of Schountz,Tony >
Sent: Tuesday, September 29, 2020 5:01 PM EDT
To: epstein ecohealthalliance.org>
CC: Ebel,Greg ; Schountz,Tony >
Subject: Re: R24 Discussion

Yes, Oct 7 from 1:00 to 1:30 MST works for me. I'll set up the zoom and send it to you.

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Sep 29, 2020, at 2:26 PM, Jon Epstein cohealthalliance.org> wrote:

Tony?

On Tue, Sep 29, 2020 at 1:10 PM Ebel,Greg > wrote:

> Works for me. Sarah is my PO for at least one of my grants.
>
> Greg
>
> **From:** Jon Epstein ecohealthalliance.org>
> **Sent:** Tuesday, September 29, 2020 11:08 AM
> **To:** Schountz,Tony >; Ebel,Greg
> **Subject:** Fwd: R24 Discussion
>
> Guys,
>
> This just came through from NIAID.
>
> I suggest that we talk to her first, then we can talk once we have her input. Want to do it on the 7th?
>
> Cheers,
>
> Jon
>
> ---------- Forwarded message ---------
> From: **Woodson, Sara (NIH/NIAID) [E]**
> Date: Tue, Sep 29, 2020 at 12:05 PM
> Subject: R24 Discussion
> To: ecohealthalliance.org <epstein
>
> Hi Jon,
>
> It's been awhile since we've spoken but I hope you are doing well. Jean forwarded me your question about hypothesis-driven research in an R24. In general, I think we should probably schedule a brief call to discuss

some of the specifics of R24s but also to hear about what you're thinking in terms of a hypothesis-driven approach (or aim). I've listed below some times that work for me/Jean/Mark, please let me know if any of those would work for your team as well.

October 5th: 9-9:30a (eastern)

October 7th: 3-3:30pm

October 14th: 10-11am, 1-2pm, or 2:30-3:30p

October 15th: 11a-noon or 3-4pm

In the interim though, here are some additional thoughts:

The R24 FOA indicates that this mechanism should be used to develop, maintain, provide a resource, but it doesn't explicitly state that hypothesis-driven research is not allowed. Our branch currently has one other funded R24 for the World Reference Collection of Emerging Viruses and Arboviruses (WRCEVA) at UTMB. This R24 does include hypothesis-driven research; they conduct small research projects that leverages having full access to the collection and to samples gathered through pursuit of adding new items to the collection. This research is usually a discreet, small project so as not to take up a lot of the budget and makes use of the resource to answer significant research questions that others haven't addressed yet and that may be difficult to work into other separate applications. I will have to search for other R24s across the institute that may have included animal model development as part of their aims, but none are coming to mind at the moment that would serve as a good example.

Sincerely, Sara

Sara E. Woodson, PhD

Program Officer

Virology Branch

Division of Microbiology and Infectious Diseases

National Institute of Allergy and Infectious Dieases, NIH

--

From: Tony Schountz on behalf of Schountz,Tony
Sent: Wednesday, October 07, 2020 3:58 PM EDT
To: Woodson, Sara (NIH/NIAID) [E]
CC: epstein ecohealthalliance.org>; Schountz,Tony >; Ebel,Greg >; jean.patterson >; Challberg, Mark (NIH/NIAID) [E]

Subject: Re: R24 Discussion

Yes, thanks much, Sara. I appreciate that you, Jean and Mark chatted with us today.

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Oct 7, 2020, at 1:51 PM, Woodson, Sara (NIH/NIAID) [E] > wrote:

Hi Tony, Jon, and Greg;
Here are the example R24's you may want to look up in NIH Reporter:

R24AI059830 PI: Jacques Robert (University of Rochester, animal model containing)
R24AI120942 PI: Scott Weaver (University of Texas Medical Branch, WRCEVA—no model development but may be relevant if thinking about including training; may also be good to link in with them for potential distribution of critical reagents along with BEI Resources)

As Mark mentioned on the phone, NIAID doesn't allow a lot of R24 grants and thus not many are funded, so there aren't many relevant examples to what you would be putting forth in your R24. Please let me know if you have other questions or concerns!
Happy writing 😊
Sincerely, Sara

-----Original Appointment-----
From: Woodson, Sara (NIH/NIAID) [E]
Sent: Wednesday, September 30, 2020 1:22 PM
To: Woodson, Sara (NIH/NIAID) [E]; ecohealthalliance.org; Schountz, Tony; Ebel,Greg; Patterson, Jean (NIH/NIAID) [E]; Challberg, Mark (NIH/NIAID) [E]; Beaubien, Candice (NIH/NIAID) [E]
Subject: R24 Discussion
When: Wednesday, October 7, 2020 3:00 PM-3:30 PM (UTC-05:00) Eastern Time (US & Canada).
Where: Skype Meeting

Please use this Zoom link for our meeting this afternoon instead…..

https://www.zoomgov.com/j/1614258516?pwd=bGVHUDFrbHVxWm91M2ZGUEdWcXF4QT09

Sincerely, Sara

From: Tony Schountz on behalf of Schountz,Tony
Sent: Thursday, September 24, 2020 10:54 AM EDT
To: epstein ecohealthalliance.org>
CC: Schountz,Tony ; Ebel,Greg <
Subject: Re: R24

Here's the zoom info:

Topic: Tony Schountz's Zoom Meeting
Time: Sep 24, 2020 09:00 AM Mountain Time (US and Canada)

Join Zoom Meeting
https://us02web.zoom.us/j/5861713088?pwd=RVJmb2VsenlWR1U3TkdiVGp4WUc2QT09

Meeting ID: 586 171 3088
Passcode: 4e5ZJe

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Sep 16, 2020, at 5:41 PM, Jon Epstein ecohealthalliance.org> wrote:

Shall we say 9 MST /11 EDT ?

Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
New York

On Wed, Sep 16, 2020, 7:09 PM Schountz,Tony wrote:

> Yes, MST. Sorry.
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University
>
> On Sep 16, 2020, at 4:43 PM, Jon Epstein ecohealthalliance.org> wrote:
>
> Is that mountain time?

Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
New York

On Wed, Sep 16, 2020, 6:27 PM Ebel,Greg wrote:

> I could do those times on Thursday.
>
> Greg

From: Schountz,Tony
Sent: Wednesday, September 16, 2020 3:59 PM
To: epstein ecohealthalliance.org>
Cc: Ebel,Greg >; Schountz,Tony

Subject: Re: R24

Jon and Greg, do Tu or Th mornings, say 9 or 10, look good for you?

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

> On Sep 16, 2020, at 3:22 PM, Jon Epstein ecohealthalliance.org> wrote:
>
> Me, too.
>
> Tuesday and thursday are fairly open if you want to suggest some times that work for you.
>
> -Jon
>
> On Wed, Sep 16, 2020 at 5:01 PM Ebel,Greg > wrote:
>
> > For me next week is a lot better.
> >
> > Greg

From: Schountz,Tony >
Sent: Wednesday, September 16, 2020 1:35 PM
To: epstein ecohealthalliance.org>
Cc: Schountz,Tony < >; Ebel,Greg

Subject: Re: R24

Jon and Greg, my week has pretty much filled up, other than tomorrow morning from 8:30 to 11:00 MST. Next week has a number of openings, though.

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

> On Sep 14, 2020, at 11:25 AM, Jon Epstein ecohealthalliance.org> wrote:
>
> Tony and Greg,
>
> My apologies, I just saw your email. I'm free again at 4:30 or 5pm EDT today, if you guys are.
>
> Otherwise, suggest some times this week when you're free.
>
> -Jon
>
> On Mon, Sep 14, 2020 at 12:12 PM Schountz,Tony wrote:
>
> > Hi Jon, we seemed to have missed you. We should reschedule this for later this week or perhaps next week.
> >
> > Thanks,
> >
> > Tony
> >
> > —
> > Tony Schountz, PhD
> > Associate Professor
> > Arthropod-borne and Infectious Disease Laboratory
> > Department of Microbiology, Immunology and Pathology

College of Veterinary Medicine
Colorado State University

On Sep 14, 2020, at 9:57 AM, Schountz,Tony wrote:

Here's a Zoom link in case we need it. I'm limited to 30 minutes.

Topic: R24 Zoom Meeting

Time: Sep 14, 2020 10:00 AM Mountain Time (US and Canada)

Join Zoom Meeting

https://us02web.zoom.us/j/5861713088?pwd=RVJmb2VsenlWR1U3TkdiVGp4WUc2QT09

Meeting ID: 586 171 3088

Passcode: 4e5ZJe

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Sep 14, 2020, at 9:51 AM, Schountz,Tony > wrote:

Hi Jon, we don't have a link to the meeting today. Did you send out a Zoom (or other) link? If not, I can send one.

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease

Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Aug 31, 2020, at 7:19 AM, Jon Epstein ecohealthalliance.org> wrote:

Sorry, I have a meeting at that time. I'm free either the hour before or after that.

Could we do 10AM MST?

On Fri, Aug 28, 2020 at 2:00 PM Schountz,Tony

wrote:

> How about September 14 at 9:00 AM MST?
>
> —
>
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University
>
> ---
>
> **From:** Ebel,Greg
>
> **Sent:** Friday, August 28, 2020 11:57 AM
> **To:** epstein ecohealthalliance.org>; Schountz,Tony
>
> **Subject:** RE: R24
>
> The morning of the 14th is OK for me.
>
> Greg
>
> **From:** Jon Epstein ecohealthalliance.org>

Sent: Friday, August 28, 2020 11:56 AM
To: Schountz,Tony

Cc: Ebel,Greg
>

Subject: Re: R24

the 14th would work for me.

-Jon

On Fri, Aug 28, 2020 at 1:54 PM Schountz,Tony

wrote:

> Monday the 14th is open for me but the rest of the week is really tough.
>
> —
>
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

From: Jon Epstein
ecohealthalliance.org>
Sent: Friday, August 28, 2020 11:52 AM
To: Schountz,Tony

Cc: Ebel,Greg

Subject: Re: R24

I'm actually off that week - we're moving the family back into NYC for the start of School (Sept 10th).

Could we meet the following week?

Thanks,

Jon

On Fri, Aug 28, 2020 at 1:45

PM Schountz,Tony

rote:

> Greg and Jon, I think we ought to schedule a conference call in a couple of weeks to hash out the R24 approach, namely to determine the goals and to identify people who need to be involved. How does the week of Sept 7 look? We're taking the kids hiking on Labor Day but otherwise my week is mostly open except for the morning of Thursday, September 10.
>
> Tony
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> —
>
> Tony Schountz, PhD
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--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

web: ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

--

From: Schountz,Tony on behalf of Schountz,Tony
Sent: Friday, August 28, 2020 1:54 PM EDT
To: epstein ecohealthalliance.org>
CC: Ebel,Greg
Subject: Re: R24

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Tony Schountz, PhD
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Arthropod-borne and Infectious Disease Laboratory
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From: Tony Schountz on behalf of Schountz,Tony >
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CC: epstein ecohealthalliance.org>; Ebel,Greg
Subject: Re: R24

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> Time: Sep 14, 2020 10:00 AM Mountain Time (US and Canada)
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> https://us02web.zoom.us/j/5861713088?pwd=RVJmb2VsenlWR1U3TkdiVGp4WUc2QT09
>
> Meeting ID: 586 171 3088
> Passcode: 4e5ZJe
>
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
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> > Tony Schountz, PhD
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> > Colorado State University

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> **Sent:** Friday, August 28, 2020 11:56 AM
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> **Cc:** Ebel,Greg
> **Subject:** Re: R24
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> > Colorado State University
> >
> > ---
> >
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> > **Sent:** Friday, August 28, 2020 11:52 AM
> > **To:** Schountz,Tony >
> > **Cc:** Ebel,Greg
> > **Subject:** Re: R24
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Tony

—

Tony Schountz, PhD
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--

Jonathan H. Epstein DVM, MPH, PhD

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--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

web: ecohealthalliance.org

From: Schountz,Tony on behalf of Schountz,Tony >
Sent: Thursday, October 08, 2020 12:35 PM EDT
To: epstein ecohealthalliance.org>; Ebel,Greg <
Subject: Re: R24

Yeah, it might be worth holding off until December to ask. □

T.

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Jon Epstein ecohealthalliance.org>
Sent: Thursday, October 8, 2020 8:28 AM
To: Ebel,Greg
Cc: Schountz,Tony >
Subject: Re: R24

Sure, but I'd prefer to avoid sharing details of what we're doing at this stage, if possible.

Cheers,
Jon

Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
New York

On Wed, Oct 7, 2020, 5:49 PM Ebel,Greg > wrote:

> Hey,
>
> Do you all want me to reach out to Scott W about the WRCEVA R24?
>
> He might say no, but I'm fully OK with asking.
>
> Greg
>
> Gregory D. Ebel
> Professor, Department of Microbiology, Immunology and Pathology
> Director, Arthropod-Borne and Infectious Diseases Laboratory
> College of Veterinary Medicine and Biomedical Sciences
> Colorado State University
>
> https://ebel.colostate.edu
> @ebellaboratory
> he/him/his

From: Tony Schountz > on behalf of Schountz,Tony >
Sent: Thursday, September 24, 2020 12:00 PM EDT
To: epstein ecohealthalliance.org>
CC: Schountz,Tony >
Subject: Re: R24
Attachment(s): "jmv.25817.pdf"

Jon, attached is the paper with the ACE2 sequences that led us down the deer mouse path for SARS2 susceptibility. I've highlighted the 7 Rhinolophus species on page 2 as well as the table with the 20 critical amino acids. (Deer mice have 17 of these 20.) So, R. pearsonii is the closest, but I suspect there may be other Rhinolophus species that have not had ACE2 sequences determined that may be closer to the 20 found in humans, and which may be more likely to be susceptible. It would be helpful if we could get as many ACE2 sequences as possible but we'd need access to lung RNA from each of them to do the PCR and sequencing. I'm suspect someone at Wuhan or elsewhere in China are already doing this. Identifying which facilitate virus entry (e.g., transfection experiments) would point to the best candidates for susceptibility and which we would want to import for one-off susceptibility experiments.

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Sep 24, 2020, at 9:37 AM, Schountz,Tony > wrote:

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

<Screen Shot 2020-09-24 at 9.36.55 AM.png>

On Sep 24, 2020, at 8:54 AM, Schountz,Tony wrote:

Here's the zoom info:

Topic: Tony Schountz's Zoom Meeting
Time: Sep 24, 2020 09:00 AM Mountain Time (US and Canada)

Join Zoom Meeting
https://us02web.zoom.us/j/5861713088?pwd=RVJmb2VsenlWR1U3TkdiVGp4WUc2QT09

Meeting ID: 586 171 3088
Passcode: 4e5ZJe

—
Tony Schountz, PhD
Associate Professor
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Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

Received: 5 March 2020 | Accepted: 30 March 2020

DOI: 10.1002/jmv.25817

SHORT COMMUNICATION

JOURNAL OF MEDICAL VIROLOGY WILEY

SARS-CoV-2 spike protein favors ACE2 from *Bovidae* and *Cricetidae*

Junwen Luan[1] | Xiaolu Jin[1,2] | Yue Lu[1,2] | Leiliang Zhang[1]

[1]Institute of Basic Medicine, Shandong Provincial Hospital Affiliated to Shandong First Medical University, Jinan, Shandong, China

[2]School of Medicine and Life Sciences, Shandong Academy of Medical Sciences, University of Jinan, Jinan, Shandong, China

Correspondence
Leiliang Zhang, PhD, Institute of Basic Medicine, Shandong Provincial Hospital Affiliated to Shandong First Medical University, Jinan, 250062 Shandong, China.
Email: armzhang@hotmail.com

Funding information
National Key Plan for Research and Development of China, Grant/Award Number: 2016YFD0500300; Shandong Academy of Medical Sciences Grant, Grant/Award Number: 2017-52; Innovation Project of Shandong Academy of Medical Sciences; Academic promotion programme of Shandong First Medical University, Grant/Award Number: 2019LJ001

Abstract

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) causes the recent COVID-19 public health crisis. Bat is the widely believed original host of SARS-CoV-2. However, its intermediate host before transmitting to humans is not clear. Some studies proposed pangolin, snake, or turtle as the intermediate hosts. Angiotensin-converting enzyme 2 (ACE2) is the receptor for SARS-CoV-2, which determines the potential host range for SARS-CoV-2. On the basis of structural information of the complex of human ACE2 and SARS-CoV-2 receptor-binding domain (RBD), we analyzed the affinity to S protein of the 20 key residues in ACE2 from mammal, bird, turtle, and snake. Several ACE2 proteins from *Primates*, *Bovidae*, *Cricetidae*, and *Cetacea* maintained the majority of key residues in ACE2 for associating with SARS-CoV-2 RBD. The simulated structures indicated that ACE2 proteins from *Bovidae* and *Cricetidae* were able to associate with SARS-CoV-2 RBD. We found that nearly half of the key residues in turtle, snake, and bird were changed. The simulated structures showed several key contacts with SARS-CoV-2 RBD in turtle and snake ACE2 were abolished. This study demonstrated that neither snake nor turtle was the intermediate hosts for SARS-CoV-2, which further reinforced the concept that the reptiles are resistant against infection of coronavirus. This study suggested that *Bovidae* and *Cricetidae* should be included in the screening of intermediate hosts for SARS-CoV-2.

KEYWORDS

ACE2, *Bovidae*, *Cricetidae*, intermediate host, SARS-CoV-2

1 | INTRODUCTION

Coronavirus disease 2019 (COVID-19), which was first reported in Wuhan, Hubei province, China, has caused over 80 422 human infections and more than 2984 deaths (as of 4 March 2020) in China.[1,2] The confirmed cases outside China are increasing, which raised major global concern. Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was identified to be the pathogen of COVID-19. SARS-CoV-2 has joined SARS-CoV and Middle East respiratory syndrome-related coronavirus (MERS-CoV) as another coronavirus that causes severe respiratory disease and human death.[3,4]

The specificity of the interaction between virus and receptor determines its host range for the virus. Spike protein (S) of SARS-CoV-2 has attracted great attention because of its role in receptor binding. Angiotensin-converting enzyme 2 (ACE2) binds to the receptor-binding domain (RBD) of SARS-CoV-2 S protein and functions as a receptor for SARS-CoV-2.[5,6] The origin of SARS-CoV-2 is considered as bat.[6] However, the intermediate host is unknown. Some studies suggest that pangolin is involved in the evolution of SARS-CoV-2.[7,8] Others suggested that snake and turtles are potential intermediate hosts for SARS-CoV-2.[9,10] In this study, we compared the key amino acids (AAs) in ACE2 from different species for the binding ability to RBD. On the basis of

potential interaction between S protein and ACE2, it was speculated that SARS-CoV-2 preserved the ability to infect *Bovidae* and *Cricetidae* but not snake or turtle.

2 | METHODS

2.1 | Sequence analysis of ACE2

A total of 93 ACE2 protein sequences were selected from 85 mammals, 4 birds, 3 turtles, and 1 snake. These ACEs with their corresponding species are listed as follows: hACE2: *Homo sapiens* (BAB40370.1), RhiACE2: *Rhinopithecus roxellana* (XP_010364367.2), MacmACE2: *Macaca mulatta* (NP_001129168.1), MuseACE2: *Mustela erminea* (XP_032187679.1), CamdACE2: *Camelus dromedarius* (XP_031301717.1), PlACE2: *Procyon lotor* (XP_031301717.1), PcACE2: *Paguma larvata* (AAX63775.1), RmACE2: *Rhinolophus macrotis* (ADN93471.1), RfACE2: *Rhinolophus ferrumequinum* (BAH02663.1), RsACE2: *Rhinolophus sinicus* (ADN93472.1), RlACE2: *Rousettus leschenaultii* (BAF50705.1), SsACE2: *Sus scrofa* (NP_001116542.1), MpfACE2: *Mustela putorius furo* (BAE53380.1), RatACE2: *Rattus norvegicus* (Q5EGZ1), MmACE2: *Mus musculus* (Q3URC9), ClfACE2: *Canis lupus familiaris* (J9P7Y2), FcACE2: *Felis catus* (A0A384DV19), MjACE2: *Manis javanica* (XP_017505752.1), RpACE2: *Rhinolophus pearsonii* (ABU54053.1), PvACE2: *Pteropus vampyrus* (XP_011361275.1), PoaACE2: *Pongo abelii* (NP_001124604.1), EcACE2: *Equus caballus* (F6V9L3), BtACE2: *Bos taurus* (Q58DD0), PtACE2: *Pan troglodytes* (A0A2J8KU96), OraACE2: *Ornithorhynchus anatinus* (F7FDA2), OvaACE2: *Ovis aries* (W5PSB6), PanACE2: *Papio Anubis* (A0A096N4X9), LaACE2: *Loxodonta africana* (G3T6Q2), SsdACE2: *Sus scrofa domesticus* (A0A220QT48), EeACE2: *Erinaceus europaeus* (A0A1S3APE5), OcACE2: *Oryctolagus cuniculus* (G1TEF4), NpACE2: *Nyctereutes procyonoides* (B4XEP4), VvACE2: *Vulpes vulpes* (A0A3Q7-RAT9), PhcACE2: *Phodopus campbelli* (C7ECU7), MaACE2: *Mesocricetus auratus* (C7ECV1), CjACE2: *Callithrix jacchus* (F7CNJ6), SusACE2: *Suricata suricatta* (XP_029786256.1), HgACE2: *Heterocephalus glaber* (A0A0N8EUX7), DoACE2: *Dipodomys ordii* (A0A1S3GHT7), ItACE2: *Ictidomys tridecemlineatus* (XP_005316051.3), CpACE2: *Cavia porcellus* (XP_023417808.1), CgACE2: *Cricetulus griseus* (A0A061HZ66), ChACE2: *Capra hircus*(A0A452EVJ5); BibtACE2: *Bos indicus x Bos taurus* (A0A4W2H3A1), BmACE2: *Bos mutus* (L8I4I4), NlACE2: *Nomascus leucogenys* (G1RE79); CsACE2: *Chlorocebus sabaeus* (A0A0D9RQZ0); MfACE2: *Macaca fascicularis* (A0A2K5X283); PpACE2: *Pan paniscus* (A0A2R9BKD8); CaACE2: *Cercocebus atys* (A0A2K5KSD8); MnACE2: *Macaca nemestrina* (A0A2K6D1N8); MalACE2: *Mandrillus leucophaeus* (A0A2K5ZV99); TsACE2: *Tarsius syrichta* (A0A1U7TY97); PrcACE2: *Propithecus coquereli* (A0A2K6GHW5); UmACE2: *Ursus maritimus* (A0A452TT30); OgACE2: *Otolemur garnettii* (H0WMI5); SbbACE2: *Saimiri boliviensis boliviensis* (A0A2K6SBD4); CciACE2: *Cebus capucinus imitator* (A0A2K5PYM0); GggACE2: *Gorilla gorillagorilla* (G3QWX4); AnACE2: *Aotus nancymaae* (A0A2K5DQI6); ChaACE2: *Chlorocebus aethiops* (Q1LZX8); AmACE2: *Ailuropoda melanoleuca* (G1MC42); VuACE2: *Vombatus ursinus* (A0A4X2M679); UaACE2: *Ursus americanus* (A0A452R1Z9); UahACE2: *Ursusarctos horribilis* (A0A3Q7TE16); PmACE2: *Physeter macrocephalus* (A0A2Y9S5T9); LvACE2: *Lipotes vexillifer* (A0A340Y3Y6); BasACE2: *Balaenoptera acutorostrata scammoni* (A0A452CBT6); DlACE2: *Delphinapterus leucas* (A0A2Y9M9H3); TtACE2: *Tursiops truncatus* (A0A2U4AJL3); NaaACE2: *Neophocaena asiaeorientalis asiaeorientalis* (A0A341BCI8); CuACE2: *Callorhinus ursinus* (A0A3Q7N3M7); NsACE2: *Neomonachus schauinslandi* (A0A2Y9GEI9); TmlACE2: *Trichechus manatuslatirostris* (A0A2Y9E393); EllkACE2: *Enhydra lutriskenyoni* (A0A2Y9KLV0); ClACE2: *Chinchilla lanigera* (C7ECU0); MdACE2: *Monodelphis domestica* (F6WXR7); LpACE2: *Lynx pardinus* (A0A485NF12); PaACE2: *Pipistrellus abramus* (C7ECT9); MbACE2: *Myotis brandtii* (S7N573); DrACE2: *Desmodus rotundus* (K9INV8); RhpACE2: *Rhinolophus pusillus* (E2DHI9); RaACE2: *Rhinolophus alcyone* (A0A0N7IQX6); RlACE2(2): *Rhinolophus landeri* (A0A0P0IB69); MylACE2: *Myotis lucifugus* (G1PXH7), GgACE2: *Gallus gallus* (F1NHR4), ApACE2: *Anas platyrhynchos* (R0LHX5), MgACE2: *Meleagris gallopavo* (G1NPB8), CaaACE2: *Cathartes aura* (A0A091MDI4), OhACE2: *Ophiophagus hannah* (V8NIH2), CpbACE2: *Chrysemys picta bellii* (XP_023964517.1), CmACE2: *Chelonia mydas* (XP_007070561.1); and PsACE2: *Pelodiscus sinensis* (XP_006122891.1). On the basis of known 20 key sites in human ACE2 interacting with SARS-CoV-2 RBD,[11] we analyzed whether these sites were conserved on other ACE2 proteins. Phylogenetic and molecular evolutionary analysis of ACE2 protein was conducted using molecular evolutionary genetics analysis version X (MEGA-X).[12] Phylogenetic tree was generated with Jones-Taylor-Thornton evolutionary model using a maximum-likelihood method.

2.2 | Structure simulation of ACE2-RBD complex

On the basis of the structure of hACE2 with SARS-CoV-2 S RBD (PDB: 6LZG), the structure of SARS-CoV-2 S and ACE2 from *Bos taurus*, *Cricetulus griseus*, *Pelodiscus sinensis*, and *Ophiophagus hannah* were simulated by SWISS-MODEL online server[13] and analyzed by Chimera software version 1.14.[14]

3 | RESULTS

3.1 | Sequence alignment of ACE2

According to the recently resolved structure of the complex of human ACE2 and SARS-CoV-2 RBD, there are 20 key AAs in hACE2 for interacting with RBM.[11] We analyzed those AAs of ACE2 protein from a list of mammals, birds, turtles, and snake, as shown in Table 1. Next, a phylogenetic tree for mammalian ACE2 proteins was constructed by MEGA-X software. There were 16 *primates* ACE2, 5 *Bovidae* ACE2, 2 *Cricetidae* ACE2, and 3 *Cetacea* ACE2 (Table 1 and Figure 1A), possessing at least 90% (18/20) critical AAs. Pangolin ACE2 preserved only 70% (14/20) AAs. Nearly half of the key residues in turtles (CpbACE2, CmACE2, and PsACE2) and snake (OhACE2) were changed (Table 1). ACE2 from *Aves*, including *Gallus gallus*, *Anas platyrhynchos*, *Meleagris gallopavo*, and *Cathartes aura*, only matched 10 to 11 AAs (Table 1).

TABLE 1 Analysis of the key AAs in ACE2 for SARS-CoV-2 RBD binding

	AA position																			
ACE2	24	27	28	30	31	34	35	37	38	41	42	45	82	83	330	353	354	355	357	393	Matched AA
hACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
RhiACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
MacmACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
PoaACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
PtACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
PanACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
NlACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
CsACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
MfACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
PpACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
CaACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
MnACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
MalACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
GggACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
ChaACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R	R	20
PrcACE2	Q	T	F	D	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	19
BtACE2	Q	T	F	E	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
OvaACE2	Q	T	F	E	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
MaACE2	Q	T	F	D	K	Q	E	E	D	Y	Q	L	N	Y	N	K	G	D	R	R	18
CgACE2	Q	T	F	D	K	Q	E	E	D	Y	Q	L	N	Y	N	K	G	D	R	R	18
ChACE2	Q	T	F	E	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
BibtACE2	Q	T	F	E	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
BmACE2	Q	T	F	E	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
PmACE2	Q	T	F	Q	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
DlACE2	Q	T	F	Q	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
NaaACE2	Q	T	F	Q	K	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	18
PhcACE2	Q	T	F	D	K	Q	E	E	D	Y	Q	L	N	Y	N	K	E	D	R	R	17
HgACE2	Q	T	F	D	K	Q	E	E	D	Y	Q	L	A	Y	N	K	D	D	R	R	17
ItACE2	L	T	F	D	K	Q	E	E	D	Y	Q	L	A	Y	N	K	G	D	R	R	17
BasACE2	Q	T	F	Q	K	H	E	E	D	Y	R	L	T	Y	N	K	G	D	R	R	17
CamdACE2	L	T	F	E	E	H	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
RlACE2	L	T	F	E	K	T	E	E	D	Y	Q	L	T	Y	K	K	G	D	R	R	16
SsACE2	L	T	F	E	K	L	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
FcACE2	L	T	F	E	K	H	E	E	E	Y	Q	L	T	Y	N	K	G	D	R	R	16
SsdACE2	L	T	F	E	K	L	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
OcACE2	L	T	F	E	K	Q	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
CjACE2	Q	T	F	D	K	H	E	E	D	H	E	L	T	Y	N	K	Q	D	R	R	16
DoACE2	L	T	F	D	N	Q	E	E	D	Y	Q	L	I	Y	N	K	G	D	R	R	16
UmACE2	L	T	F	E	K	Y	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16

(Continues)

TABLE 1 (Continued)

	AA position																				
ACE2	24	27	28	30	31	34	35	37	38	41	42	45	82	83	330	353	354	355	357	393	Matched AA
SbbACE2	Q	T	F	D	K	H	E	E	D	H	E	L	T	Y	N	K	Q	D	R	R	16
CciACE2	Q	T	F	D	K	H	E	E	D	H	E	L	T	Y	N	K	Q	D	R	R	16
AnACE2	Q	T	F	D	K	H	E	E	D	H	E	L	T	Y	N	K	Q	D	R	R	16
AmACE2	L	T	F	E	K	Y	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
UaACE2	L	T	F	E	K	Y	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
UahACE2	L	T	F	E	K	Y	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
LvACE2	R	T	F	Q	K	H	E	E	D	Y	Q	L	T	F	N	K	G	D	R	R	16
TtACE2	R	T	F	Q	K	R	E	E	D	Y	Q	L	T	Y	N	K	G	D	R	R	16
LpACE2	L	T	F	E	K	H	E	E	E	Y	Q	L	T	Y	N	K	G	D	R	R	16
MpfACE2	L	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	K	R	D	R	R	15
ClfACE2	L	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	K	G	D	R	R	15
RpACE2	R	T	F	D	K	H	E	E	D	H	E	L	D	Y	N	K	D	D	R	R	15
LaACE2	L	T	F	D	T	Q	E	E	D	Y	Q	L	D	F	N	K	G	D	R	R	15
VvACE2	L	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	K	G	D	R	R	15
CpACE2	Q	T	F	D	E	L	K	E	D	Y	Q	L	A	Y	N	K	N	D	R	R	15
TsACE2	Q	T	F	D	K	Q	E	E	D	H	Q	L	S	Y	N	N	S	D	R	R	15
TmlACE2	L	T	F	D	T	Q	E	E	D	Y	Q	L	N	F	N	K	G	D	R	R	15
ClACE2	Q	T	F	D	N	E	K	E	D	Y	Q	L	A	Y	N	K	D	D	R	R	15
MuseACE2	L	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	K	R	D	R	R	14
PlACE2	L	T	F	E	N	N	E	E	E	Y	Q	L	T	Y	N	K	G	D	R	R	14
MjACE2	E	T	F	E	K	S	E	E	E	Y	Q	L	N	Y	N	K	H	D	R	R	14
PvACE2	L	T	F	E	K	T	E	E	D	Y	Q	L	A	Y	K	K	G	D	R	K	14
EcACE2	L	T	F	E	K	S	E	E	E	H	Q	L	T	Y	N	K	G	D	R	R	14
NpACE2	L	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	R	G	D	R	R	14
OgACE2	Q	T	F	D	N	R	E	E	E	H	Q	L	T	Y	N	K	D	D	R	R	14
VuACE2	R	E	F	E	T	K	E	E	E	Y	Q	L	T	F	N	K	G	D	R	R	14
NsACE2	L	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	K	H	D	R	R	14
ElkACE2	P	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	K	R	D	R	R	14
RhpACE2	L	K	F	N	D	S	E	E	D	Y	Q	L	N	Y	N	K	G	D	R	R	14
RmACE2	E	K	F	D	K	S	K	E	D	Y	E	L	N	Y	K	K	G	D	R	R	13
RsACE2	E	I	F	D	K	T	K	E	D	H	Q	L	N	Y	N	K	G	D	R	R	13
RatACE2	K	S	F	N	K	Q	E	E	D	Y	Q	L	N	F	N	H	G	D	R	R	13
MmACE2	N	T	F	N	N	Q	E	E	D	Y	Q	L	S	F	N	H	G	D	R	R	13
CuACE2	L	T	F	E	K	S	E	E	E	Y	Q	F	T	Y	N	K	H	D	R	R	13
RlACE2(2)	L	T	F	D	D	S	A	E	N	Y	Q	L	N	F	N	K	G	D	R	R	13
PcACE2	L	T	F	E	T	Y	E	Q	E	Y	Q	V	T	Y	N	K	G	D	R	R	12
RfACE2	L	K	F	D	D	S	E	E	N	H	Q	L	N	F	N	K	G	D	R	R	12
SusACE2	L	T	F	E	Q	H	E	Q	E	Y	L	V	A	Y	N	K	G	D	R	R	12

TABLE 1 (Continued)

	AA position																			
ACE2	24	27	28	30	31	34	35	37	38	41	42	45	82	83	330	353	354	355	357	393	Matched AA
MdACE2	D	T	F	D	D	A	K	E	E	H	Q	L	T	Y	N	K	N	D	R	R	12
DrACE2	E	T	F	E	N	T	E	E	E	Y	Q	L	T	Y	N	N	K	D	R	R	12
RaACE2	L	I	F	D	N	S	E	E	N	H	Q	L	N	F	N	K	G	D	R	R	12
OraACE2	E	Q	F	T	Q	K	Q	E	D	Y	Q	L	K	F	N	K	N	D	R	R	11
EeACE2	E	K	F	D	D	R	Q	E	N	Y	E	L	N	Y	N	N	G	D	R	R	11
MbACE2	K	I	F	E	N	S	K	E	D	H	E	L	T	Y	N	K	G	D	R	R	11
MylACE2	K	I	F	E	N	S	A	E	D	H	E	L	T	Y	N	K	G	D	R	R	11
GgACE2	E	T	F	A	E	V	R	E	D	Y	E	L	R	F	N	K	N	D	R	R	11
ApACE2	Q	M	F	A	E	V	R	E	D	Y	E	L	N	F	N	K	N	D	R	R	11
MgACE2	E	T	F	A	E	V	R	E	D	Y	E	L	R	F	N	K	N	D	R	R	11
CpbACE2	E	N	F	S	Q	V	R	E	D	Y	A	L	K	Y	N	K	K	D	R	R	11
CmACE2	E	N	F	S	Q	V	R	E	D	Y	A	L	K	Y	N	K	K	D	R	R	11
PsACE2	E	N	F	S	E	V	Q	E	D	Y	A	L	K	Y	N	K	K	D	R	R	11
PaACE2	E	R	F	V	K	H	E	E	N	H	E	L	G	F	D	K	N	D	R	R	10
CaaACE2	Q	I	F	E	E	P	R	E	N	Y	E	L	S	F	N	K	N	D	R	R	10
OhACE2	...	K	F	E	Q	A	R	T	D	Y	N	I	M	F	N	K	E	D	R	R	9

Note: hACE2, *Homo sapiens* (BAB40370.1), RhiACE2, *Rhinopithecus roxellana* (XP_010364367.2), MacmACE2, *Macaca mulatta* (NP_001129168.1), MuseACE2, *Mustela erminea* (XP_032187679.1), CamdACE2, *Camelus dromedarius* (XP_031301717.1), PlACE2, *Procyon lotor* (XP_031301717.1), PcACE2, *Paguma larvata* (AAX63775.1), RmACE2, *Rhinolophus macrotis* (ADN93471.1), RfACE2, *Rhinolophus ferrumequinum* (BAH02663.1), RsACE2, *Rhinolophus sinicus* (ADN93472.1), RlACE2, *Rousettus leschenaultii* (BAF50705.1), SsACE2, *Sus scrofa* (NP_001116542.1), MpfACE2, *Mustela putorius furo* (BAE53380.1), RatACE2, *Rattus norvegicus* (Q5EGZ1), MmACE2, *Mus musculus* (Q3URC9), ClfACE2, *Canis lupus familiaris* (J9P7Y2), FcACE2, *Felis catus* (A0A384DV19), MjACE2, *Manis javanica* (XP_017505752.1), RpACE2, *Rhinolophus pearsonii* (ABU54053.1), PvACE2, *Pteropus vampyrus* (XP_011361275.1), PoaACE2, *Pongo abelii* (NP_001124604.1), EcACE2, *Equus caballus* (F6V9L3), BtACE2, *Bos taurus* (Q58DD0), PtACE2, *Pan troglodytes* (A0A2J8KU96), OraACE2, *Ornithorhynchus anatinus* (F7FDA2), OvaACE2, *Ovis aries* (W5PSB6), PanACE2, *Papio Anubis* (A0A096N4X9), LaACE2, *Loxodonta africana* (G3T6Q2), SsdACE2, *Sus scrofa domesticus* (A0A220QT48), EeACE2, *Erinaceus europaeus* (A0A1S3APE5), OcACE2, *Oryctolagus cuniculus* (G1TEF4), NpACE2, *Nyctereutes procyonoides* (B4XEP4), VvACE2, *Vulpes vulpes* (A0A3Q7RAT9), PhcACE2, *Phodopus campbelli* (C7ECU7), MaACE2, *Mesocricetus auratus* (C7ECV1), CjACE2, *Callithrix jacchus* (F7CNJ6), SusACE2, *Suricata suricatta* (XP_029786256.1), HgACE2, *Heterocephalus glaber* (A0A0N8EUX7), DoACE2, *Dipodomys ordii* (A0A1S3GHT7), ItACE2, *Ictidomys tridecemlineatus* (XP_005316051.3), CpACE2, *Cavia porcellus* (XP_023417808.1), CgACE2, *Cricetulus griseus* (A0A061HZ66), ChACE2, *Capra hircus*(A0A452EVJ5); BibtACE2, *Bos indicus x Bos taurus* (A0A4W2H3A1), BmACE2, *Bos mutus* (L8I4I4), NlACE2, *Nomascus leucogenys* (G1RE79); CsACE2, *Chlorocebus sabaeus* (A0A0D9RQZ0); MfACE2, *Macaca fascicularis* (A0A2K5X283); PpACE2, *Pan paniscus* (A0A2R9BKD8); CaACE2, *Cercocebus atys* (A0A2K5KSD8); MnACE2, *Macaca nemestrina* (A0A2K6D1N8); MalACE2, *Mandrillus leucophaeus* (A0A2K5ZV99); TsACE2, *Tarsius syrichta* (A0A1U7TY97); PrcACE2, *Propithecus coquereli* (A0A2K6GHW5); UmACE2, *Ursus maritimus* (A0A452TT30); OgACE2, *Otolemur garnettii* (H0WMI5); SbbACE2, *Saimiri boliviensis boliviensis* (A0A2K6SBD4); CciACE2, *Cebus capucinus imitator* (A0A2K5PYM0); GggACE2, *Gorilla gorillagorilla* (G3QWX4); AnACE2, *Aotus nancymaae* (A0A2K5DQI6); ChaACE2, *Chlorocebus aethiops* (Q1LZX8); AmACE2, *Ailuropoda melanoleuca* (G1MC42); VuACE2, *Vombatus ursinus* (A0A4X2M679); UaACE2, *Ursus americanus* (A0A452R1Z9); UahACE2, *Ursusarctos horribilis* (A0A3Q7TE16); PmACE2, *Physeter macrocephalus* (A0A2Y9S5T9); LvACE2, *Lipotes vexillifer* (A0A340Y3Y6); BasACE2, *Balaenoptera acutorostrata scammoni* (A0A452CBT6); DlACE2, *Delphinapterus leucas* (A0A2Y9M9H3); TtACE2, *Tursiops truncatus* (A0A2U4AJL3); NaaACE2, *Neophocaena asiaeorientalis asiaeorientalis* (A0A341BCI8); CuACE2, *Callorhinus ursinus* (A0A3Q7N3M7); NsACE2, *Neomonachus schauinslandi* (A0A2Y9GEI9); TmlACE2, *Trichechus manatuslatirostris* (A0A2Y9E393); EllkACE2, *Enhydra lutriskenyoni* (A0A2Y9KLV0); ClACE2, *Chinchilla lanigera* (C7ECU0); MdACE2, *Monodelphis domestica* (F6WXR7); LpACE2, *Lynx pardinus* (A0A485NF12); PaACE2, *Pipistrellus abramus* (C7ECT9); MbACE2, *Myotis brandtii* (S7N573); DrACE2, *Desmodus rotundus* (K9INV8); RhpACE2, *Rhinolophus pusillus* (E2DHI9); RaACE2, *Rhinolophus alcyone* (A0A0N7IQX6); RlACE2(2), *Rhinolophus landeri* (A0A0P0IB69); MylACE2, *Myotis lucifugus* (G1PXH7), GgACE2, *Gallus gallus* (F1NHR4), ApACE2, *Anas platyrhynchos* (R0LHX5), MgACE2, *Meleagris gallopavo* (G1NPB8), CaaACE2, *Cathartes aura* (A0A091MDI4), OhACE2, *Ophiophagus hannah* (V8NIH2), CpbACE2, *Chrysemys picta bellii* (XP_023964517.1), CmACE2, *Chelonia mydas* (XP_007070561.1); and PsACE2, *Pelodiscus sinensis* (XP_006122891.1).
Abbreviations: AA, amino acid; ACE2, angiotensin-converting enzyme 2; RBD, receptor-binding domain; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

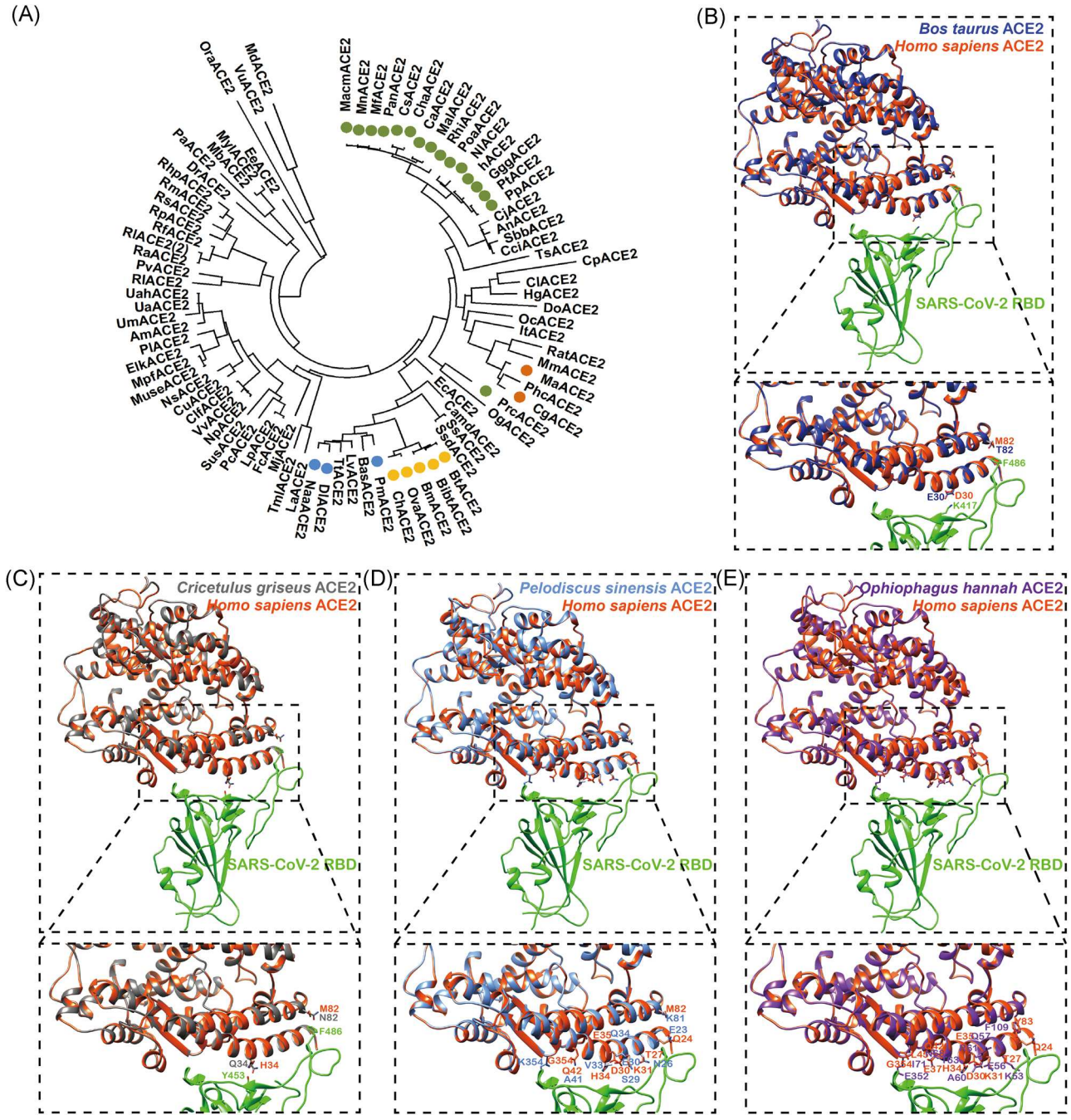

FIGURE 1 Structure simulation of SARS-CoV-2 RBD with ACE2 from different species. A, Phylogenetic tree of mammalian ACE2. ACE2 proteins from a total of 85 mammals were analyzed by MEGA-X and the phylogenetic tree was constructed using a maximum-likelihood method. The green, yellow, orange, and blue represent ACE2 from *Primates*, *Bovidae*, *Cricetidae*, and *Cetacea*, respectively. B, Structural simulation of the protein complex of *Bos taurus* ACE2 and SARS-CoV-2 RBD. *Bos taurus* ACE2, *Homo sapiens* ACE2, and SARS-CoV-2 RBD are in medium blue, orange red, and green, respectively. C, Structural simulation of the protein complex of *Cricetulus griseus* ACE2 and SARS-CoV-2 RBD. *Cricetulus griseus* ACE2, *Homo sapiens* ACE2, and SARS-CoV-2 RBD are in dim gray, orange red, and green, respectively. D, Structural simulation of the protein complex of *Pelodiscus sinensis* ACE2 and SARS-CoV-2 RBD. *Pelodiscus sinensis* ACE2, *Homo sapiens* ACE2, and SARS-CoV-2 RBD are in cornflower blue, orange red, and green, respectively. E, Structural simulation of the protein complex of *Ophiophagus hannah* ACE2 and SARS-CoV-2 RBD. *Ophiophagus hannah* ACE2, *Homo sapiens* ACE2, and SARS-CoV-2 RBD are in purple, orange red, and green, respectively. ACE2, angiotensin-converting enzyme 2; MEGA-X, Molecular Evolutionary Genetics Analysis version X; RBD, receptor-binding domain; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2

3.2 | Structure simulation of the protein complex of SARS-CoV-2 RBD and *Bovidae/Cricetidae*/turtle/snake ACE2

Recently, the structure of SARS-CoV-2 RBD with human ACE2 has been resolved. To investigate whether *Bovidae/Cricetidae* ACE2 maintained the binding affinity with SARS-CoV-2 RBD, we simulated the potential structure of the protein complex. T82 and E30 in *Bos taurus* ACE2 kept the contact to F486 and K417 in SARS-CoV-2 S (Figure 1B). N82 and Q34 in *Cricetulus griseus* ACE2 maintained the contact to F486 and Y453 in SARS-CoV-2 S (Figure 1C). We concluded that *Bovidae/Cricetidae* ACE2 could associate with SARS-CoV-2 S (Figure 1B,C).

To investigate the potential association between SARS-CoV-2 and ACE2 from turtle and snake, we simulated the potential structure of turtle/snake ACE2 with SARS-CoV-2 RBD. The AA correlated to hACE2 Q42 is changed to A (A41) in turtle (Figure 1D). We also noticed that the AA correlated to hACE2 H34 is changed to A (A60) in a snake (Figure 1E). When the contact AA was mutated to smaller AA (A), the contact force for protein-protein interaction will be reduced. Moreover, the corresponding AA of K31 was changed to E (E30) in turtle and Q (Q57) in snake ACE2 (Figure 1D). K31 in hACE2 was critical for SARS-CoV RBD binding and ACE2-K31D mutant abolished its association with SARS-CoV RBD.[15] Taken together, turtle and snake ACE2 are unlikely to bind to S protein of SARS-CoV-2.

4 | DISCUSSION

SARS-CoV, MERS-CoV, and SARS-CoV-2 have caused severe human infectious diseases in the last 2 decades. These three human coronaviruses originated from bats, but the intermediate hosts were different. SARS-CoV came from the *Paguma larvata*,[16] and the intermediate host for MERS-CoV is *Camelus dromedaries*.[17] The new coronavirus SARS-CoV-2 has recently caused a serious pandemic in China and other countries. However, it is not clear which animals are involved in the evolution of SARS-CoV-2 and which animals may be infected by SARS-CoV-2. RBD region in S protein of pangolin coronavirus is similar to that of SARS-CoV-2,[7,8] indicating the involvement of pangolin in the recombination of SARS-CoV-2. By analyzing the codon usage of SARS-CoV-2, people suggested that snake might be a potential host for SARS-CoV-2.[9] Another study indicated that turtle is a potential intermediate host for SARS-CoV-2 based on the key AAs in ACE2 for interacting with SARS-CoV RBD.[10] The late study raised the concerns of SARS-CoV-2 infection in the turtle aquaculture and pet turtle. Most of the coronaviruses hosts are mammals; with a few of exceptions are birds. Considering that all known hosts for coronaviruses are thermostatic animals, it is unlikely that reptiles will be infected with SARS-CoV-2.

There are 20 key AAs in ACE2 critical for binding S protein of SARS-CoV-2.[11] On the basis of these 20 AAs, we analyzed the corresponding AAs in ACE2 from a list of mammal, bird, turtle, and snake. We found that the ACE2 of turtles and snake lost the capability to associate with S protein (Table 1 and Figure 1D,E). These reptiles should be ruled out from the potential host list for SARS-CoV-2. *Aves* ACE2 was unlikely to associate with SARS-CoV-2 RBD because they lost the critical K corresponding to K31 in human ACE2 (Table 1). Pangolin ACE2 was predicted to recognize SARS-CoV-2 RBD less efficiently because it only preserved 14 of 20 critical AAs (Table 1). Interestingly, we found that ACE2 proteins from *Primates*, *Bovidae*, *Cricetidae*, and *Cetacea* were capable to recognize RBD of SARS-CoV-2 by maintaining the majority of key residues in ACE2 for associating with SARS-CoV-2 RBD. Swine ACE2 (CpACE2) with 15 of 20 matched critical AAs was shown to support SARS-CoV-2 entry.[6] *Bovidae/Cricetidae* ACE2 matched more AAs than swine ACE2, thus they should recognize SARS-CoV-2 RBD. It would strengthen our conclusion if we have biochemical evidence for the S-ACE2 interaction analysis for *Bovidae/Cricetidae* ACE2. On the basis of human ACE2 and SARS-CoV-spike complex structure model (PDB ID: 2AJF), we and others recently predicted that hamster ACE2 could associate with SARS-CoV-2 and hamster might be a candidate small animal model for SARS-CoV-2 infection.[18,19] Indeed, golden Syrian hamster (*Mesocricetus auratus*) has been established as a model to study the pathogenesis and transmission of COVID-19.[19] One of *Cetacea*, *Neophocaena asiaeorientalis asiaeorientalis* (Yangtze finless porpoise), lives in the middle and lower reaches of the Yangtze River and its lakes, where Wuhan located nearby.[20] It will be interesting to investigate whether Yangtze finless porpoise could be infected with SARS-CoV-2 or related coronavirus.

In conclusion, we found that *Bovidae/Cricetidae* ACE2 but not turtle/snake ACE2 could recognize SARS-CoV-2 RBD. More attention should be paid to *Bovidae* and *Cricetidae* in hunting the potential intermediate host for SARS-CoV-2.

ACKNOWLEDGMENTS

The authors would like to thank Dr Shan Gao for the discussion. This study is supported by grants from National Key Plan for Research and Development of China (2016YFD0500300), Shandong Academy of Medical Sciences Grant (2017-52), the Innovation Project of Shandong Academy of Medical Sciences, and Academic Promotion Program of Shandong First Medical University (2019LJ001). Molecular graphics and analyses performed with UCSF Chimera, developed by the Resource for Biocomputing, Visualization, and Informatics at the University of California, San Francisco, with support from NIH P41-GM103311.

CONFLICT OF INTERESTS

The authors declare that there are no conflict of interests.

AUTHOR CONTRIBUTIONS

LZ conceived the work. JL and XJ collected and analyzed the data. JL and YL contributed to graphics processing. LZ wrote the manuscript. All authors approved the final version for publication.

ORCID

Leiliang Zhang http://orcid.org/0000-0002-7015-9661

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How to cite this article: Luan J, Jin X, Lu Y, Zhang L. SARS-CoV-2 spike protein favors ACE2 from *Bovidae* and *Cricetidae*. *J Med Virol*. 2020;1–8. https://doi.org/10.1002/jmv.25817

From: Tony Schountz > on behalf of Schountz,Tony <
Sent: Thursday, September 24, 2020 11:37 AM EDT
To: Schountz,Tony
CC: epstein ecohealthalliance.org>; Ebel,Greg <
Subject: Re: R24

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

ACE2 Residues Involved in Spike Interactic

Suscept
Not susc
Unknow

Twenty Ace2 Residues Involved in SARS-CoV-2 Receptor Binding

	ACE2	AA position																		
Common Name	**Species name**	24	27	28	30	31	34	35	37	38	41	42	45	82	83	330	353	354	355	357
Human	*Homo sapiens*	Q	T	F	D	K	H	E	E	D	Y	Q	L	M	Y	N	K	G	D	R
Syrian hamster	*Mesocricetus auratus*	Q	T	F	D	K	Q	E	E	D	Y	Q	L	N	Y	N	K	G	D	R
Leschenault's rousette	*Rousettus leschenaultii*	L	T	F	E	K	T	E	E	D	Y	Q	L	T	Y	K	K	G	D	R
Domestic cat	*Felis catus*	L	T	F	E	K	H	E	E	E	Y	Q	L	T	Y	N	K	G	D	R
Pearson's horseshoe bat	*Rhinolophus pearsonii*	R	T	F	D	K	H	E	E	D	H	E	L	D	Y	N	K	D	D	R
Least horseshoe bat	*Rhinolophus pusillus*	L	K	F	N	D	S	E	E	D	Y	1	L	N	Y	N	K	G	D	R
Ferret	*Mustela putorius*	L	T	F	E	K	Y	E	E	E	Y	Q	L	T	Y	N	K	R	D	R
Big-eared horseshoe bat	*Rhinolophus macrotis*	E	K	F	D	K	S	K	E	D	Y	E	L	N	Y	K	K	G	D	R
Chinese rufous horseshoe bat	*Rhinolophus sinicus*	E	I	F	D	K	T	K	E	D	H	Q	L	N	Y	N	K	G	D	R
Lander's horseshoe bat	*Rhinolophus landeri*	L	T	F	D	D	S	A	E	N	Y	Q	L	N	F	N	K	G	D	R
Jamaican fruit bat	*Artibeus jamaicensis*	D	T	F	E	K	T	E	E	E	Y	E	L	A	Y	N	K	N	D	R
Norway rat	*Rattus norvegicus*	K	S	F	N	K	Q	E	E	D	Y	Q	L	N	F	N	H	G	D	R
House mouse	*Mus musculus*	N	T	F	N	N	Q	E	E	D	Y	Q	L	S	F	N	H	G	D	R
Greater horseshoe bat	*Rhinolophus ferrumequinum*	L	K	F	D	D	S	E	E	N	H	Q	L	N	F	N	K	G	D	R
Vampire bat	*Desmodus rotundus*	E	T	F	E	N	T	E	E	E	Y	Q	L	T	Y	N	N	K	D	R
Halcyon horseshoe bat	*Rhinolophus alcyone*	L	I	F	D	N	S	E	E	N	H	Q	L	K	F	N	K	N	D	R
Brandt's bat	*Myotis brandii*	K	I	F	E	N	S	K	E	D	H	E	L	T	Y	N	K	G	D	R
Little brown bat	*Myotis lucifugus*	K	I	F	E	N	S	A	E	D	H	E	L	T	Y	N	K	G	D	R
Japanese house bat	*Pipistrellus abramus*	E	R	F	V	K	H	E	E	N	H	E	L	G	F	D	K	N	D	R

20 Residues (white/blue) fro
5 Residues (blue) fr

On Sep 24, 2020, at 8:54 AM, Schountz,Tony wrote:

Here's the zoom info:

Topic: Tony Schountz's Zoom Meeting
Time: Sep 24, 2020 09:00 AM Mountain Time (US and Canada)

Join Zoom Meeting
https://us02web.zoom.us/j/5861713088?pwd=RVJmb2VsenlWR1U3TkdiVGp4WUc2QT09

Meeting ID: 586 171 3088
Passcode: 4e5ZJe

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony
Sent: Wednesday, July 12, 2017 8:16 PM EDT
To: 石正丽 <zlshi
Subject: Re: Re: Bat ID Abstract Submission

Hi Zhengli,

I hope your travel home was peaceful. I wanted to thank you for your attendance and presentation at the bat ID symposium. I think it was a very good meeting and I hope others benefited from it. We are already planning to host it again in 2020.

If you have an email distribution list for the conference you're hosting next year, could you please add me to it? It looks like a great meeting and if I can get travel arranged I would like to come.

Thank you,

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: 石正丽 <zlsh
Sent: Wednesday, April 26, 2017 6:32 PM
To: Schountz,Tony
Subject: Re: Re: Bat ID Abstract Submission

Dear Tony,
Thank you very much for your information and organising the meeting!
Looking forward to meeting you!
Best regards,

Zhengli,

> -----原始邮件-----
> **发件人:** "Schountz,Tony" >
> **发送时间:** 2017年4月27日 星期四
> **收件人:** "Schountz,Tony" >
> **抄送:** "zlshi@wh.iov.cn" <zlshi
> **主题:** Re: Bat ID Abstract Submission
>
> Dear Dr. Shi,
>
> We have you scheduled to give a 15 min talk (12 minutes plus 3 minutes for questions) at the bat infectious diseases symposium, probably Friday morning, June 30. I should have the program draft up next week.
>
> Thanks,
>
> Tony
>
> > On Mar 29, 2017, at 7:37 AM, Tony Schountz wrote:
> >
> > Thank you for submitting an abstract to the Bat ID Symposium. A decision on its disposition will be made in May.
> >
> > ## Bat ID Abstract Submission
> >
> > | | |
> > |---|---|
> > | **Presenting author email address** * | |
> > | **Presentation Type** * | Oral Presentation |
> > | **Please choose ONE or TWO categories for your abstract** * | • Coronaviruses |
> > | **Title** * | SARS coronavirus may have originated from frequent recombination events between SARS-like coronaviruses in a single horseshoe bat habitat |

Authors *	Hu B, Zeng L-P, Yang X-L, Ge X-Y, Zhang W, Li B, Luo D-S, Zhang Y-Z, Wang M-N, Daszak P, Wang L-F, Cui J, Shi Z-L.
Institutions *	CAS Key Laboratory of Special Pathogens and Biosafety, Center for Emerging Infectious Diseases of Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China; Yunnan Institute of Endemic Diseases Control and Prevention, Dali, China; EcoHealth Alliance, New York, New York, USA; Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore
Upload your abstract *	us_bat_conference_zhengli_shi_oral.docx 16.38 KB · DOCX

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony
Sent: Wednesday, April 26, 2017 10:42 PM EDT
To: 石正丽 <zlshi >
Subject: Re: Re: Bat ID Abstract Submission

Hi Zhengli,

Yes, we are excited for the symposium. Quite a few more abstracts this time, so I am optimistic we can continue having the symposium at 3 year intervals.

Let me know if there's anything I can do to help you.

Thanks,

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: 石正丽 <zlsh
Sent: Wednesday, April 26, 2017 6:32 PM
To: Schountz,Tony
Subject: Re: Re: Bat ID Abstract Submission

Dear Tony,
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Looking forward to meeting you!
Best regards,

Zhengli,

> -----原始邮件-----
> **发件人:** "Schountz,Tony"
> **发送时间:** 2017年4月27日 星期四
> **收件人:** "Schountz,Tony"
> **抄送:** "zlshi
> **主题:** Re: Bat ID Abstract Submission
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> Dear Dr. Shi,
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> We have you scheduled to give a 15 min talk (12 minutes plus 3 minutes for questions) at the bat infectious diseases symposium, probably Friday morning, June 30. I should have the program draft up next week.
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> > | | |
> > |---|---|
> > | **Presenting author email address** * | |
> > | **Presentation Type** * | Oral Presentation |
> > | **Please choose ONE or TWO categories for your abstract** * | • Coronaviruses |
> > | **Title** * | SARS coronavirus may have originated from frequent recombination events between SARS-like coronaviruses in a single horseshoe bat habitat |

Authors *	Hu B, Zeng L-P, Yang X-L, Ge X-Y, Zhang W, Li B, Luo D-S, Zhang Y-Z, Wang M-N, Daszak P, Wang L-F, Cui J, Shi Z-L.
Institutions *	CAS Key Laboratory of Special Pathogens and Biosafety, Center for Emerging Infectious Diseases of Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China; Yunnan Institute of Endemic Diseases Control and Prevention, Dali, China; EcoHealth Alliance, New York, New York, USA; Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore
Upload your abstract *	us_bat_conference_zhengli_shi_oral.docx 16.38 KB · DOCX

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
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Colorado State University

From: Schountz,Tony
Sent: Saturday, May 12, 2018 11:15 AM EDT
To: 胡犇 <huben
Subject: Re: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Thank you, Ben. Should I make my own reservation?

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: 胡犇 <huben
Sent: Friday, May 11, 2018 6:47 PM
To: Schountz,Tony
Cc: 石正丽; 周鹏
Subject: Re: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Dear Dr.Schountz:
Here is the hotel information:
name: Optics Valley Kingdom Plaza Hotel Wuhan,
address: No.1 Wu Jia Wan, Hongshan District, Wuhan, Hubei Province, China.

Best
Ben

-----原始邮件-----
发件人:"Schountz,Tony"
发送时间:2018-05-12 00:01:20 (星期六)
收件人: "胡犇" <huben
抄送: "Schountz,Tony" , "石正丽" <zlsh >, "周鹏" <peng.zhou >
主题: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Hi Ben,

I have my flight booked and will arrive in Wuhan at 10:00 PM on October 19 (All Nippon Airways**NH 937**). Can you tell me the name and address of the hotel? I will need it for my visa and for my university administrators.

Thank you,

Tony

> On Apr 9, 2018, at 8:06 AM, 胡犇 <huben > wrote:
>
> Dear Dr.Schountz:
>
> The 8th International Symposium on Emerging Viral Diseases will be held in October 20-22, 2018, in Wuhan, China. The biennial symposium is organized by Wuhan Institute of Virology, Chinese Academy of Sciences and has become an important event for leading Chinese and international virologists to discuss cutting-edge science on emerging viruses as well as to foster global collaborations.
>
> Prof Zhengli Shi and Dr.Peng Zhou had a nice experience last year in Colorado when attending the symposium on bat-borne infectious diseases, and we know you have made great contributions to bat virus researches. We sincerely hope that you can attend the symposium. Please find enthe formal invitation letter for the meeting.
>
> If you have any question regarding the conference, please contact me.
>
> Thank you!

Best regards

Ben Hu Ph.D

Research Assistant

Secretary of the 8th International Symposium on Emerging Viral Diseases

Wuhan Institute of Virology, Chinese Academy of Sciences
Wuhan 430071, P.R. China

<Invitation letter Tony Schountz.pdf>

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony
Sent: Wednesday, August 08, 2018 10:00 PM EDT
To: 胡犇 <huben
CC: 石正丽 <zlshi
Subject: Re: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Thank you, Ben. My understanding is that it needs to be an original for the visa application.

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: 胡犇 <huben
Sent: Wednesday, August 8, 2018 7:38 PM
To: Schountz,Tony
Cc: 石正丽
Subject: Re: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Hi Dr.Shountz:
There is no problem about the invitation letter with the official seal. I can prepare it today.
Is a scanned copy of this letter acceptable for visa application or the embassy must need an original copy?
Thanks
Ben

> -----原始邮件-----
> **发件人:**"Schountz,Tony"
> **发送时间:**2018-08-09 02:15:14 (星期四)
> **收件人:** "胡犇" <huben >
> **抄送:** "石正丽" <zlshi >
> **主题:** Re: Invitation to the 8th International Symposium on Emerging Viral Diseases
>
> Hi Ben,
>
> I'm having trouble getting my visa for my visit. Apparently, I need the letter from you that has some kind of seal stamped on it, and this letter requires my passport number is listed on it. That number is My legal name is **William A Schountz** and this is the name on my passport so the letter should be addressed with that name. Can you mail the letter directly to me at:
>
> William Schountz
>
> It would be helpful to get the letter by the end of next week because I need my passport back by September 14 for upcoming travel. I cannot get the passport back until I have the visa approved.
>
> Thanks,
>
> Tony
>
> > On Aug 6, 2018, at 5:27 PM, 胡犇 <huben wrote:
> >
> > Thanks a lot for the abstract, Dr.Schountz.
> >
> > Best
> >
> > Ben

在 2018-08-07 04:36:28，"Schountz,Tony" 写道：

Hi Ben,

Attached is my abstract. I should have quite a bit more information for the talk as we have many bats infected with the virus and are getting some very interesting results.

Thanks,
Tony

On Apr 9, 2018, at 8:06 AM, 胡犇 <huben > wrote:

Dear Dr.Schountz:

The 8th International Symposium on Emerging Viral Diseases will be held in October 20-22, 2018, in Wuhan, China. The biennial symposium is organized by Wuhan Institute of Virology, Chinese Academy of Sciences and has become an important event for leading Chinese and international virologists to discuss cutting-edge science on emerging viruses as well as to foster global collaborations.

Prof Zhengli Shi and Dr.Peng Zhou had a nice experience last year in Colorado when attending the symposium on bat-borne infectious diseases, and we know you have made great contributions to bat virus researches. We sincerely hope that you can attend the symposium. Please find enthe formal invitation letter for the meeting.

If you have any question regarding the conference, please contact me.

Thank you!

Best regards

Ben Hu Ph.D

Research Assistant

Secretary of the 8th International Symposium on Emerging Viral Diseases

Wuhan Institute of Virology, Chinese Academy of Sciences
Wuhan 430071, P.R. China

<Invitation letter Tony Schountz.pdf>

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony
Sent: Wednesday, August 29, 2018 10:13 AM EDT
To: 胡犇 <huben >
Subject: Re: Re: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Hi Ben,

Yes, I received my visa last week. I used a company called CIBTvisas to handle it.

See you in October.

Thanks,

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: 胡犇 <huben >
Sent: Wednesday, August 29, 2018 8:08 AM
To: Schountz,Tony
Subject: Re: Re: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Dear Dr.Schountz:

May I ask whether your application for China visa goes well? Did the embassy accept the scanned copy of the invitation letter as supporting document?

If you successfully get the visa, please kindly update me.

Thanks.

Sincerely

Ben

-----原始邮件-----
发件人:"Schountz,Tony" >
发送时间:2018-08-09 10:00:26 (星期四)
收件人: "胡犇" <huben
抄送: "石正丽" <zlsh
主题: Re: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

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Tony

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Associate Professor
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From: 胡犇 <huben
Sent: Wednesday, August 8, 2018 7:38 PM
To: Schountz,Tony
Cc: 石正丽
Subject: Re: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Hi Dr.Shountz:
There is no problem about the invitation letter with the official seal. I can prepare it today.
Is a scanned copy of this letter acceptable for visa application or the embassy must need an original copy?
Thanks
Ben

-----原始邮件-----
发件人:"Schountz,Tony" >
发送时间:2018-08-09 02:15:14 (星期四)
收件人: "胡犇" <huben >
抄送: "石正丽" <zlshi
主题: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Hi Ben,

I'm having trouble getting my visa for my visit. Apparently, I need the letter from you that has some kind of seal stamped on it, and this letter requires my passport number is listed on it. That number is . My legal name is **William A Schountz** and this is the name on my passport so the letter should be addressed with that name. Can you mail the letter directly to me at:

William Schountz

It would be helpful to get the letter by the end of next week because I need my passport back by September 14 for upcoming travel. I cannot get the passport back until I have the visa approved.

Thanks,

Tony

On Aug 6, 2018, at 5:27 PM, 胡犇 <huben wrote:

Thanks a lot for the abstract, Dr.Schountz.

Best

Ben

在 2018-08-07 04:36:28，"Schountz,Tony" 写道：

Hi Ben,

Attached is my abstract. I should have quite a bit more information for the talk as we have many bats infected with the virus and are getting some very interesting results.

Thanks,
Tony

On Apr 9, 2018, at 8:06 AM, 胡犇 <huben > wrote:

Dear Dr.Schountz:

The 8th International Symposium on Emerging Viral Diseases will be held in October 20-22, 2018, in

Wuhan, China. The biennial symposium is organized by Wuhan Institute of Virology, Chinese Academy of Sciences and has become an important event for leading Chinese and international virologists to discuss cutting-edge science on emerging viruses as well as to foster global collaborations.

Prof Zhengli Shi and Dr.Peng Zhou had a nice experience last year in Colorado when attending the symposium on bat-borne infectious diseases, and we know you have made great contributions to bat virus researches. We sincerely hope that you can attend the symposium. Please find enthe formal invitation letter for the meeting.

If you have any question regarding the conference, please contact me.

Thank you!

Best regards

Ben Hu Ph.D

Research Assistant

Secretary of the 8th International Symposium on Emerging Viral Diseases

Wuhan Institute of Virology, Chinese Academy of Sciences
Wuhan 430071, P.R. China

<Invitation letter Tony Schountz.pdf>

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony
Sent: Wednesday, July 12, 2017 8:14 PM EDT
To: 胡犇 <huben >
Subject: Re: Re: Re: Requesting invitation letter for visa application
Attachment(s): "Bat ID Program 2017 June 23.pdf"

Hi Ben,

Did you get a PDF copy of the program? If not, I've attached it here.

The symposium was fantastic. We will probably have it again in 2020.

Thanks,

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: 胡犇 <huben
Sent: Tuesday, June 20, 2017 9:03 PM
To: Schountz,Tony
Subject: Re: Re: Re: Requesting invitation letter for visa application

Dear Dr. Schountz:

The exciting conference is approaching. Although unfortunately I cannot attend the meeting due to the limited budget on international travel of our project, my colleagues, Prof. Zhengli Shi and Dr. Peng Zhou will go to Fort Collins and give two oral presentations.

May I ask for a pdf version of the conference program to forward to them?

Thank you so much!

Sincerely

Ben

> -----原始邮件-----
> **发件人:** "Schountz,Tony" <
> **发送时间:** 2017年4月12日 星期三
> **收件人:** "胡犇" <huben
> **抄送:**
> **主题:** Re: Re: Requesting invitation letter for visa application
>
> You're very welcome, Ben. I look forward to meeting all of you at the symposium.
>
> Tony
>
> —
> Tony Schountz, PhD
> Associate Professor
> Arthropod-borne and Infectious Disease Laboratory
> Department of Microbiology, Immunology and Pathology
> College of Veterinary Medicine
> Colorado State University

From: 胡犇 <huben
Sent: Tuesday, April 11, 2017 7:34 PM
To: Schountz,Tony
Subject: Re: Re: Requesting invitation letter for visa application

Dear Dr. Schountz:
Thank you so much for your kind help!
Sincerely
Ben

-----原始邮件-----
发件人: "Schountz,Tony" < >
发送时间: 2017年4月11日 星期二
收件人: "胡犇" <huben
抄送:
主题: Re: Requesting invitation letter for visa application

Ben, I have attached a Word file that you can edit with the names and addresses of the four participants. So, just make a copy for each one and use them.

Thank you,

Tony

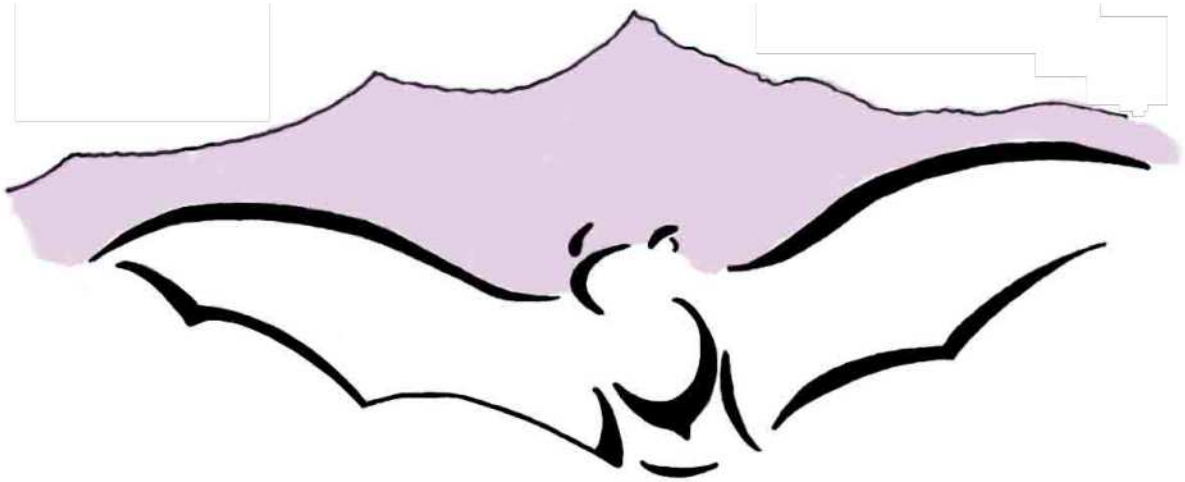
On Apr 11, 2017, at 3:56 AM, 鑀＄妵 <huben > wrote:

Dear Dr.Schountz:
I am a researcher at Wuhan Institute of Virology, Chinese Academy of Sciences. My colleagues and I are studying bat viruses and we have submitted four abstracts to the 2nd International Symposium on Infectious Diseases of Bats which is going to be held in Fort Collins in June.
The title for the 4 abstracts are:
1) SARS coronavirus may have originated from frequent recombination events betwwen SARS-like coronaviruses in a single horseshoe bat habitat (oral)
2) Dampening of STING-dependent IFN production: an implication of virus tolerance in bats? (oral) 锛墊 noticed from the web that this abstract has already been confirmed as oral presentation)
3) Genomic characterization of diverse BatCoV HKU10 and three novel alphacoronaviruses (poster)
4) Genetically diverse filoviruses in Rousettus and Eonycteris spp. bats, China, 2009 and 2015. (poster)
As it is a unique conference specializing on our research area, we are very eager to attend. However, it usually takes at least two months for us to get the US visa due to the complicated procedure of applying for travel permit to Chinese Academy of Sciences and then one month of administrative processing by US embassy. So in order we can make our visit to Colorado in late June, we have to start the process of travel permit and visa application now.
To apply for a travel permit, we are required to submit an invitation letter from the conference organizer. I know for the bat-borne disease meeting, we will know the results of the acceptance of the abstract by May. But it will be late for us to apply for the travel permit and US visa.
Could you please kindly provides four invitation letters to us indicating we will attend the meeting and give presentations? (oral or posters)
It does not matter whether the abstracts will be finally selected as he invitation letters are only for visa application.
We deeply appreciate your understanding and assistance.
Thank you very much!
Best regards

Ben Hu Ph.D
Research Assistant
Wuhan Institute of Virology, CAS

鈥?/div>
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

Infectious Diseases of Bats Symposium



June 29-July 1, 2017
University Center for the Arts
1400 Remington St
Colorado State University
Fort Collins, CO 80524

Table of Contents

Program

Venue: **University Center for the Arts**, Colorado State University

Thursday, June 29

5:30 p.m. Registration, PowerPoint file transfer, lobby, **University Center for the Arts**

6:00 p.m. Reception - *Wine, beer and snacks*, **University Center for the Arts**

Friday, June 30

7:00 a.m. Registration, University Center for the Arts

8:00 a.m. Tony Schountz. Colorado State University. **Welcoming remarks**

8:10 a.m. Session I - Filoviruses (Joseph Prescott, Moderator)

8:10 a.m. **Studies of horizontal transmission of Marburg virus among experimentally infected fruit bats**
Jonathan S. Towner[1,2], Amy J. Schuh[1], Brian R. Amman[1], Megan E. B. Jones[1,2], Tara K. Sealy[1], Uebelhoer LS, Spengler JR, Stuart T. Nichol[1]

[1]Viral Special Pathogens Branch, Centers for Disease Control and Prevention, Atlanta, USA, [2]Department of Pathology, College of Veterinary Medicine, University of Georgia, Athens, USA

8:30 a.m. **Investigations of Long-term Protective Immunity against Marburg Virus Reinfection in Egyptian Rousette Bats**
Amy Schuh, Amman BR, Sealy TK, Spengler JR, Nichol ST and Towner JS

Viral Special Pathogens Branch, Division of High-Consequence Pathogens and Pathology, Centers for Disease Control and Prevention, Atlanta, GA 30333, USA

8:45 a.m. **Innate immune response to filoviruses and the role of filoviral interferon-inhibiting domains in bat and human cells**
Ivan V. Kuzmin[1,2], Toni M. Schwarz[3], Philipp A. Ilinykh[1,2], Ingo Jordan[4], Thomas G. Ksiazek[1,2,5], Ravi Sachidanandam[6], Christopher F. Basler[3, 7], and Alexander Bukreyev[1,2,5]

[1] Department of Pathology, The University of Texas Medical Branch, Galveston, Texas, USA; [2] Galveston National Laboratory, The University of Texas Medical Branch, Galveston, Texas, USA; [3] Department of Microbiology, Icahn School of Medicine at Mount Sinai, New York, New York, USA; [4] ProBioGen AG, Berlin, Germany; [5] Department Microbiology & Immunology, The University of Texas Medical Branch, Galveston, Texas, USA; [6] Department of Oncological Sciences, Icahn School of Medicine at Mount Sinai, New York, New York, USA; [7] Current Address: Center for Microbial Pathogenesis, Institute for Biomedical Sciences, Georgia Research Alliance, Eminent Scholar in Virology, Georgia State University, Atlanta, Georgia, USA

9:00 a.m. **Broad based surveillance for ebolaviruses: PREDICT in Sierra Leone, Liberia, and Guinea.**
Brian Bird[1], Goldstein T[1], Anthony S[2], Gbakima A[3], Saylors K[3], Jean Louis F[3], Wolking D[1], Epstein J[4], Karesh W[4], Kreuder-Johnson C[1], Mazet J[1]

One Health Institute UC Davis School of Veterinary Medicine[1], Center for Infection and Immunity Columbia University[2], Metabiota Inc.[3], EcoHealth Alliance[4]

9:15 a.m. **Quantifying signatures of resistance and tolerance to filoviruses in bat cell lines**
Cara E. Brook[1], Melinda Ng[2], Esther Ndungo, Rohit K. Jangra, Andrew P. Dobson, Andrea L. Graham, Bryan T. Grenfell, C. Jessica E. Metcalf[1]*, Kartik Chandran[1]*
[1]Department of Ecology and Evolutionary Biology, Princeton University;
[2]Department of Microbiology and Immunology, Albert Einstein College of Medicine
*These senior authors contributed equally to this work.

9:30 a.m. **Serologic evidence of exposure to filoviruses in fruit bats, Singapore**
Laing ED[1], Ian H Mendenhall[2], Linster M[2], Low DHW[2], Chen Y[2], Yan L[1], Sterling SL[1], Borthwick S[2], Neves ES[2], Lim JSL[2], Skiles M[2], Lee BPY[4], Wang LF[2], Broder CC[1], Smith GJD[2, 5]

Uniformed Services University, Bethesda, MD, USA[1], Duke-National University of Singapore Medical School, Singapore[2], North Carolina State University, Raleigh, NC, USA[3], National Parks Board, Singapore[4], Duke Global Health Institute, Duke University, Durham, North Carolina, USA[5]

9:45 a.m. **Predicting undiscovered filovirus reservoirs and patterns of disease emergence**
David Hayman

Molecular Epidemiology and Public Health Laboratory, Hopkirk Research Institute, Massey University, New Zealand

10:00 a.m. Break

10:30 a.m. Session II - Coronaviruses A (Joel Rovnak, Moderator)

10:30 a.m. **Bats as possible animal origin of MERS-CoV**
Susanna K. P. Lau

Department of Microbiology, The University of Hong Kong, Hong Kong, China

10:45 a.m. **Rapid detection of MERS coronavirus ancestors in bats**
Prof. Patrick CY Woo

Department of Microbiology, The University of Hong Kong, Hong Kong.

11:00 a.m. **Global patterns in coronavirus diversity**
Simon J Anthony[1,2,3]; Johnson, C.K[4]; Greig, D.J[4]; Kramer, S[1,5]; Che, X[1]; Wells, H[1]; Hicks, A.L[1]; Joly, D.O[6, 7]; Wolfe, N.D[6]; Daszak, P[3]; Karesh, W[3]; Lipkin, W.I[1,2]; Morse, S.S[2]; PREDICT Consortium[8]; Mazet, J.A.K[4]; Goldstein, T[4]

[1]Center for Infection and Immunity, Mailman School of Public Health, Columbia University, 722 West 168th Street, New York, NY, 10032 (USA); [2]Dept of Epidemiology, Mailman School of Public Health, Columbia University, 722 West 168th Street, New York, NY (USA); [3]EcoHealth Alliance, 460 West 34th Street, NY, New York (USA); [4]One Health Institute & Karen C Drayer Wildlife Health Center, School of Veterinary Medicine, University of California Davis, California (USA); [5]Dept of Environmental Health Sciences, Mailman School of Public Health, Columbia University, 722 West 168th Street, New York, NY (USA); [6]Metabiota, Inc. One Sutter, Suite 600, San Francisco, CA, 94104 (USA); [7]Wildlife Conservation Society, New York, NY, (USA)

11:15 a.m. **SARS coronavirus may have originated from frequent recombination events between SARS-like coronaviruses in a single horseshoe bat habitat**
Ben Hu[1], Lei-Ping Zeng[1], Xing-Lou Yang[1], Xing-Yi Ge[1], Wei Zhang[1], Bei Li[1], Dong-Sheng Luo[1], Yun-Zhi Zhang[2], Mei-Niang Wang[1], Peter Daszak[3], Lin-Fa Wang[4], Jie Cui[1], Zheng-Li Shi[1]

[1] CAS Key Laboratory of Special Pathogens and Biosafety, Center for Emerging Infectious Diseases, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China; [2]Yunnan Institute of Endemic Diseases Control and Prevention, Dali, China; [3]EcoHealth Alliance, New York City, New York, USA; [4]Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore.

11:30 a.m. **A metagenomic approach identifying a MERS-related coronavirus in a bat from South Africa**
Marike Geldenhuys[1], Marinda Mortlock[1], Jaqueline Weyer[2], Oliver Bezuidt[3], Ernest Seamark[4], Teresa Kearney[5,6], Cheryl Gleasner [7], Tracey Erkkila[7], Helen Cui[7] and Wanda Markotter[1]

[1] Centre for Viral Zoonosis, Department of Medical Virology, Faculty of Health sciences, University of Pretoria, Pretoria, South Africa. [2] Centre for Emerging, Zoonotic and Parasitic Diseases,

National Institute for Communicable Diseases, Sandringham, South Africa. [3] Centre for Microbial Ecology and Genomics, University of Pretoria, Pretoria, South Africa. [4] AfricanBats NPC, South Africa and Centre for Wildlife Management, University of Pretoria, Pretoria, South Africa. [5] Animal, Plant and Environmental Sciences, University of the Witwatersrand, Johannesburg, South Africa

12:00 p.m. Lunch and Poster Session

2:00 p.m. Session III - Rhabdoviruses (Ashley Malmlov, Moderator)

2:00 p.m. **New insights into the antiviral innate immune response of *Desmodus rotundus***
Sarkis Sarkis, Marie-Claude Lise, Edith Darcissac, Stéphanie Dabo, Christine Neuveut, Benoît de Thoisy, Eliane Meurs, Anne Lavergne and Vincent Lacoste

Institut Pasteur de la Guyane, French Guiana/ France

2:15 p.m. **A comparative study of the autophagy pathway during virus infection of bat (natural) and human (accidental) host cells**
Eric D. Laing[1], Spencer L. Sterling[1], Dawn L. Weir[1], Sasha E. Larsen[2], Linfa Wang[3], Brian C. Schaefer[1], and Christopher C. Broder[1]

[1]Department of Microbiology, Uniformed Services University, Bethesda, MD, USA; [2]Department of Pharmacology, Uniformed Services University, Bethesda, MD, USA; [3]Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore

2:30 p.m. **Lagos bat virus in South Africa, 2013-2017**
Jessica Coertse[1], Le Roux, K.[2], Richardson, E.[3], White, W.[3], Markotter, W.[1]

[1]Centre for Viral Zoonoses, Department of Medical Virology, Faculty of Health Sciences, University of Pretoria, South Africa; [2]Allerton Provincial Veterinary Laboratory, Pietermaritzburg, KwaZulu-Natal, South Africa; [3]KwaZulu-Natal Bat Interest Group, KwaZulu-Natal, South Africa

2:45 p.m. **Characterization of a novel Rhabdovirus isolated from insectivorous bat (*Pipistrellus kuhlii*) in Italy**
Davide Lelli[1], Alice Prosperi[1], Chiara Chiapponi[1], Paola Debenedictis[2], Anna Maria Gibellini[3], Stefania Leopardi[2], Enrica Sozzi[1], Dino Scaravelli[4], Ana Moreno[1], Antonio Lavazza[1]

[1]Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna, Via Bianchi 9 - 25124 Brescia, Italy; [2]Istituto Zooprofilattico Sperimentale delle Venezie, OIE Collaborating Centre and National Reference Centre for Research on Infectious Diseases at the Animal-Human Interface, Viale dell'Università 10 - 35020 Legnaro (PD), Italy; [3]Wildlife Rehabilitation Center WWF of Valpredina via Pioda n.1, 24060 Cenate Sopra(BG), Italy; [4]University of Bologna, Department of Veterinary Medical Sciences, via Tolara di sopra 50 - 40064 Ozzano Emilia (BO), Italy

3:00 p.m. Session IV - Paramyxoviruses (Danielle Adney, Moderator)

3:00 p.m. **Age-specific dynamics of maternally- and infection- derived immunity within African bat populations**
Alison J Peel[1], Kate S Baker[2], David TS Hayman[3], Andrew A Cunningham[4], James LN Wood[5], Romain Garnier[5] and Olivier Restif[5]
[1] Environmental Futures Research Institute, Griffith University, Nathan, QLD, Australia; [2] Institute for Integrative Biology, University of Liverpool, UK; [3] Molecular Epidemiology and Public Health Laboratory, Hopkirk Research Institute, Massey University, Palmerston North, New Zealand; [4] Institute of Zoology, Zoological Society of London, Regent's Park, London, UK; [5] Department of Veterinary Medicine, University of Cambridge, Cambridge, UK

3:15 p.m. **Detection of rubula- and related viruses in an Egyptian fruit bat (*Rousettus aegyptiacus*) colony in South Africa**
Marinda Mortlock[1], Jacqueline Weyer[2], Janusz Paweska[2] and Wanda Markotter[1]

[1]Centre for Viral Zoonoses, Department of Medical Virology, Faculty of Health Science, University of Pretoria, South Africa; [2]Centre for Emerging, Zoonotic and Parasitic Diseases, National Institute for Communicable Diseases, Sandringham, Johannesburg, South Africa

3:30 p.m. Break

4:00 p.m. **Influenza-like virus and paramyxovirus screening in Brazilian bats**

Angélica Cristine Campos[1]; Luiz Gustavo Góes[1]; Cristiano Carvalho[2]; Guilherme Ambar[5]; Luciano M. Thomazelli[1]; Jhiovana Cristielly Costa[1]; Mariana Cristine de Souza[1]; Adriana Ruckert[3]; Débora C. Oliveira[3]; Luzia F. Martorelli[3]; Ana Paula Kataoka[3]; Marcelo S. Nardi[4]; Juliana L. Summa[4]; Roberta Marcatti de Azevedo[4]; Wagner A. Pedro[2]; Luzia H. Queiroz[2]; Ariovaldo P. Cruz-Neto[5] and Edison Durigon[1]

[1] Departamento de Microbiologia, Instituto de Ciências Biomédicas (ICB), Universidade de São Paulo (USP), São Paulo-SP; [2] Faculdade de Medicina Veterinária de Araçatuba, Universidade Estadual Paulista (UNESP), Araçatuba- SP; [3] Centro de Controle de Zoonozes (CCZ) do Município de São Paulo-SP; [4] Divisão Técnica de Medicina Veterinária e Manejo da Fauna Silvestre (DEPAVE-3), Secretaria do Verde e Meio Ambiente, Prefeitura do Município de São Paulo, São Paulo-SP; [5] Departamento de Zoologia, Instituto de Biociências, Universidade Estadual Paulista (UNESP), Rio Claro-SP

4:15 p.m. **Hendra virus dynamics and spillover**

Raina Plowright[1], Maureen Kessler[1], Alison Peel[2], Hamish McCallum[2], Peggy Eby[3]

[1]Department of Microbiology and Immunology, Montana State University; [2]Environmental Futures Research Institute, Griffith University, Queensland, Australia; [3]University of New South Wales, Australia.

4:30 p.m. Session V - Methodology in Bat-borne Viruses (Danielle Adney, Moderator)

4:30 p.m. **Using serology to understand the dynamics of concurrent viral infections in pteropid bats**

Jonathan H. Epstein[1], Noam Ross[1], Ariful Islam[1], Dan Crowley[1,2], Gary Crameri[3], Christopher Broder[4], Linfa Wang[5], and Peter Daszak[1].

[1]EcoHealth Alliance, NY USA; [2]Columbia University Mailman School of Public Health, NY USA; [3]CSIRO Australian Animal Health Laboratory, Geelong, VIC, AUS; [4]Uniformed Services University, MD USA; [5]Duke-NUS, Singapore

4:45 p.m. **Estimating viral richness and viral sharing in bats: integrating previously-published and newly-acquired field data**

Kevin J. Olival[1], Noam Ross[1], Evan A. Eskew[1], Anna R. Willoughby[1], Carlos Zambrana-Torrelio[1], Peter Daszak[1], and PREDICT Consortium[2]

[1] EcoHealth Alliance, New York, NY 10001, USA; [2] http://www.vetmed.ucdavis.edu/ohi/predict/publications/Authorship.cfm

5:00 p.m. **Open Discussion**

6:00 p.m. Recess

Saturday, July 1

7:30 a.m. Registration, North Ballroom, University Center for the Arts

8:00 a.m. Session II - Coronaviruses B (Rebekah Kading, Moderator)

8:00 a.m. **Optimised sampling efforts and screening assays identify several MERS-related coronaviruses in South African bats**

Wolfgang Preiser[1,2], Ndapewa L. Ithete[1], Nadine Cronjé[1], Tasnim Suliman[1]

[1]Division of Medical Virology, Faculty of Medicine & Health Sciences, University of Stellenbosch, South Africa; [2]National Health Laboratory Service (NHLS) Tygerberg, Cape Town, South Africa

8:15 a.m. **Coronavirus diversity in bats from urban, rural and forest areas of Atlantic and Amazon Forest biomes, Brazil.**
Luiz Gustavo Góes[1]; Angélica Cristine Campos[1]; Cristiano Carvalho[2]; Guilherme Ambar[5]; Douglas Oliveira[1]; Caroline Alvarenga[1]; Jhiovana Cristielly Costa[1]; Adriana Ruckert[3]; Débora C. Oliveira[3]; Luzia F. Martorelli[3]; Ana Paula Kataoka[3]; Marcelo S. Nardi[4]; Juliana L. Summa[4]; Roberta Marcatti de Azevedo[4]; Luzia H. Queiroz[2]; Ariovaldo P. Cruz-Neto[5] and Edison Durigon[1]

[1]Departamento de Microbiologia, Instituto de Ciências Biomédicas (ICB), Universidade de São Paulo (USP), São Paulo-SP; [2] Faculdade de Medicina Veterinária de Araçatuba, Universidade Estadual Paulista (UNESP), Araçatuba- SP; [3] Centro de Controle de Zoonozes (CCZ) do Município de São Paulo-SP; [4] Divisão Técnica de Medicina Veterinária e Manejo da Fauna Silvestre (DEPAVE-3), Secretaria do Verde e Meio Ambiente, Prefeitura do Município de São Paulo, São Paulo-SP; [5] Departamento de Zoologia, Instituto de Biociências, Universidade Estadual Paulista (UNESP), Rio Claro-SP

8:30 a.m. **Preliminary Evidence of a Novel Alphacoronavirus and Secondary Acquisition of Tymoviridae and Partitiviridae in Little Brown Bats (*Myotis lucifugus*) in Southcentral Alaska.**
Douglas Causey[1], Jonathan C. Rupp*[1], Maegan Lange[1], Megan Howard[2], Anitha Sundarajan[3], Jonny Sena[3], Faye D. Schilkey[3], Molly Murphy[4], Sarah Cooperman[1], Eric Bortz[1]

[1]Dept. of Biological Sciences, University of Alaska Anchorage; [2]Battelle Memorial Institute; [3]National Center for Genome Resources, Santa Fe NM; [4]Dept. of Veterinary Medicine, University of Alaska Fairbanks

8:45 a.m. **Are big brown bat cells different than human cells in their innate immune response to coronavirus and viral ligands?**
Arinjay Banerjee[1], Robert Brownlie[3], Noreen Rapin[1], Trent Bollinger[2], Darryl Falzarano[1,3] and Vikram Misra[1]

[1]Department of Microbiology, Western College of Veterinary Medicine, University of Saskatchewan, Canada. [2]Department of Pathology, Western College of Veterinary Medicine, University of Saskatchewan, Canada. [3]VIDO-InterVac, University of Saskatchewan, Canada.

9:00 a.m. **Session V - Influenza** (Corey Campbell, Moderator)

9:00 a.m. **Reverse genetic analysis of bat influenza viruses: A journey full of surprises.**
Martin Schwemmle

Institute of Virology, University of Freiburg Medical Center

9:30 a.m. **Towards understanding bat influenza A-like viruses**
Wenjun Ma[1], Bin Zhou[2], Jingjiao Ma[1], Qingfang Liu[1], Jinhwa Lee[1], Michael Duff[1], Juergen A. Richt[1], David E. Wentworth[2]
[1]Department of Diagnostic Medicine/Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan, Kansas, United States of America.
[2]Virology, J. Craig Venter Institute, Rockville, Maryland, United States of America.

9:45 a.m. **Experimental Infection of Jamaican Fruit Bats (*Artibeus jamaicensis*) with a Rescued Bat HL18NL11 Influenza A-like Virus**
Tony Schountz[1], Ashley Malmlov[1], Jingjiao Ma[2], Jinhwa Lee[2], Corey Campbell[1], Tawfik Aboellail[1], Ann Hawkinson[3] and Wenjun Ma[2]

[1]Department of Microbiology, Immunology and Pathology, College of Veterinary Medicine and Biomedical Sciences, Colorado State University; [2]Department of Diagnostic Medicine and Pathobiology, College of Veterinary Medicine, Kansas State University; [3]School of Biological Sciences, University of Northern Colorado

10:00 a.m. Break

10:00 a.m. Session VI - Ecology (Paul Cryan, Moderator)

10:30 a.m. **Seroprevalence of alphaviruses, flaviviruses and Rift Valley fever virus in Ugandan bats**
Rebekah C Kading[1,2], Kityo R[3], Mossel E[1], Borland E[1], Nakayiki T[4], Nalikka B[3], Nyakarahuka L[4], Ledermann J[1], Panella N[1], Gilbert A[5,6], Crabtree M[1], Kerbis Peterhans J[7], Towner J[8], Amman B[8], Sealy T[8], Nichol S[8], Powers A[1], Lutwama J[4], Miller B[1]

[1] Centers for Disease Control and Prevention, Division of Vector-borne Diseases, Arbovirus Diseases Branch, Fort Collins, CO. [2]Current Affiliation: Colorado State University, Department of Microbiology, Immunology and Pathology, Fort Collins, CO. [3]Makerere University, Department of Biological Sciences, Kampala, Uganda. [4]Uganda Virus Research Institute, Entebbe, Uganda. [5]Centers for Disease Control and Prevention, Division of High Consequence Pathogens, Rabies and Poxvirus Branch, Atlanta, GA. [6]Current Affiliation: United States Department of Agriculture, Animal and Plant Health Inspection Service, Fort Collins, CO. [7]College of Professional Studies, Roosevelt University &Collections & Research, The Field Museum of Natural History, Chicago, IL. [8]Centers for Disease Control and Prevention, Division of High Consequence Pathogens, Viral Special Pathogens Branch

10:45 a.m. **Presence of zoonotic bat pathogens correlate with reproductive seasons in South African bat populations**
Wanda Markotter[1], Muriel Dietrich[1], Teresa Kearney[2,3], Stewart McCulloch[1], Marinda Mortlock[1], Ernest Seamark[4,5] and Janusz Paweska[6]

[1] Centre for Viral Zoonoses, Department of Medical Virology, Faculty of Health Sciences, University of Pretoria, South Africa. [2] Ditsong National Museum of Natural History, Pretoria, South Africa. [3] Plant and Environmental Sciences, University of the Witwatersrand, Johannesburg, South Africa. [4] AfricanBats, Kloofsig, South Africa. [5] Centre for Wildlife Management, Faculty of Natural and Agricultural Sciences, University of Pretoria, Pretoria, South Africa. [6] Centre for Emerging, Zoonotic and Parasitic Diseases, National Institute for Communicable Diseases, Sandringham, South Africa.

11:00 a.m. **Body mass index of the Egyptian fruit bat, *Rousettus aegyptiacus*: An indicator of infection status**
Low J. de Vries[1], Stewart McCulloch[1], Janusz Paweska[2] and Wanda Markotter[1]

[1]Centre for Viral Zoonoses, Department of Medical Virology, Faculty for Health Science, University of Pretoria, South Africa; [2]Center for Emerging, Zoonotic and Parasitic Diseases, National Institute for Communicable Diseases, Sandringham, Johannesburg, South Africa

11:15 a.m. **Environmental constraints drive the viral diversity of two sympatric Amazonian bat species**
Arielle Salmier, Sourakhata Tirera, Benoit de Thoisy, Alain Franc, Edith Darcissac, Damien Donato, Christiane Bouchier, Vincent Lacoste and Anne Lavergne

Institut Pasteur de la Guyane, French Guiana/ France

11:30 a.m. **Seasonal and individual predictors of grey-headed flying fox (*Pteropus poliocephalus*) foraging movements in Adelaide, South Australia**
Cecilia A. Sánchez[1,2], Terry B. Reardon[3], Wayne S.J. Boardman[4] and Sonia Altizer[1,2]

[1]Odum School of Ecology, University of Georgia, Athens, GA, USA; [2]Center for the Ecology of Infectious Diseases, University of Georgia, Athens, GA, USA; [3]South Australian Museum, Adelaide, South Australia, Australia; [4]University of Adelaide, Adelaide, South Australia, Australia

11:45 a.m. **Uganda Bat calls library-developing a tool to survey arthropod-borne viruses associated with Chiroptera**
Robert Martin Kityo[1], Rebekah Kading[2], Betty Nalikka[1], Julius Lutwama[3]

[1]Makerere University, College of Natural Science – Department of Zoology, Entomology and Fisheries Science Kampala Uganda; [2]Colorado State University; [3]Uganda Virus research institute

12:00 p.m. Lunch

1:00 p.m. Session V - Immunology of Bats (Tony Schountz, Moderator)

1:00 p.m. **Dampening of STING-dependent IFN production: an implication of virus tolerance in bats?**
Jiazhen Xie[1], Chenxi Ma [1], Yang Li[1], Jie Cui[1], Linfa Wang [2], Zhengli Shi [1] and Peng Zhou[1*]

[1]Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan 430071, China; [2]Emerging Infectious programme, Singapore Duke-NUD Medical School, Singapore 169857, Singapore

1:15 p.m. **Regulation of immune activation and dampened inflammation in Pteropid bats**
Aaron T. Irving[1], Katarina Luko[1], Matae Ahn[1], Kong Pui San[1], & Lin-Fa Wang[1]

[1]Duke-NUS Medical School, Singapore

1:30 p.m. **Delineating the phenotype and function of the B cell population in the fruit-eating bat, *Pteropus Alecto.***
Pravin Periasamy[1,2], Martínez Gómez JM[1,2], Wang LF[3] , and Alonso S[1,2]

[1]Department of Microbiology and Immunology, [2]Immunology Programme, Yong Loo Lin School of Medicine, Life Sciences Institute, National University of Singapore, Singapore. [3]DUKE-NUS, Singapore.

1:45 p.m. **Integrative measures for assessing "health" in free-ranging bats – zoonotic and conservation implications from a One Health perspective**
DeeAnn M. Reeder, Kenneth A. Field

Department of Biology, Bucknell University

2:00 p.m. Session VI - White Nose Syndrome (Joel Rovnak, Moderator)

2:00 p.m. **Host-pathogen interactions during white-nose syndrome**
Ken Field[1], Sophia M Reeder[1], Jonathan M Palmer[2], Brent J Sewall[3], Jenni M Prokkola[4], Greg Turner[5], Thomas M Lilley[6], Marianne Gagnon[3], J Paul White[7], Joseph Johnson[8], Christopher Hauer[3], and DeeAnn M Reeder[2]

[1]Department of Biology, Bucknell University, Lewisburg, PA; [2]Center for Forest Mycology Research, Northern Research Station, US Forest Service, Madison, WI; [3]Department of Biology, Temple University, Philadelphia, PA; [4]University of Eastern Finland, Joensuu, Finland; [5]Wildlife Diversity Division, Pennsylvania Game Commission, Harrisburg, PA; [6]Institute of Integrative Biology, University of Liverpool, Liverpool L69 3BX, UK; [7]Wisconsin Department of Natural Resources, Madison, WI; [8]Biological Sciences, Ohio University, Athens, OH

2:15 p.m. **Resistance or Tolerance – How do European bats cope with *Pseudogymnoascus destructans*?**
Marcus Fritze[1,2],Voight CC[2], Czirjak GA[2], Puechmaille SJ[1,3]

[1] Zoology Institute,University of Greifswald,Soldmann-Str. 14, D - 17487 Greifswald, Germany; [2] Leibniz institute for Zoo and Wildlife Research, Alfred-Kowalke-Str. 17, 10315 Berlin, Germany and [3]School of Biology and Environmental Sciences, University College Dublin, Belfield, D4 Dublin Ireland

2:30 p.m. **Modeling the impact of White-nose syndrome on two western bat species**
C. Reed Hranac[1], Brandon J. Klüg-Baerwald[2], Yvonne A. Dzal[3], Cori Lausen[4], Jonathan C. Marshall[1,5], Sarah H. Olson[6] , David T. S. Hayman[1]

[1]Hopkirk Research Institute, Massey University, Private Bag, 11 222, Palmerston North 4442, New Zealand; [2] Department of Biology University of Regina, Regina, SK, Canada, 3737 Wascana Parkway, Regina, SK S4S 1T8; [3] Department of Zoology, University of British Columbia, Vancouver, BC, Canada #4200-6270 University Boulevard, Vancouver, BC V6T 1Z6, [4] Wildlife Conservation Society Canada, Kaslo, BC, Canada, P.O. Box 606, 202 B Ave, Kaslo, BC V0G 1M0; [5] Institute of Fundamental Sciences Massey University, Private Bag 11 222, Palmerston North 4442, New Zealand; [6] Wildlife Conservation Society, Wildlife Health Program 212 South Wallace Avenue, Suite 101, Bozeman, MT, 59715, USA

2:45 p.m. **Variable behaviors influence species susceptibility to disease – surviving white-nose syndrome.**
Paul M. Cryan

U.S. Geological Survey (USGS), USGS Fort Collins Science Center, 2150 Centre Ave., Bldg. C, Fort Collins, Colorado

3:00 p.m. Break

3:30 p.m. Session VI - Other Infectious Agents of Bats (Anna Fagre, Moderator)

3:00 p.m. **Emerging Insights into the Geographic Distribution, Genetic Diversity and Evolutionary Origin of Bat-borne Hantaviruses**
Satoru Arai[1], Se Hun Gu[2], Son Truong Nguyen[3], Vuong Tan Tu[3], Blaise Kadjo[4], Burton K. Lim[5], Joseph S. Masangkay[6], Saw Bawm[7], Joseph A. Cook[8], Shigeru Kyuwa[9], Keiko Tanaka-Taya[1], Shigeru Morikawa[1] and Richard Yanagihara[2]

[1]National Institute of Infectious Diseases, Tokyo, Japan; [2]University of Hawaii at Manoa, Honolulu, HI, USA; [3]Institute of Ecology and Biological Resources, Vietnam Academy of Science and Technology, Hanoi, Vietnam; [4]University of Félix Houphouët-Boigny, Abidjan, Côte d'Ivoire; [5]Royal Ontario Museum, Toronto, Canada; [6]University of the Philippines Los Baños, Laguna, Philippines; [7]University of Veterinary Science, Nay Pyi Taw, Myanmar; [8]University of New Mexico, Albuquerque, New Mexico, U.S.A.; [9]University of Tokyo, Tokyo, Japan;

3:15 p.m. **Neotropical Bats that Co-habit with Humans Function as Dead-End Hosts for Dengue Virus**
Amanda Vicente-Santos[1,2], Andres Moreira-Soto[1,4], Claudio Soto-Garita[1], Luis Guillermo Chaverri[3], Andrea Chaves[2], Jan Felix Drexler[4,5], Juan Alberto Morales[6], Alejandro Alfaro-Alarcón[6], Bernal Rodríguez-Herrera [2] and Eugenia Corrales-Aguilar [1*]

[1]Virology-CIET (Research Center for Tropical Diseases), Microbiology, University of Costa Rica, San José, Costa Rica. [2]Biology, University of Costa Rica, San José, Costa Rica. [3]Exact and Natural Sciences School, National Distance Education University, San José, Costa Rica. [4]Institute of Virology, University of Bonn Medical Centre, 53127 Bonn, Germany.[5]German Centre for Infection Research, Bonn-Cologne, Germany.[6] Department of Pathology, School of Veterinary Medicine, National University, Costa Rica

3:30 p.m. **Novel Gammaherpesvirus in Bats: discerning the secrets of these oncogenic viruses**
Sonu Subudhi, Noreen Rapin, Janet Hill[1] and Vikram Misra

Department of Veterinary Microbiology, University of Saskatchewan, Saskatoon, Canada

3:45 p.m. **Experimental Infection of Jamaican Fruit Bats (*Artibeus jamaicensis)* with Zika Virus**
Ashley Malmlov[1], Kaitlyn Miedema[1], Tawfik Aboellail[2], Corey L Campbell[1], Miles Eckley[1], Nunya Chotiwan[1], Rebekah C. Gullberg[1], Rushika Perera[1] and Tony Schountz[1]

[1]Arthropod-Borne and Infectious Diseases Laboratory, Department of Microbiology, Immunology and Pathology, College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, Colorado, USA and [2]Veterinary Diagnostic Laboratories, Department of Microbiology, Immunology and Pathology, College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, Colorado, USA

4:00 p.m. **Long-term monitoring of *Bartonella* bacteria in a captive colony of fruit bats and experimental evidence of bat flies as vectors of bartonella**

Clifton McKee[1,2], Colleen Webb[1], Michael Kosoy[2], Ying Bai[2], Lynn Osikowicz[2], Richard Suu-Ire[3], Yaa Ntiamoa-Baidu[4], Andrew Cunningham[5], James Wood[6], David Hayman[7]

[1]Department of Biology, Colorado State University; [2]Division of Vector-Borne Diseases, Centers for Disease Control and Prevention; [3]Wildlife Division, Forestry Commission of Ghana; [4]Department of Animal Biology and Conservation Science, University of Ghana; [5]Institute of Zoology, Zoological Society of London; [6]Department of Veterinary Medicine, University of Cambridge; [7]Institute of Veterinary, Animal and Biomedical Sciences, Massey University

4:15 p.m. **Open Discussion**

5:00 p.m. Adjourn

POSTER PRESENTATIONS

1. James N. Aegerter, Ashley C. Banyard, Anthony R. Fooks, Graham C. Smith·
Predicting the epizootiology of temperate bat disease: Is it all about the bats?

2. Danielle E. Anderson, Kristmundur Sigmundsson, So Young Kim, Brian Ho Wenkae, Jasmine Tan[1] and Lin-Fa Wang. **Comparative loss of function screens highlight common cellular pathways required by mumps virus for replication in bats and humans**

3. Victoria Avanzato, Neeltje van Doremalen, Christine Carrington, Janine Seetahal, Tony Schountz, Vincent Munster
Development Implementation of a RT-PCR Assay to Detect Henipaviruses in Trinidad Bats

4. Jonathan C. Rupp, Maegan Lange, Megan Howard, Anitha Sundarajan, Jonny Sena[3], Faye D. Schilkey, Molly Murphy, Douglas Causey, Eric Bortz.
Genomic characterization and pathogenic potential of a novel evolutionarily-divergent alphacoronavirus isolated from *M. lucifigus* bats in Alaska.

5. Douglas Causey, Jonathan C. Rupp, Maegan Lange, Megan Howard, Anitha Sundarajan, Jonny Sena, Faye D. Schilkey, Molly Murphy, Eric Bortz
Preliminary Evidence of Secondary Acquisition of Tymoviridae and Partitiviridae in Little Brown Bats (*Myotis lucifugus*) in Southcentral Alaska.

6. Marcy Kanuka, Ashley Malmlov, Christine Cornish, Kathleen Parker, Cassandra Tang Wing, Diana Stone, Tony Schountz and Sonia Cheetham
Molecular Screening of Zika and Dengue Viruses in Bats (*Artibeus jamaicensis, Glossophaga longirostris and Molossus molossus*) from Grenada, West Indies.

7. Diana Stone, Christine Cornish, Amy C. Lyons, Yan-Jang S. Huang, Dana L. Vanlandingham, Stephen Higgs, Bradley Blitvich, Abiodun A. Adesiyun, Sharlene Santana, Leith Leiser-Miller, Sonia Cheetham.
Serologic evaluation of Alphavirus and Flavivirus exposure in bats in Grenada

8. Fagre AC, Kityo R, Lee J, Mossel E, Crabtree, M, Nalikka B, Nakayiki T, Kerbis J, Gilbert, A, Bergren, N, Nyakarahuka L, Lutwama J, Stenglein M, Byas A, Malmlov A, Bergren N, Rice L, Miller B, Schountz T & Kading, RC.
Isolation and molecular characterization of Bukakata orbivirus, a novel virus from a Ugandan bat, and associated pathology in experimentally infected Jamaican fruit bats (*Artibeus jamaicensis*)

9. Robert J. Fischer, Seth D. Judson, Sarah H. Olson, Vincent J. Munster
Using GIS to Guide Ebola Virus Disease Ecology Field Investigations

10. Hannah Frank, David Enard, Chase Mendenhall, Ji-Yeun Lee, Ellie Armstrong, Stefan Prost, Seth Judson, Jamieson O'Marr, Gretchen Daily, Dmitri Petrov, Scott Boyd and Elizabeth Hadly[1,6,7]
Bat - infection interactions: Signals of evolution, ecology, immunity and deforestation

11. Yupadee Hengjan, Didik Pramono, Hitoshi Takemae, Ryosuke Kobayashi, Karla Cristine Doysabas, Keisuke Iida, Takeshi Ando, Supratikno, Chaerul Basri Yuli Sulistya Fitriana, Eko M.Z. Arifin, Yasushige Ohmori, Ken Maeda, Srihadi Agungpriyono and Eiichi Hondo
Daytime behavior of *Pteropus vampyrus* and *Acerodon jubatus* in the natural habitats: a cue of viral transmission

12. Yutthana Joyjinda, Supaporn Wacharapluesadee, Prateep Duengkae, Apaporn Rodpan, Teerada ponpinit, Thongchai Kaewpom, Sangchai Yingsakmongkol, Kevin J Olival, Thiravat Hemachudha
The study of whole spike gene of bat coronavirus from Thailand using Next Generation Sequencing

13. Jun Li & Vincent Munster
Assessment of the cross-species potential of two emerging coronaviruses, SARS-CoV and MERS-CoV, by Protein-Protein Molecular Docking analyses

14. Kessler MK, Kamath PL, Smith CS, Goldspink LK, Plowright RK
Hendra virus phylogeography in eastern Australia

15. Tamar Kutateladze, Lela Urushadze, Davit Putkaradze, Magda Dgebuadze, Giorgi Babuadze, Ioseb Natradze, Lillian Orciari, and AndresVelasco-Villa
Viral Zoonosis in Georgian Bats

16. Aiah Lebbie, Jonathan Towner, Ibrahim Bakarr Brian Amman, Amy Schuh, Jonathan Johnny, Tara Sealy, James Graziano, Celine Taboy, John Klena, Immah Conteh, Stuart Nichol, Alusine Koroma, Ibrahim Foday and Richard Wadsworth
Forestalling Future Outbreaks: Enhancing Capacity for Surveillance of Viral Hemorrhagic Fever Viruses in Sierra Leone

17. Matovu Benard, Nalikka Betty and Kityo Robert
Ecological aspects of bats in a cave frequented by members of the local community in Kaptum Cave in eastern Uganda.

18. Rebekah McMinn, Michael Letko, Neeltje van Doremalen, Kerri Miazgowicz, Vincent Munster[1]
Middle East respiratory syndrome coronavirus spike plasticity in the context of the common vampire bat (*Desmodus rotundus***) DPP4 receptor.**

19. Alison J. Peel, Victoria Boyd, Raina K. Plowright, Olivier Restif, Gary Crameri, John Giles, Hamish McCallum, Konstans Wells
Viral community dynamics of Australian Flying foxes

20. Ponpinit T, Wacharapluesadee S, Duengkae P, Kaewpom T, Yinsakmongkon S, Rodpan A, Hemachudha T
The glycoprotein of Nipah virus in Thai bats associated with Nipah virus in Bangladesh

21. Jonathan C. Rupp, Maegan Lange, Megan Howard, Anitha Sundarajan, Jonny Sena, Faye D. Schilkey, Molly Murphy, Douglas Causey, Eric Bortz.
Genomic characterization and pathogenic potential of a novel evolutionarily-divergent alphacoronavirus isolated from *M. lucifigus* **bats in Alaska.**

22. Salmier A., de Thoisy B., Crouau-Roy B., Lacoste V. and Lavergne A.
Spatial pattern of genetic diversity and selection in the MHC class II DRB of three Neotropical bat species

23. Ken Cameron, Stephanie Seifert, Shauna Milne-Price, Alain Ondzie, Trent Bushmaker, Jean-Vivien Mombouli, Sarah Olson and Vincent J. Munster
Establishing a field collection scheme to investigate the role of African fruit bats as the natural reservoir of ebolaviruses

24. Lela Urushadze, Ying Bai, Lynn Osikowicz, Ioseb Natradze, Ketevan Sidamonidze, Davit Putkaradze, and Michael Kosoy
Co-infection in Georgian Bats

25. Megan E. Vodzak, MS, MPH, Ohnmar Aung, MBBS, MA , Marc T. Valitutto, VMD, Kyaw Y. N. Tun, BVSc, MSc, PhD , Heather S. Davies, MS , Michael E. von Fricken, PhD, MPH Suzan Murray, DVM, DACZM, and Dawn M. Zimmerman, DVM, MS
Caves of Myanmar: a high-risk human-wildlife interface for zoonotic disease

26. Supaporn Wacharapluesadee, Prateep Duengkae, Aingorn Chaiyes, Sangchai Yinsakmongkon[3] Pattarapol Maneeorn[4], Patcharakiti Phengsakul, Wachirapon Khumbucha, Thongchai Kaewpom, Apaporn Rodpan, Thiravat Hemachudha
Prevalence Patterns of Coronaviruses in Lyle's flying fox (*Pteropus lylei*) in Thailand

27. Xing-Lou Yang, Yun-Zhi Zhang, Ren-Di Jiang, Hua Guo, Wei Zhang, Bei-Li, Ning Wang, Li-Wang, Cecilia Waruhiu, Ji-Hua Zhou, Shi-Yue Li, Peter Daszak, Lin-Fa Wang, Zheng-Li Shi
Genetically Diverse Filoviruses in *Rousettus* and *Eonycteris* spp. Bats, China, 2009 and 2015

28. Miles Eckley, Ann Hawkinson, Tyler Sherman, Tony Schountz, Corey L Campbell
Development of a monoclonal antibody to Jamaican fruit bat CD3γ.

29. Candace Cotter, Tony Schountz, Corey L Campbell.
Bats and Immunity: Anti-Viral IFNγ Responses Differ Among Hosts.

30. Janine F.R. Seetahal, Orchid M. Allicock, Stephen C. Sameroff, Christopher Oura, Vernie Ramkissoon, W. Ian Lipkin, Christine V.F. Carrington
Virome analysis of neotropical bats on the Caribbean island of Trinidad

31. Periasamy P, Martínez Gómez JM, Wang LF, and Alonso S.
Delineating the phenotype and function of major lymphocyte populations in the fruit-eating bat, Pteropus Alecto.

32. Cara E. Brook, Hafaliana C. Ranaivoson, Christopher C. Broder, Andrew A. Cunningham, Andrea L. Graham, Jean-Michel Héraud, Louise Wong, James L.N. Wood, Andrew P. Dobson, C. Jessica E. Metcalf
Seasonal serological signals in viral infections for Madagascar fruit bats

Oral Presentation Abstracts

Studies of horizontal transmission of Marburg virus among experimentally infected fruit bats
Jonathan S. Towner[1,2], Amy J. Schuh[1], Brian R. Amman[1], Megan E. B. Jones[1,2], Tara K. Sealy[1], Uebelhoer LS, Spengler JR, Stuart T. Nichol[1]

[1]Viral Special Pathogens Branch, Centers for Disease Control and Prevention, Atlanta, USA, [2]Department of Pathology, College of Veterinary Medicine, University of Georgia, Athens, USA

Objectives: To investigate under experimental conditions the dynamics of Marburg virus replication in a known reservoir host and determine if 1) the virus can be transmitted from infected bats to immunologically naïve bats in the absence of arthropod vectors, and 2) identify the route(s) of virus shedding and therefore likely exposure. **Methods**: Using age-matched captive borne juvenile bats, we inoculated a total of 12 animals with Marburg virus 371 bat isolate and co-housed these animals with 24 naïve contact bats for 9 months under BSL-4 conditions and tested for evidence of virus shedding and transmission. **Results**: Marburg virus shedding was detected in oral, rectal and urine specimens from the inoculated bats through 19 days post infection. During the same time frame, Marburg virus was detected in oral specimens from contact bats, indicating that they were orally exposed to the virus from the inoculated animals. In the late study phase, we found that Marburg virus was horizontally transmitted from the donor bats to naïve contact bats by finding Marburg virus RNA in blood and oral specimens from contact bats, followed by the detection of Marburg virus IgG antibodies in these same animals. **Conclusions**: This study demonstrates, in the absence of any arthropod vectors, 1) direct filovirus transmission from a natural reservoir to another animal, 2) Marburg virus is shed primarily in saliva and urine, and perhaps feces, with some bats acting as super-shedders accounting for more than 80% of the cumulative virus shed, and 3) that this virus/reservoir host system can serve as an bona-fide experimental model for investigating how filoviruses are maintained long-term in nature and what drivers might influence occasional spillover to humans and other animals.

Investigations of Long-term Protective Immunity against Marburg Virus Reinfection in Egyptian Rousette Bats
Schuh AJ, Amman BR, Sealy TK, Spengler JR, Nichol ST and Towner JS

Viral Special Pathogens Branch, Division of High-Consequence Pathogens and Pathology, Centers for Disease Control and Prevention, Atlanta, GA 30333, USA

Objectives: The Egyptian rousette bat (ERB; *Rousettus aegyptiacus*) is as a known natural reservoir host for Marburg virus (MARV). Following infection of ERBs with MARV, virus-specific IgG antibodies rapidly decline and by 3 months post infection the bats are MARV seronegative. Therefore, it is unclear whether reinfection plays a role in MARV maintenance. **Methods:** To address this question, ERBs that had been “naturally” or experimentally infected with MARV 17 to 24 months prior were challenged with homologous virus. Following challenge, evidence of MARV replication in the blood and viral shedding from the oral mucosa was monitored for 14 days, MARV IgG antibody responses were monitored for 21 days and tissues obtained at necropsy at 21 days were tested for the presence of MARV RNA. **Results:** No evidence of MARV replication in the blood or shedding from the oral mucosa was detected in either group of bats through 14 days post inoculation. A robust MARV IgG antibody response occurred by seven days post inoculation in all bats, indicating the occurrence of a secondary immune response. **Conclusions:** This study demonstrates that both “natural” and experimental infection of ERBs with MARV induces long-term protective immunity against reinfection and suggests that other factors such as the twice-yearly influx of susceptible juveniles, large colony sizes and population connectivity, drive MARV transmission dynamics in wild populations of ERBs.

Innate immune response to filoviruses and the role of filoviral interferon-inhibiting domains in bat and human cells
Ivan V. Kuzmin[1,2], Toni M. Schwarz[3], Philipp A. Ilinykh[1,2], Ingo Jordan[4], Thomas G. Ksiazek[1,2,5], Ravi Sachidanandam[6], Christopher F. Basler[3, 7], and Alexander Bukreyev[1,2,5]

[1] Department of Pathology, The University of Texas Medical Branch, Galveston, Texas, USA, [2] Galveston National Laboratory, The University of Texas Medical Branch, Galveston, Texas, USA; [3] Department of Microbiology, Icahn School of Medicine at Mount Sinai, New York, New York, USA; [4] ProBioGen AG, Berlin, Germany; [5] Department Microbiology & Immunology, The University of Texas Medical Branch, Galveston, Texas, USA; [6] Department of Oncological Sciences, Icahn School of Medicine at Mount Sinai, New York, New York, USA; [7] Current Address: Center for Microbial Pathogenesis, Institute for Biomedical Sciences, Georgia Research Alliance, Eminent Scholar in Virology, Georgia State University, Atlanta, Georgia, USA

Objectives: Innate immune responses in bat (Rousettus aegyptiacus) and human cells to the filoviruses Marburg (MARV) and Ebola (EBOV) were investigated to determine the ability of these viruses to subvert antiviral insults from different host species.
Methods: The innate immune response to filoviruses in bat and humans cells was profiled by deep sequencing and also analyzed by qRT-PCR. Bat mRNAs encoding IFNalpha, beta, gamma, lambda, and interferon stimulated genes (ISG) 54 and 56, were cloned and examined for their antiviral effect in response to MARV and EBOV infection in bat and human cells. Rates of infection and the effects of the major filoviral IFN-inhibiting domains (IID), VP35 and VP24, were analyzed in cells from both host species.
Results: We demonstrated that EBOV and MARV replicate to similar levels in all tested cell lines, indicating that permissiveness for EBOV at cell and organism levels do not necessarily correlate. Filoviruses, particularly MARV, induced a potent innate immune response in rousette cells that was generally stronger than in human cells. Both EBOV VP35 and VP24 IID were found to suppress the innate immune response in rousette cells, but only VP35 IID appeared to promote virus replication. Along with IFN-alpha and IFN-beta, IFN-gamma was demonstrated to control filovirus infection in bat cells but not in human cells suggesting host species specificity of the antiviral effect. The antiviral effects of bat IFNs appeared not to correlate with induction of bat ISG54 and ISG56, which were detected in human cells expressing bat IFN-alpha and IFN-beta.
Conclusions: Rousettus aegyptiacus cells mount robust innate immune responses to filovirus infection. Filovirus IIDs are active in both rousette and human cells; however, the VP35 IID plays a greater role in promotion of viral replication in rousette cells than in human cells. IFN-gamma plays a greater role in control of filovirus infections in rousette non-immune cells than in human cells. At least in part, the antiviral effect of IFN-gamma results from 'cross talk' leading to activation of the type I IFN response. The data are useful for understanding the interactions of filoviruses with natural (Rousettus aegyptiacus) and accidental hosts (humans).

Broad based surveillance for ebolaviruses: PREDICT in Sierra Leone, Liberia, and Guinea
Bird B[1], Goldstein T[1], Anthony S[2], Gbakima A[3], Saylors K[3], Jean Louis F[3], Wolking D[1], Epstein J[4], Karesh W[4], Kreuder-Johnson C[1], Mazet J[1]

One Health Institute UC Davis School of Veterinary Medicine[1], Center for Infection and Immunity Columbia University[2], Metabiota Inc.[3], EcoHealth Alliance[4]

Objectives: Developing and operationalizing strategies to reduce zoonotic pathogen spillover, amplification, and spread are nowhere more relevant than in Sierra Leone, Guinea, and Liberia. The devastating loss of lives associated with the Ebola virus outbreak revealed the urgent need for increased animal and public health sector capacity strengthening. Put into historical context, this epidemic was more than 60 times larger than any previous Ebola outbreak, spread to 7 additional countries, and stretched emergency response efforts to the utmost limits of capacity. **Methods**: PREDICT is working to improve understanding of wildlife reservoirs, spillover hosts, and origins of these viruses; ascertain the potential of virus-spillover into other non-typical hosts, such as livestock or companion animals; gain a greater understanding of high-risk human behavioral activities; and improve disease surveillance and laboratory capacities through workforce development in line with Global Health Security Agenda priorities. **Results**: Due to the impact on these three countries, USAID's PREDICT Project developed a focused effort to better address the threat of ebolaviruses by investigating the virus' animal origins, while strengthening in-country capacity to build and reinforce emerging disease surveillance and detection systems. In each country, teams are conducting concurrent sampling of from multiple animal taxa (dogs, cats, livestock, wildlife) and applying broad based molecular approaches to detect all known and other potential novel ebolaviruses. As of April 2017, over 6,500 animals have been sampled including over 3,500 bats in the three countries, with laboratory testing underway. Without identifying reservoirs of infection and how widely they are distributed across the region, prevention programs to reduce transmission from animals to people will have limited impact, and it is likely that future spillover of ebolaviruses from animals into humans will continue to occur. **Conclusions**: As we have seen over the years in Central and Eastern Africa where filovirus outbreaks have repeatedly occurred, effective control of these rare "spillover" events is possible and, when the right technical capacities are in place, these outbreaks can even be limited to a small number of human cases.

Quantifying signatures of resistance and tolerance to filoviruses in bat cell lines
Cara E. Brook[1], Melinda Ng[2], Esther Ndungo, Rohit K. Jangra, Andrew P. Dobson, Andrea L. Graham, Bryan T. Grenfell, C. Jessica E. Metcalf[1]*, Kartik Chandran[1]*

[1]Department of Ecology and Evolutionary Biology, Princeton University;
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Objectives: Previous work has demonstrated that a single amino acid change in the filovirus receptor, NPC1, in *Eidolon helvum* cells make them refractory to Ebola virus infection, hinting at a possible coevolutionary history between virus and bat host. We sought to expand on this nascent evidence of the evolution of pathogen resistance. **Methods:** We carried out a series of plaque assays, in which we challenged bat (EidNi/41.3, RoNi/7.1, PaKiT01), U2OS, and Vero cell lines with multicycle replicating pseudotype Ebola and Marburg filoviruses. Because of the agar overlay inherent to the plaque assay, viral transmission was restricted to neighboring cells. We visualized this transmission by photographing the timecourse of infection spread across the cell monolayer, and processing the images to quantify the proportion infected at a given time point as the proportion of photograph illuminated by GFP-tagged virus. We then fit spatially-structured traditional epidemiological models to the resulting data, in order to disentangle the mechanisms underpinning diverse trajectories of tolerance and resistance in different virus-cell line relationships. **Results:** Our modeling highlights diverse, species-specific evolutionary relationships between particular bat cell lines and particular filoviruses, which necessitate mechanisms of pathogen resistance in order to recapture data trajectories in some cases (chiefly *E. helvum* and Ebola and *P. alecto* and Marburg) and mechanisms of tolerance in others. **Conclusions:** Our work highlights the power of interdisciplinary approaches, combining quantitative epidemiology with cell biology and adds to growing evidence suggestive of unique species-specific coevolution between bats and filoviruses.

Serologic evidence of exposure to filoviruses in fruit bats, Singapore
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Objectives: Bats are known natural hosts of Nipah virus and Maburg virus, and the collective evidence suggests that bats are also the natural hosts of ebolaviruses. Reston virus, an *Ebolavirus* species, is known to circulate in species of bats in the Philippines. To examine whether ebolaviruses and marburgviruses are more broadly present in Southeast Asia, we tested sera from three fruit bat species endemic in Singapore and widely distributed throughout Southeast Asia for evidence of past exposure to known species of ebolaviruses and marburgviruses. **Methods:** Sera were collected from the above-mentioned bat species from 2011 to 2016 in Singapore to screen for evidence of exposure to filoviruses. Venous blood was diluted 1:10 in 1×PBS and tested using a Bio-Plex® bead-based multiplex assay that simultaneously probes sera for immunoglobulins specific to the viral envelope glycoprotein from representative strains of all previously described *Ebolavirus* and *Marburgvirus* spp. We employed methods developed by Peel AJ *et al.* to establish a median fluorescence intensity (MFI) cutoff value. We screened 409 samples with this *Ebolavirus/Marburgvirus* spp. Bio-Plex® assay. **Results:** Positive results indicated that bats were previously infected with viruses related to the ebolaviruses from which the virus surface proteins were derived. Of the species tested, 10% of *Eoncyteris spelaea*, 8% of *Cynopterus brachyotis*, and 4% of *Penthetor lucasi* had positive sera results for antibodies specific to ebolaviruses.
Conclusion: These serological results demonstrated that viruses related to ebolaviruses have previously infected all three species of fruit bats, and may circulate in the populations, but we have not detected the virus in any samples. We conducted next generation sequencing on urine and feces, bat cell lines and screened numerous samples from bats in Singapore and have detected no evidence of the virus. As there is no evidence of Ebola virus disease in humans in Singapore or Southeast Asia, we think that these serological findings are evidence of novel, yet undescribed viruses related to known ebolaviruses.

Predicting undiscovered filovirus reservoirs and patterns of disease emergence
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Objectives: How can we discover unidentified filovirus hosts and where should we be searching for the viruses? Filoviruses *Ebolavirus* (EBOV) and *Marburgvirus* cause hemorrhagic fevers with high mortality rates, posing significant threats to public health and wildlife conservation. The viruses have sporadically emerged over the last 40 years at least, and yet the hosts of EBOV in particular remain poorly known and characterized. Here different studies help inform field surveillance through the identification of bat traits that predict filovirus reservoirs and ecological processes that facilitate emergence. **Methods:** Different modeling approaches were used. A mathematical model with seasonal birthing synthesized filovirus and bat data to determine if biannual birthing

might facilitate pathogen persistence. Regression analyses on serological data tested the model predictions. A machine learning approach provided additional information on bats, integrating multiple host trait data. Fragmentation analyses using satellite land cover data and Ebola virus disease outbreak index cases in humans (i.e. spillover from wildlife reservoirs) tested the hypothesis that forest fragmentation was correlated with emergence. **Results:** Synthesis of filovirus and bat data through models suggests bi-annual breeding and longer incubation periods, such as reported for Egyptian fruit bats and EBOV in experimental studies, allow viral persistence in bat colony sizes often found in nature. Serological data and machine learning approaches support the findings, with bats from species with two annual birth pulses more likely to be seropositive (odds ratio 4.4, 95% confidence interval 2.5-8.7) than those with one, suggesting biannual birthing may allow filovirus persistence. Machine learning algorithms suggest species' geographic range overlap may facilitate filovirus persistence. Finally, fragmentation analyses suggest Ebola virus disease outbreaks occurred mostly in hotspots of forest fragmentation. **Discussion:** These analyses suggest surveillance for filoviruses, especially ebolaviruses, might be targeted to young bats from species with biannual birthing in areas of fragmented forested habitat. The link between forest fragmentation and EBOV outbreaks suggests there is common ground between biodiversity conservation and disease risk mitigation. Together these results will help the research community identify where, when and in which species to continue the search for filovirus hosts.

Bats as possible animal origin of MERS-CoV

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Objectives: Bats are important reservoir for emerging viruses including coronaviruses. Although dromedary camels are believed to be the immediate animal source of the recent MERS epidemic, the evolutionary origin of MERS-CoV remains obscure. While horseshoe bats are the primary reservoir of ancestors of SARS-CoV, the possible role of bats in the emergence of MERS-CoV is less clear. When MERS-CoV was first discovered, it was found to be most closely related to *Tylonycteris* bat CoV HKU4 (Ty-BatCoV HKU4) and *Pipistrellus* bat CoV HKU5 (Pi-BatCoV HKU5) previously discovered in lesser bamboo bat (*Tylonycteris pachypus*) and Japanese pipistrelle (*Pipistrellus abramus*) respectively in Hong Kong. Subsequently, two other lineage C betacoronaviruses, BtVs-BetaCoV/SC2013 and Coronavirus Neoromicia/PML-PHE1/RSA/2011 (NeoCoV) were also detected in bats from China and Africa respectively. Interestingly, a lineage C betacoronavirus, Erinaceus CoV VMC/DEU, has also been found in European hedgehogs, which are phylogenetically closely related to bats, in Europe. Although NeoCoV represents the closest bat counterpart of MERS-CoV in most genome regions, the spike (S) protein, important for host receptor binding, is genetically divergent from that of MERS-CoV. On the other hand, Ty-BatCoV HKU4 possessed an S protein being most closely related to MERS-CoV. The spike of Ty-BatCoV HKU4, but not that of Pi-BatCoV HKU5, was able to utilize the MERS-CoV receptor, human dipeptidyl peptidase 4 (hDPP4) or CD26, for cell entry. These findings suggested that bats may be the primary host of the ancestor of MERS-CoV. **Methods**:To better understand the evolutionary path of MERS-CoV, we collected bat samples from various regions in China. **Results**: Diverse CoVs were detected, including a potentially novel lineage C betacoronavirus. Compared to Ty-BatCoV HKU4 and Pi-BatCoV HKU5, the virus was even more closely related to MERS-CoV and NeoCoV in most regions of its genome. In contrast, the S1 region was less closely related MERS-CoV than Ty-BatCoV HKU4 but more closely related to MERS-CoV than Pi-BatCoV HKU5. To determine if this virus can utilize hDPP4 as receptor, binding experiments using S1-receptor-binding domain (RBD), cell entry studies using pseudovirus assays and structural modelling of the RBD-hDPP4 interphase were performed. **Conclusions**: The results suggested a stepwise evolutionary process among lineage C betacoronaviruses in gaining the ability to bind hDPP4, and support a bat origin of MERS-CoV.

Rapid detection of MERS coronavirus ancestors in bats

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Objectives: Since its first appearance in 2012, the Middle East Respiratory Syndrome (MERS) has affected more than 25 countries in four continents with more than 1,300 cases and a high fatality rate of more than 30%. A novel lineage C betacoronavirus (betaCoV), MERS-CoV, has been confirmed to be the etiological agent. Human dipeptidyl peptidase 4 (hDPP4) was found to be the cellular receptor for MERS-CoV. Subsequent detection of MERS-CoV and its antibodies in dromedaries in various countries in the Middle East and North Africa have implied that these animals are probably the reservoir for MERS-CoV. Other lineage C betaCoVs in bats [e.g. *Tylonycteris* bat CoV HKU4 (Ty-BatCoV-HKU4), *Pipistrellus* bat CoV HKU5 (Pi-BatCoV-HKU5)] and hedgehogs were found to be closely related to MERS-CoV. So far, detection of MERS-CoV and discoveries of its closely related CoVs are most efficiently achieved through RT-PCR. Although RT-PCR is highly sensitive, its turn-around-time is about four hours and the test requires expensive equipment, stringent laboratory set-up and personal attention to prevent laboratory PCR product cross contamination which may lead to false-positive results.

Methods: Recently, we have developed a monoclonal antibody-based rapid nucleocapsid protein (NP) detection assay for on-site diagnosis of MERS-CoV, which can be finished in 30 minutes. **Results and Conclusions**: This rapid test is highly specific for MERS-CoV for human and dromedary samples, as samples containing other human CoVs (HCoV-OC43, HCoV-229E, HCoV-NL63 and HCoV-HKU1) or dromedary CoV UAE-HKU23 all showed negative results. However, we hypothesize that the rapid test can pick up betaCoVs closely related to MERS-CoV; and hence would be useful for the discovery of MERS-CoV ancestors. To test this hypothesis, we examine the usefulness of this rapid test to detect four alphaCoVs and four lineage B, C and D betaCoVs in fecal samples of bats.

Global patterns in coronavirus diversity

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Objectives: Since the emergence of SARS-CoV and MERS-CoV it has become clear that bats are important reservoirs of coronaviruses (CoVs). Despite this, only 16% of all CoV sequences in Genbank come from bats. The remaining 84% largely consist of known pathogens of public health or agricultural significance, indicating that current research effort is heavily biased towards describing known diseases rather than the 'pre-emergent' CoV diversity circulating in bats. Our study addresses this critical gap, and focuses on the evolutionary and ecological drivers of CoV diversity in resource poor countries, where the risk of zoonotic emergence is believed to be highest. **Methods**: We surveyed the diversity of CoVs in multiple host taxa from 20 countries in Africa, Asia and Latin America to explore the factors driving viral diversity at a 'global' scale. Partial CoV sequences were identified using consensus PCR, which was chosen in part because it could be easily implemented in resource poor settings. Sequences were then parsed into phylogenetic clusters (operational taxonomic units) and analyzed using ecological and epidemiologic approaches. **Results**: In total we identified sequences representing 100 discrete clusters, 91 of which were found in bats, and showed that patterns of CoV diversity correlate with those of bat diversity. This cements bats as the major evolutionary reservoirs and ecological drivers of CoV diversity. Preliminary co-phylogenetic reconciliation analysis indicated that frequent host switching has contributed to CoV evolution, and that regional variation exists in the dynamics of this process. **Conclusions**: Overall our study represents a model for exploring global viral diversity and advances our fundamental understanding of CoV biodiversity and the potential risk factors associated with zoonotic emergence.

SARS coronavirus may have originated from frequent recombination events between SARS-like coronaviruses in a single horseshoe bat habitat

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Objectives: Horseshoe bats are recognized as the natural reservoirs of Severe Acute Respiratory Syndrome coronavirus (SARS-CoV), as an increasing number of SARS-like coronaviruses (SL-CoV) have been detected in this bat family since 2005. However, knowledge gaps remain between currently known bat SL-CoVs and the direct progenitor of SARS-CoV. Further information is needed to better understand where and how SARS-CoV originated from bat reservoirs. **Methods:** We have conducted a 5-year surveillance of SL-CoV in a cave inhabited by horseshoe bats in Yunnan, China. Full-length genome sequencing of 11 novel bat SL-CoVs discovered in this single location was performed and genomic characterization, phylogenetic analysis and recombination analysis were conducted. Efficiency of human ACE2 usage was also evaluated in HeLa cells for several newly identified strains. **Results:** Our findings revealed that genetically diverse bat SL-CoVs were circulating in this single location, including different strains with high sequence similarity to SARS-CoV in the highly variable N-terminal

domain (NTD) and receptor-binding domain (RBD) of S protein and the ORF8 region, respectively. Meanwhile, compared with other SL-CoVs, strains identified from this cave exhibited higher sequence similarity to SARS-CoV in the non-structural proteins. Evidence supported that frequent recombination events have occurred within the S gene and around ORF8 between bat SL-CoVs in this cave and may have promoted the generation of the pandemic SARS-CoV. Cell entry studies demonstrated that different newly identified SL-CoVs with variants of S protein are all able to use human ACE2 as the receptor, which represent a potential risk of emergence if given the opportunity to spillover. **Conclusions:** We have identified an epicenter of SL-CoVs where the director progenitor of SARS-CoV likely originated via sequential recombination events. These findings offered important new insight into understanding the geographical and evolution origin of SARS-CoV and highlights the need to pursue the surveillance of bat SL-CoVs to make better preparation for future emergence of SARS-like disease in humans.

A metagenomic approach identifying a MERS-related coronavirus in a bat from South Africa

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A Middle East Respiratory Syndrome (MERS) related coronavirus was previously detected in a Cape serotine bat (*Neoromicia capensis*) from the KwaZulu Natal Province in South Africa. Though the virus showed significant similarity to human MERS coronavirus (MERS-CoV), it was too divergent to be considered the direct progenitor of the virus causing human MERS-CoV outbreaks. **Objectives:** As part of a broader viral discovery surveillance program investigating excreted zoonotic viruses from bats, we implemented metagenomic techniques to collectively screen the virome of 60 *Neoromicia* bats constituting 6 species from 4 South African provinces sampled from 2007-2015. **Methods:** Using a viral particle enrichment methodology, total nucleic acids from faecal and rectal specimens were sequenced on Illumina's MiSeq and NextSeq500. Coding complete genome sequencing was performed with further amplicon sequencing on Illumina's MiSeq. Bayesian (BEAST) phylogenetic comparisons and pairwise estimations were performed with full genome representatives of all 4 betacoronavirus lineages. **Results:** We detected a MERS-related betacoronavirus from the same *Neoromicia* species. The virus shared a 97.2% overall nucleotide identity to another *Neoromicia* MERS-related virus identified in South Africa, and 85.5-85.6% nucleotide identity to human and camel (alternative hosts) strains of MERS-CoV. Significant discrepancies between bat-borne and human/camel MERS-CoV genomes were attributed to the low (63.7-64.3%) amino acid similarities of the spike genes, which is responsible for receptor attachment. Genome comparisons between betacoronavirus lineages of emerging viruses, namely MERS-CoV and the equivalent Severe Acute Respiratory Syndrome (SARS) coronaviruses, indicate that the relative phylogenetic distances between *Neoromicia* MERS-related strains and human/camel MERS-CoV are far greater than the distances between SARS-related bat viruses and human SARS viruses. **Conclusions:** Continued surveillance within the *Neoromicia* genus may yield additional MERS-related viruses sharing greater similarity to the human and camel MERS strains (as was shown with detected SARS-related bat viruses). Alternatively, if the progenitor of MERS-CoV originated from the *Neoromicia* genus, the currently identified diversity would suggest that significant receptor adaptation was required within dromedary camels (or unknown intermediate hosts) prior to being transmitted to humans. Continued viral surveillance in regions inhabited by both these hosts may aid in understanding the emergence of MERS.

New insights into the antiviral innate immune response of *Desmodus rotundus*

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The common vampire bat, *Desmodus rotundus*, is the main reservoir of rabies virus in South America. Mechanisms that allow persistence of viruses in bats are not well-defined. During the last decade, innate immunity has emerged as one of the implicated mechanisms. As a non-model organism, no tools were available regarding *D. rotundus*, there was therefore a crying need for characterizing their immune system. Given that the interferon (IFN) system provides the first line of defense upon viral recognition, we investigated the IFN-I response in an immortalized cell line, established from a *D. rotundus* embryonic lung, stimulated with synthetic

dsRNA (poly I:C). We observed that stimulation induced high levels of expression of all PRRs involved in dsRNA recognition, as well as a rapid up-regulation of both IFN-α1 and β. Furthermore, in characterizing some of the ISGs such as OAS1, PKR and ADAR, we identified two OAS1 genes, tentatively named *OAS1a* and *OAS1b*. Upon stimulation, *OAS1b* appeared to be the most inducible ISG tested. These results not only provide evidence of the intact signaling pathway of the IFN-I in our cellular model, but also that *OAS1b* may be a major player in antiviral activity in *D. rotundus*. In the frame of the present work, we generated a sum of insightful tools specific of the common vampire bat useable to the study of a number of different viruses, the first of which is the rabies virus.

A comparative study of the autophagy pathway during virus infection of bat (natural) and human (accidental) host cells

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Objectives: In contrast to other terrestrial animals, infection of bats with ebolaviruses and henipaviruses does not cause symptomatic disease. Whether bats have antiviral mechanisms to control these infections or how these viruses persist at a cellular level is largely unknown. Autophagy is a cellular protein homeostatic process, which has been implicated as a cell-autonomous innate defense mechanism against a broad array of intracellular infections. Bats are longer lived compared to other similarly sized mammals and increased proteostatic processes have been observed in long-lived mammalian species. **Methods:** In this study, we performed an investigation of autophagy in cell lines from the black flying fox (*Pteropus alecto*), a natural host of Hendra virus and Australian bat lyssavirus (ABLV), and human cells. ABLV, a neurotropic virus, was used as a model bat-borne virus to examine the interactions between an intracellular virus infection and autophagy in host cells. **Results:** Autophagy activation was observed in *P. alecto* brain tissue-derived primary and secondary cells infected with replication competent ABLV 1 and 2 days post infection. Compared to a human neuroblastoma cell line, *P. alecto* kidney and brain cells exhibited a higher level of basal autophagy. Treatment of bat and human cell lines with pharmacological activators of autophagy reduced ABLV replication. Quantification of ABLV titers and protein levels after infection of bat and human cells lines demonstrated that bat cells were less permissive to ABLV infection. Lentiviral knockdown of autophagy-related gene-5 (ATG-5) in bat and human cell lines did not result in a significant silencing of the autophagy pathway, however, a trending increase of ABLV replication levels was observed in the ATG-5 knockdown cells. Pre- and post-infection treatment of human neuroblastoma cells with BEZ235, an mTOR- and PI3K-inhibitor, significantly decreased virus replication in a dose-dependent manner. **Conclusions:** To our knowledge this is the first study to explore whether the autophagy pathway has a role as an antiviral defense mechanism during virus infection in bats. Ongoing experiments aimed at the interplay between autophagy and apoptosis will be critical to supporting our hypothesis that autophagy is an antiviral defense mechanism in bats.

Development of a minimally invasive individual identification technique for continuous monitoring of African bat species

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Objectives; An ever increasing number of potentially zoonotic diseases are associated with bat populations throughout the world, and as such the continuous monitoring and surveillance of these populations has become essential, not only for disease epidemiology but also in order to address the lack of knowledge available for biology, ecology and life histories of the majority of bat species. This requires the development of an ethically acceptable, cost effective, durable and reliable marking system to facilitate monitoring of individual bats. In order to address annual population structure, potential movement patterns and individuals' infection or exposure status we tested the ability to uniquely mark 11 bat species from six families, ranging in mass from 4g to 120g, using wing tattoos. Specific serological monitoring of Lagos bat virus exposure in *Rousettus aegyptiacus,* focussing on the presence and duration of neutralising antibodies has been undertaken since 2012. **Methods;** Non-toxic black ink was applied into the interdermal layers of the propatagial membrane of the bat by means of a tattoo system with nine-pronged needles. The tattooing procedure was performed on individual bats from a captive colony of *R.*

aegyptiacus (n=287) and free-flying, wild populations of the aforementioned species (n=2559). The robustness and longevity of this system was assessed from recaptures of tattooed individuals representing four of the above species in the wild, and observations of the captive colony of *R. aegyptiacus*. **Results;** This technique provides a simple, durable and cost effective marking system for both immediate and medium term monitoring, with no observed detrimental effects to the individuals to date. The longest periods between application and observation of tattoos has been; 927 days for *R. aegyptiacus*, 292 days for *N. thebaica*, 126 days for *M. natalensis* and 89 days for *Rh. smithersii.* Over 100 *R. aegyptiacus* recapture events have demonstrated individuals' seroconversion, antibody maintenance and loss against LBV. **Conclusion;** This technique has shown potential to facilitate monitoring individual bats' infection or exposure status in both captive and wild settings, with individual seroconversion and titer loss against LBV being observed, as well as providing an effective mark-recapture identification for population and movement studies.

Characterization of a novel Rhabdovirus isolated from insectivorous bat (*Pipistrellus kuhlii*) in Italy
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Objectives: *Rhabdoviridae* is one of the most ecologically diverse families of RNA viruses with clinical importance. Herein we report the isolation and the genome characterization of a novel rhabdovirus detected from a bat collected within a survey implemented in Italy on emerging viruses of bats. **Methods:** A fresh carcass of an adult female of *Pipistrellus kuhlii* spontaneously dead in a wildlife rehabilitation center in Northern Italy was fully necropsied. Tissue samples from different organs (lung, hearth, intestine) were subjected to viral isolation on cell culture. Virus identification was performed using negative staining electron microscopy (nsEM) and NGS sequencing. Molecular and phylogenetic analyses were performed. **Results:** Anamnesis reported sensory depression, inappetence, normal body mass and injuries of patagium consistent with a cat bitten. The death occurred three days after the admission to the rehabilitation center and no pathological lesions indicative of infectious diseases were observed at necropsy. CPE was observed on VERO cells inoculated with a pool of organs and nsME performed on cells supernatants revealed characteristic bullet-shaped viral particles referable to rhabdovirus. Tests aimed to exclude rabies and related lyssaviruses resulted negative. The complete genome size was 11,780 nt comprised 5 genes encoding the canonical rhabdovirus structural proteins and an additional transcriptional unit (U1) encoding a small protein (157 aa) located between the G and L genes (3'-N-P-M-G-U1-L-5'). BLAST analysis showed the highest nucleotide identity (65%) to Le Dantec virus (LDV) (human, 1965 Senegal) the prototype strain of the putative genus Ledantevirus. The most highly conserved protein L shared 70% and 69% of aa identity with LDV and Keuraliba virus (KEUV) (gerbil, 1968 Senegal) respectively. Phylogenetic tree based on full-genome sequence confirm the belonging of the new isolate to the ledantevirus group. **Conclusions:** A novel rhabdovirus was identified from *Pipistrellus kuhlii*, the most common species in urban areas in Italy. This finding represents (beside lyssaviruses) the only bat-borne rhabdovirus isolated in Europe. Specific diagnostic tools for viral detection will be set up for epizootiological investigations aimed to define the viral ecology and diffusion in bats population in Italy, in order also to further characterize and clarify its zoonotic potential.

Age-specific dynamics of maternally- and infection- derived immunity within African bat populations
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Objectives: Predicting and managing spillover of emerging infectious diseases to domestic animals and humans depend on data on reservoir host distribution, ecology and immunology as well as the mechanisms governing pathogen transmission among its populations. However, such data are generally sparse. This is exemplified by old-world fruit bats, which have been linked to an increasing number of zoonotic viruses, but whose ecology is

challenging to study and immunology has only recently begun to be elucidated. Even where appropriate data are available, fission-fusion population structures make it challenging to separate out the dynamical effect of pathogen reintroduction into the study population through movement from the transmission dynamics expected within a closed population. Island populations provide ideal natural experiments and involve simplifications analogous to the assumptions often made in modelling studies (e.g. single, closed population of a single species), allowing exploration of underlying processes. Here, building on an extensive body of work on straw-coloured fruit bats (*Eidolon helvum*), we aim to further elucidate fundamental processes governing viral dynamics, including the role of maternally-derived antibodies (MatAb). **Methods:** We focus on two viruses for which *E. helvum* is a reservoir (Lagos bat virus (LBV) and African henipavirus) and look for evidence of the presence of MatAb in wild *E. helvum* from continental and island populations. We use rare age-specific data to model waning rates of maternally- and infection- derived antibodies. These results then informed the parameterisation of a stochastic seasonal birth model to explore population-level persistence in the presence of MatAb, in both naive and non-naive populations. **Results:** Statistical modelling supported age as the strongest determinant of seroprevalence for both henipavirus and LBV, in addition to highly significant correlations between mother-offspring pairs. Age-specific seroprevalences predicted rapid loss of maternal immunity and effectively lifelong infection-induced immunity (particularly for LBV). The inclusion of MatAb had considerable implications on viral persistence within populations in a dynamic birth pulse model. **Conclusions:** This study helps to better understand endemic viral dynamics in bat populations, and the implications of considering the presence of MatAb in broader wildlife disease systems.

Detection of rubula- and related viruses in an Egyptian fruit bat (*Rousettus aegyptiacus*) colony in South Africa

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Objectives: More than 22 viral families have been associated with bats globally, eight of which with the Egyptian fruit bat (*Rousettus aegyptiacus*) occurring across sub-Saharan Africa and parts of the Middle East. Among numerous other zoonotic viruses, this species has also been associated with zoonotic henipaviruses (family *Paramyxoviridae*). More recently, a newly described zoonotic rubulavirus, Sosuga virus, was detected in this species from Uganda. The occurrence and diversity of these viruses remain unknown in Southern Africa. **Methods:** A broadly reactive hemi-nested RT-PCR assay targeting the *Avula-Rubulavirus* genera within the *Paramyxoviridae* family was used for nucleic acid detection. Spleen and kidney samples from bats collected during 2012-2016 from a cave in the Limpopo Province of South Africa, were retrospectively screened for the presence of rubulavirus RNA. Virus isolation, next-generation Illumina sequencing and amplicon sequencing were used to obtain full gene or genome sequences for comparison. **Results:** A total number of 137 bats were screened of which 5.84% of spleen samples tested positive. We detected several rubulavirus-related viruses grouping in a sister clade to the *Rubulavirus* genus. This clade contains other bat-associated rubulaviruses including the zoonotic Sosuga virus. Additionally, a co-infection with a virus closely related to human mumps virus was detected in one of the bats sampled. Preliminary results also suggest seasonality of these viruses in the colony, as positive individuals were predominantly detected in winter months. This phenomenon coincides with the loss of maternal antibodies i.e. an influx of susceptible individuals into the colony. **Conclusion:** The first evidence of bat-associated rubulaviruses from *R. aegyptiacus* in South Africa, some of which are related to know human pathogens, are reported. Additionally, a considerable diversity was detected from a small sample size. Enhanced surveillance might shed light on the prevalence of these viruses within the targeted colony. Considering the potential excretion of these viruses during the winter months might be the next step in determining their transmission potential. This is of importance as the specific cave is situated within a rural settlement surrounded by free-roaming livestock and is frequented by humans for religious practices.

Influenza-like virus and paramyxovirus screening in Brazilian bats

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Objectives: Bats are recognized as natural reservoirs of emergent viruses related to severe human disease outbreaks including Rabies, Nipah, Hendra and SARS coronavirus. Since the discovery of Hendra and Nipah emergent paramyxovirus in late 1990s in flying foxes bats from Australia and Asia, others bat-borne paramyxovirus have been identified in bats across the globe including bats species from Australia, Asia, Africa and America. Recently, new members of the influenza A virus where detected in bats from Guatemala and Peru, amplifying the host variety of Influenza virus A group. Despite the recent detection of Influenza-A and Paramyxovirus in South American bats and the spill-over events of paramyxovirus from bats to humans only few studies had analyzed the occurrence of influenza-like virus and paramyxovirus in Brazilian's bats. These study aims to analyze the occurrence and diversity of influenza-like virus and paramyxovirus in Brazilian bats. **Methods:** A total of 1071 samples including distinct tissues (intestine, lung, kidney and spleen), rectal and oral swabs, and serum (821 individuals/47 species) from urban area and Atlantic Forest biome were analyzed. The Total Nucleic Acid was extracted and cDNA synthesis was performed. Samples were screened by Pan-Flu PCR assay targeting the Influenza PB1 gene and by a Semi-Nested Pan-paramyxovirinae PCR assay targeting the L gene. **Results:** PCR fragments for both assays were observed in electrophoresis analysis. The amplicons were purified and sequenced by Sanger method. Sequencing confirmed the presence of 3 distinct Paramyxovirus lineages in eight bats. Morbillivirus-like was detected in insectivorous bat's *Molossus rufus* (intestine) and *Myotis nigricans* (lung)*;* Unclassified Paramyxovirus and one possible Henipa-like virus was found in hematophagous bats *Desmodus rotundus* in kidney samples*.* **Conclusions:** This study report the lack of detection of influenza-like in a high number of bat samples and may indicate the absence or the lower prevalence of these virus group in bats from Brazil. Our results also suggest the presence of paramyxovirus genotypes in bats commonly found in rural and urban area, including a probably Henipa-like virus in hematophagous bats, species that already had been described as vectors of rabies and others paramyxovirus with unknown zoonotic potential.

Hendra virus dynamics and spillover

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Hendra virus provides a model system for understanding the dynamics of emerging bat viruses and spillover. One factor constraining our ability to study Hendra virus spillover is the limited knowledge of the biology of the virus within its reservoir hosts. We present three different hypotheses for how within-host pathogen dynamics in bats may interact with among host factors to drive dynamics of emerging bat virus spillover. These hypotheses include: pulsed viral excretion due to seasonal epidemics, local persistence due to waning immunity within bats, or episodic shedding from persistently infected bats. We discuss the evidence for each hypothesis and show that differentiation among these scenarios is essential for predicting and managing spillover.

Using serology to understand the dynamics of concurrent viral infections in pteropid bats

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Objectives: Fruit bats of the genus *Pteropus* are reservoirs for henipaviruses throughout their range. *Pteropus medius* is the natural reservoir for Nipah virus in India and Bangladesh, and mechanisms of spillover to humans primarily involves contamination of date palm sap with excreta. Serological dynamics have provided insight into patterns of Nipah virus infection in this host, but other viruses, including Nipah-like viruses have been identified through pathogen discovery techniques. Little is known about infection patterns of other viruses within this species, or their likelihood of infecting other animals or people. **Methods**: We screened sera from a single population of *P. medius* in Bangladesh collected quarterly over six years for IgG antibodies against henipaviruses (NiV, HeV, CEDV), filoviruses (EBOV, MARV), and Menangle virus, using assays containing virus-specific solubilized glycoproteins or F proteins in a Luminex platform. **Results and Conclusions:** Here we present preliminary observations of comparative temporal patterns for multiple viral agents that suggest co-circulation in this population. We also discuss challenges in interpretation of serology

when studying viral infections in wildlife, particularly when multiple antigenically related viruses may be present.

Estimating viral richness and viral sharing in bats: integrating previously-published and newly-acquired field data

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Objectives: A handful of studies published over the last 8 years have sought to identify the host, ecological, and evolutionary factors that best explain species-level differences in viral richness in bats. Similarly, a few studies have also aimed to answer the golden question: Do bats carry a significantly larger number of total viruses, or a larger number or proportion of zoonotic viruses than other mammals? Our objective is to address these critical questions using statistical models and large datasets collated from the literature and acquired from the field. **Methods:** We collated data from the past 75 years of published for over 2800 mammal-virus associations, representing 754 mammal species and 586 ICTV-named viral species. We fit a series of generalized additive models to these data to identify and examine the functional form of significant predictor variables for total and zoonotic viral richness. Using our best-fit models we also estimate expected viral richness for each host species under a scenario of 'maximum' research effort. We map these viruses in geographic space. We also use species accumulation curves to estimate viral richness from standardized, field-acquired data from the USAID PREDICT project (http://www.healthmap.org/predict/). Network models and statistics were used to compare patterns of viral sharing among bats between the literature and field-acquired datasets. **Results:** For the all mammal analyses: The best-fit model for total viral richness per wild mammal species explained 49.2% of the total deviance, and included a per-species measure of disease-related research effort, phylogenetically corrected body mass, geographic range, mammal sympatry, and taxonomy (order) After controlling for research effort, the proportion of zoonotic viruses per species is predicted by phylogenetic relatedness to humans, host taxonomy and human population within a species range—which may reflect human–wildlife contact. We demonstrate that bats harbor a significantly higher proportion of zoonotic viruses than all other mammalian orders. For the bat field-acquired data we show significant differences in viral richness estimates across bat genera and viral family, as well as differences in the rates of saturation. Clustering in bat host-virus networks follow some predictable patterns and identify additional bat species to target for viruses of interest. **Conclusions:** These host-specific analyses and estimates of viral richness, including the unobserved or 'missing' viruses, allow us to better identify and target which species and regions should be preferentially targeted to characterize the global bat virome.

Optimised sampling efforts and screening assays identify several MERS-related coronaviruses in South African bats

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Objectives: Bats are considered reservoir hosts for all mammalian alpha- and beta-coronaviruses (α-, β-CoV). Following the emergence of SARS in 2002/03 and the subsequent identification of *Rhinolophus sinicus* as the likely ancestral SARS-CoV source, a wide diversity of bat CoV has been described worldwide. We work in transdisciplinary collaborations with ecologists and zoologists to define CoV diversity and ecology in South African bats. In addition to general "opportunistic" surveillance, species-specific studies of *Neoromicia capensis* and *Rhinolophus spp* are conducted, including longitudinal studies of bat colonies to determine shedding patterns and diversity of viruses present. **Methods:** Since 2011, 24 different bat species have been sampled along rainfall and altitudinal gradients across different biomes; namely Fynbos, Forest, Nama Karoo, Grassland, and Savanna. Sample types include faecal pellets, saliva and urine swabs, and when voucher specimens are sacrificed for museum collections, also blood and organs. Sequences of the 816bp RGU fragment (Drexler et al., 2010) for species classification were used to construct ML trees in MEGA v7. **Results:** An improved screening method greatly increased the CoV detection rate. Of 686 samples tested, 92 from 9 bat species were screening-positive: 66 for α-CoV, 19 for β-CoV, and 7 for both. The majority of sequences identified are α-CoVs, with ~20% prevalence for *N. capensis*. Preliminary analyses of partial RdRp, nucleocapsid and spike gene fragments of novel β-CoV identified in Neoromicia and Pipistrellus bats are closely related to BtCoV PML-PHE1/RSA/2011 (NeoCoV), previously found by us in a *N. capensis* and belonging to the same viral species as the recently emerged MERS-CoV, responsible for the ongoing

outbreak in the Arabian Peninsula. **Conclusions:** Extensive, dedicated sampling efforts allowed detection of α- and β-CoV from a wide range of bat species across large parts and different biomes of South Africa. An improved screening PCR approach yielded significantly more positive samples. There is substantial CoV diversity in southern African bats, including, most importantly, additional MERS-CoV-related CoV, which will hopefully help to address the unresolved question of the origin of this zoonotic pathogen.

Coronavirus diversity in bats from urban, rural and forest areas of Atlantic and Amazon Forest biomes, Brazil.

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Objectives: Epidemiological and phylogenetic studies indicate that four out of six coronavirus capable of infecting humans are the result of spill over events of virus from bats to humans. Despite the great diversity of coronaviruses in bats, the large number of bat species in Brazil (15% of the world's bat diversity) and the presence regions classified as hotspot for zoonotic pathogen emergence only few studies have analyzed the circulation of coronaviruses in Brazilian's bats. This study aims to evaluate the diversity of CoV circulating in bats in Brazil, covering different species, habitats, and life history of the hosts. **Methods:** We analyzed 840 bats from 53 species and five bat families with a pancoronavirus detection assay. Intestine, lungs, serum and rectal/oral swabs were obtained from bats from forest, urban, and rural areas located in the Atlantic and Amazon Forest biomes. **Results:** Distinct coronavirus lineages were detected in in bats from all sites screened. The coronavirus RNA was detected in 27 individuals from eleven bat species including *Artibeus lituratus(4), Carollia perspicillata (5), Eumops glaucinus(1), Glossophaga soricina (3), Mimon crenulatum(1), Molossus rufus(2), Molossus molossus (1), Myotis nigricans(1), Myotis riparus (1), Phyllostomus discolor(1)* and *Sturnira lilium (7)*. The analysis of coronavirus phylogenetic relation from nucleotide sequences obtained showed the circulation of the 25 Alphacoronavirus genotypes (α-CoV) and two Betacoronavírus (β-CoV), distributed in thirteen lineages (eleven α-CoV and two β-CoV). Results indicate the presence of a great coronavirus diversity in bats from Brazil including potential new and already described lineages. We describe the detection of a bat coronavirus genetically related with Alphacoronavirus-1 species, which are a group of closely related viruses with an evolutionary history of recombination and cross-species transmission between domestic and livestock animals. We also report the circulation of Betacoronavirus lineage "C", related to emergent highly pathogenic coronavirus CoV-MERS, in South American bats commonly found in urban areas, representing the first detection of coronavirus Clade C in this subcontinent. **Conclusions:** Our report points to the great diversity of CoV genotypes in New World bats, more specifically in the Atlantic Forest Biome, providing a better understanding of CoV diversity, host range and biogeographic distribution.

Preliminary Evidence of a Novel Alphacoronavirus and Secondary Acquisition of Tymoviridae and Partitiviridae in Little Brown Bats (*Myotis lucifugus*) in Southcentral Alaska.

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Objective: We sought to analyze the virome of the most common bat species in Alaska, *Myotis lucifugus*, the little brown bat. Swabs, tissue, and fecal samples were collected from habitats in close proximity to barns, farm buildings, and human habitations in southcentral Alaska. **Methods**: Total RNA extracts were screened by RT-PCR and CoV ORF1a, and primary RNA samples were used in library preparation for short-read, paired-end next generation sequencing on an Illumina HiSeq platform. **Results**: Sanger sequencing of amplicons confirmed the presence of an alpha-coronavirus phylogenetically related to

persistent alphacoronaviruses detected in bats in Colorado and the Rocky Mountains. Aligning to a reference *M. lucifigus* virus from Colorado, bat alphacoronavirus CDPHE15/USA/2006, we assembled a full-length genome (28,515nt) identifying the novel alphacoronavirus/bat/Alaska/s7/2014. A high degree of thermodynamically stable stem-loop RNA structures are predicted by Mfold within 700nt of 5' and 3' termini of genome**.** While nucleotide conservation to the Colorado virus was 96%, notable amino acid differences were identified in coronavirus proteins. In two distinct bat samples, preliminary results indicate the likely presence of tymovirus (eg. Dulcama mottle virus) probably acquired through ingestion of insects feeding on infected plants. In addition, initial results indicate presence of alpha-partitivirus closely aligned to *Rosellina*-type associated with spruce/alder and other partitivirus-like sequences. Secondary acquisition of virus obtained by feeding or incidental infection by fungi (eg. gamma-partitivirus associated with *P. destructans*) has been previously described for bats collected from similar ecological settings (eg. Thapa et al. 2016). **Conclusions**: We continue to further refine these initial for better resolution of the virome of Alaska bats.

Are big brown bat cells different than human cells in their innate immune response to coronavirus and viral ligands?

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Objectives: Bats are hosts for viruses such as those that closely resemble coronaviruses (CoV) that cause severe acute respiratory syndrome (SARS), Middle East respiratory syndrome (MERS) and porcine epidemic diarrhoea (PED). Despite the serious nature of these diseases in other mammalian hosts, bats naturally infected with CoV or experimentally infected with MERS-CoV do not demonstrate clinical signs of disease. We challenged big brown bat (*Eptesicus fuscus*) cells and human cells with MERS-CoV or viral ligands to study the differences in their interferon and inflammatory responses. **Methods:** *E. fuscus* kidney cell line and bone marrow derived cells, human fibroblast and epithelial cells were challenged with either MERS-CoV or poly(I:C), a double stranded RNA surrogate. Transcripts for several innate immune response genes were quantified using qRT-PCR. Interaction between the bat TNF promoter and a potential repressor of the promoter, c-Rel, was detected by chromatin co-immunoprecipitation and bat c-Rel, TLR3, RIGI and MDA5 transcripts were knocked-down using specific siRNA. **Results:** Both human and bat cells, when stimulated with poly(I:C), contained higher levels of transcripts for interferon beta than unstimulated cells. In contrast, only human cells expressed robust amount of RNA for TNFα, a cell signaling protein involved in systemic inflammation. We further observed that poly(I:C) signaled primarily through TLR3 in big brown bat cells. We examined the bat TNFα promoter and found a potential repressor (c-Rel) binding motif. We demonstrated that c-Rel binds to the putative c-Rel motif in the promoter and knocking down c-Rel transcripts significantly increased basal levels of TNFα transcripts. Both human and bat cells support replication of MERS-CoV to comparable levels. **Conclusions:** We have identified a novel transcription repressor, c-Rel, that inhibits an increase in TNFα transcripts in bat cells after poly(I:C) stimulation. We have also showed for the first time that poly(I:C) signals through TLR3 in bat cells. We are currently studying the modulation of the innate immune response in bat cells by MERS-CoV and individual MERS-CoV and bat coronavirus proteins. Identifying adaptations in the bat innate immune response might allow us to extrapolate the knowledge in identifying potential drug targets in spill-over species, such as humans.

Reverse genetic analysis of bat influenza viruses: A journey full of surprises.

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Our understanding of conventional influenza A viruses was recently challenged by the identification of two novel genome sequences of influenza A-like viruses from bat specimens by next-generation sequencing. Serological surveys indicate that these viruses circulate in various bat species in Central and South America. However, no viable viruses could be isolated from bats, impeding further characterization of these viruses. Interestingly, analysis of the viral surface proteins revealed that the entry machinery of these viruses differ significantly from all known conventional influenza A viruses and may only support entry into bat cells. This talk will summarize recent progress obtained by reverse genetic analysis of bat influenza A-like viruses, including the observation that the host tropisms of these viruses might be larger than anticipated.

Towards understanding bat influenza A-like viruses

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Objectives: Bats harbor many viruses, which are periodically transmitted to humans resulting in outbreaks of disease (e.g., Ebola, SARS-CoV). Recently, bat influenza A-like virus HL17NL10 and HL18NL11 sequences were identified; however, no viruses were isolated from bats. This discovery aroused great interest in understanding the evolutionary history and pandemic potential of bat-influenza virus. **Methods**: Using synthetic genomics, we rescued a modified bat-influenza virus that had the HA and NA coding regions replaced with those of A/PR/8/1934 (H1N1). **Results**: This modified bat-influenza virus replicated efficiently in vitro and in mice, resulting in severe disease. The results indicate that internal genes of bat influenza A-like viruses are functional to support virial genome transcription and virus replication. Mini-genome replication studies and virus reassortment experiments demonstrated that bat influenza A-like virus has very limited genetic and protein compatibility with Type A or Type B influenza viruses, yet it readily reassorts with another divergent bat influenza A-like virus. **Conclusions**: In conclusion, our data indicate that the bat influenza A-like viruses recently identified are authentic viruses that pose little, if any, pandemic threat to humans; however, they provide new insights into the evolution and basic biology of influenza viruses.

Experimental Infection of Jamaican Fruit Bats (*Artibeus jamaicensis*) with a Rescued Bat HL18NL11 Influenza A-like Virus

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Objectives: Nucleotide sequences of two novel influenza A-like viruses, HL17NL10 and HL18NL11, were recently discovered in New World little yellow shouldered fruit bats (*Sturnira lilium*) and flat-faced fruit bats (*Artibeus planirostris*), respectively. Serological studies indicated high prevalence to these viruses among many species of Phyllostomidae leaf-nosed fruit bats of Central and South America, including Jamaican fruit bats (*Artibeus jamaicensis*). **Methods**: Infectious viruses have not been isolated from bats, therefore an infectious clone of HL18NL11 was generated by reverse genetics technologies that produced particles resembling influenza viruses from transfected cells by electron microscopy. Susceptibility of Jamaican fruit bats to rescued HL18NL11 bat influenza A-like virus was determined during a 28-day challenge experiment via intranasal inoculation. **Results**: The bats exhibited no overt clinical signs of disease nor fever. However, rectal swabs had up to 10^4 $TCID_{50}$ equivalents of HL18NL11 vRNA by real-time PCR in each bat on days 2, 4 and 7 post inoculation, but not day 15 or 28, and in the lungs of one of the bats on day 28 when they were euthanized. Serology showed moderate antibody titers to nucleoprotein by ELISA. Histopathology revealed mild pathology, particularly in the one bat with detectable vRNA in its lung. This bat's lungs showed multifocal mild-to-moderate histiocytic and lymphoplamacytic interstitial pneumonia. Pleocellular infiltrates were especially prominent around adventitia of pulmonary arterioles. Immunohistochemistry with mouse antibody to recombinant H18N11 nucleoprotein revealed virus antigen in the lungs of this bat. **Conclusions**: This is the first study to demonstrate susceptibility to bat influenza viruses and suggests that viral persistence up to 28 days may occur in some bats, supporting the hypothesis that Jamaican fruit bats may be a natural reservoir host of the HL18NL11 virus.

Seroprevalence of alphaviruses, flaviviruses and Rift Valley fever virus in Ugandan bats

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Objectives: Arboviruses including Rift Valley fever virus (RVFV), chikungunya virus (CHIKV) and Sindbis viruses have previously been isolated from naturally-infected East African bats, however the role of bats in arbovirus transmission cycles is poorly understood. The aim of this study was to investigate the exposure history of Ugandan bats to a panel of arboviruses. **Methods**: Insectivorous and fruit bats were captured from multiple locations throughout Uganda between 2009 – 2013. All bat captures were conducted under the approval of IACUC protocols 1731AMMULX (Maramagambo samples) and 010-015 (all other samples). Bats were captured using harp traps or mist nets, taking appropriate biosafety precautions. All serum samples were frozen at -80°C until they were tested for neutralizing antibodies against West Nile virus (WNV), yellow fever virus (YFV), Dengue 2 virus (DENV-2), Zika virus (ZIKAV), CHIKV, o'nyong-nyong virus (ONNV), Babanki virus (BABV), and RVFV by plaque reduction neutralization test (PRNT). **Results**: Sera from up to 626 bats were screened for neutralizing antibodies against each virus. Key findings include the presence of antibodies against ONNV in approximately 15% (44/303) of Egyptian rousette bats (*Rousettus aegyptiacus*) from Maramagambo forest in western Uganda, and antibodies against RVFV in Ethiopian epauletted fruit bats (*Epomophorus labiatus*) captured from Kawuku (5/52) and Egyptian rousette bats from Kasokero cave (3/54). **Conclusions**: Antibodies reactive to flaviviruses were widespread across bat taxa and sampling locations.The data presented demonstrate the widespread exposure of bats in Uganda to arboviruses, and highlight particular virus-bat associations that warrant further investigation.

Presence of zoonotic bat pathogens correlate with reproductive seasons in South African bat populations
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In 2003 we initiated passive surveillance on bats in South Africa with the initial objective to identify rabies–related lyssaviruses, but this has since expanded to include several other possible zoonotic viral and bacterial pathogens. The project has identified viruses in the following families; *Rhabdo, Paramyxo, Bunya, Filo*, *Adeno-, Herpes-, Picorna, Orthomyxo, Circo, Parvo, Papilloma* and *Coronaviridae* as well as the following bacterial pathogens; *Leptospira*, *Rickettsia and Bartonella.* **Objectives:** To determine longitudinal circulation of pathogens we initiated seasonal sampling from 2012 in two cave systems in South Africa. This sampling specifically focused on the reproductive seasons of *Rousettus aegyptiacus* and *Miniopterus natalensis*. **Methods:** Serum was analysed for rabies related lyssavirus, Lagos bat virus, antibodies using a virus neutralization assays. Tissue, urine saliva and fecal samples were tested for the presence of viral nucleic acids using RT-PCR/PCR specific for several viral families. Illumina MiSeq 16S rRNA gene sequencing on low-biomass individual bat samples was used to identify bacterial pathogens. **Results:** Longitudinal studies, specifically focused on measuring the presence of LBV antibodies in *Rousettus aegyptiacus*, indicated cyclic fluctuation of antibodies with a marked increase shortly after the parturition period, which identified this as a high risk period for spill-over. We showed that seasonal bat reproduction is a major driver shaping temporal variations in microbial community structure. A strong temporal shift in oral, fecal and urinary microbiota was also associated with bat reproduction, with significant associations between the microbiota and the sex, or reproductive status. **Conclusion**: This cumulative evidence can be used to indicate periods of increased viral and bacterial circulation, which can be used to make public and veterinary health decisions on spill-over risks.

Body mass index of the Egyptian fruit bat, *Rousettus aegyptiacus*: An indicator of infection status
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Body mass in conjunction with forearm length has long been used to determine body mass indices for bats. These indices have been further linked to diseases detected in bats, with a low body mass index being a potential indicator of infected bats. **Objectives**: We correlated body measurements to body mass, enabling us to determine

the best measurement that could be used to build body mass indices which can be correlated to disease status of *Rousettus aegyptiacus.* **Methods**: This study focuses on the Egyptian fruit bat (*Rousettus aegyptiacus*) in the Limpopo Province of South Africa. Data was gathered over a two year period, 2015 and 2016, and consisted of measurements of various body parts. **Results**: Wilcoxon Matched pair tests indicated a significant difference in body weight between the two sampling years (V = 34476, p = 0.002466). A strong correlation was found between body mass and forearm length when both years are considered (S = 17252000, p-value < 2.2e-16), as well as for the first (S = 3487900, p-value < 2.2e-16) and second year (S = 1250500, p-value < 2.2e-16) of the study with a strong correlation value; R > 0.78 in all cases. The correlation between mass and forearm length was significant for both males and females during both years (p-value < 2.2e-16), but the correlation value was always lower for females. Other body measurements correlated significantly with body mass, but only forearm length showed a strong correlation. **Discussion**: Forearm length is thus an indicator of body mass in Egyptian fruit bats, as has been found for insectivorous bats. As such, body mass in conjunction with forearm length could be used to build body mass indices, which could be used as a preliminary indicator of disease status for *Rousettus aegyptiacus.*

Environmental constraints drive the viral diversity of two sympatric Amazonian bat species
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Amazonia is a major biodiversity hotspot which encompasses a great diversity of bat species, as well as a wide variety of climates and vegetation formations. Landscape characteristics (*e.g*. climate, vegetation structure, anthropogenic disturbances) are relevant predictors of species richness and influence the host-pathogens relationships. However, the effects of contrasting environmental conditions on the viral diversity harbored by Amazonian bats have yet to be investigated. Through a metagenomic approach we characterized the viral diversity of two sympatric Amazonian bat species: the common vampire bat, *Desmodus rotundus* (*Phyllostomidae*) and the insectivorous bat, *Molossus molossus* (*Molossidae*). Then, through a statistical approach, we assessed the impact of the landscape characteristics by comparing the viral richness harbored by different populations of vampires and insectivorous bats inhabiting different environments (*e.g.*, forests, edge habitats, anthropized and urban areas). We identified 10,983 viral sequences related to 48 viral families known to infect a wide range of hosts (*i.e.*, bacteria, plants, insects and vertebrates). Most viruses detected reflect the dietary habits, especially within the insectivorous bat species which presented the highest diversity of plant and insect-related viral families. Diversity tests and phylogenetic relationships reconstructed for several mammal-related viral families (*e.g.*, *Bunyaviridae*, *Circoviridae*, *Foamyviridae*, *Herpesviridae*, *Papillomaviridae*) revealed a preferential transmission route within phyla of bats, as well as a potential association of viral diversity with the host's gut microbiota. Three structuring poles related to species traits and environments were identified, explaining the distribution of viral diversity and showed a strong correlation between the type of environment, host phylogeny, diet and viral diversity. The substantial viral richness detected in forest environments is likely due to a wider diversity of prey and favored by more frequent contacts between hosts and overlapping habitats. These findings provide significant insight into viral bat diversity in Amazonia and emphasize that environmental constraints and host features are the main drivers of viral diversity in bat species.

Seasonal and individual predictors of grey-headed flying fox (*Pteropus poliocephalus*) foraging movements in Adelaide, South Australia
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Objectives: The distribution of flying foxes in Australia is influenced by the unpredictable availability of their preferred diet, especially eucalypt blossoms. Recently, human activities, including destruction of native habitat and planting of non-native vegetation that provides predictable foraging, have altered the distribution and movements of flying foxes. The consequences of this change are important for both bat and human health, given that bats are reservoirs of Australian bat lyssavirus and Hendra virus, both of which cause fatal disease in humans. In 2010, grey-headed flying foxes (*Pteropus poliocephalus)* established a permanent roost in Adelaide, South Australia, several hundred kilometers outside their previous range. Despite incurring juvenile mortality due to extreme heat events, the population now numbers approximately 7000 and is expected to continue growing. **Methods:** As part of a larger study to characterize the health and behavior of the Adelaide flying fox population, we deployed lightweight GPS loggers on bats to track their foraging movements. Loggers recorded a bat's position every 30 seconds when flying and every 45 minutes when stationary, and also recorded acceleration,

speed, and altitude data. Forty foraging sites were ground-truthed to identify feeding resources. **Results:** Five flying foxes were tracked in winter 2016 and 9 in summer 2017, resulting in 112 nights of movement data. Bats exhibited individual variation in movement patterns, with some foraging repetitively, and others ranging more widely over the landscape. The nightly distance traveled depended on the interaction between sex and the ratio of weight to forearm length, but not on season. In the summer, bats foraged predominantly on urban resources, with figs and eucalypts being especially popular. **Conclusions:** This work provides insight into a recently-established, understudied bat population and is useful both to local Adelaide stakeholders as well as other urban citizens seeking to manage the bats that share their space. Foraging on urban resources, especially in residential yards, could increase the chances for disease transmission from flying foxes to humans and pets. Individual predictors of movement should be considered when building models of bat movement and disease risk.

Uganda Bat calls library-developing a tool to survey arthropod-borne viruses associated with Chiroptera
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Objectives: We continue to conduct studies of bats in different parts and habitats of Uganda with a number of particular goals: -

i. To continue to understand the occurrence and ecology of bats that may be reservoirs and/or vectors of viruses in Uganda (BM presentation),
ii. To develop a micro-chiroptera calls Library for the country
iii. Continue the development a fast approach that can be used to quickly survey and identify the bat fauna of different parts of Uganda.
iv. To investigate the roles of different species of bats in the ecology of viruses (RK presentation),

Methods: Through a DTRA supported project we particularly targeted to understand bat ecology and their potential roles in virus ecology. This was done through graduate training and research, training in field techniques of capture and processing of bats for detection of and characterization of viruses a pillar institutional players and a compilation of reference calls of micro-chiropteran bats for Uganda. Field biosurveillance training was held with participants from NADDEC, UVRI and Makerere University at Zika forest. A graduate student now preparing his dissertation, was recruited and completed an ecological study on bats in the Kaptum cave. Insect bats are captured using Mist nets, Herp traps and Hand net capture at roost sites. Bats are either free flown, ziplined or light tagged and hand released from which voucher calls are collected. Collected calls are processed using Kaleidoscope Pro version 31.7 for large files that need to be split for examination and processing in Sonobat4.0.6p. **Results**: Cumulatively, voucher calls for 50 species of micro chiropteran bats (over 50% of the Ugandan species) have been collected. Several of these are represented by multiple bats that way taking care of potential intra specific variations, potential ecological variations each of which could affect the call produced by the species. This presentation specifically shares our findings on call characteristics for a sample of the species and highlights the great overlap in signatures for species of Molosid bats, species of the Genus *Scotophilus*, while showing very nicely segregated call signals for Hipposiderid, Rhinolophid and a good number of verspertilionid bats. **Conclusions**: Our next steps are to attempt to collect voucher calls from species we haven't, collect additional calls from species already recorded but from few individuals, and to work with partners to develop a tool that could be used to rapidly identify calls collected from bat detection surveys from different parts of the country.

Dampening of STING-dependent IFN production: an implication of virus tolerance in bats?
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Objectives: Bats are known to harbour a number of zoonotic viruses, many of which are highly pathogenic in human but result in no clinical symptoms in bats. The mechanism of how bats coexist with viruses is still largely unknown. We previously reported the contraction of type I IFN locus and unusual constitutively expression of IFNA in bats. We hypothesis this may help bat to inhibit virus replication. However, as immune response can also do harm to the host, then how bats tolerate viruses and viral induced immune responses become a question. **Methods:** To address this question, we scanned a list of DNA and RNA sensors in bats. We then focus on STING, which played a key role in multiple DNA sensing pathways, for understanding how bats tolerate DNA viruses. We also tested the functionality of bat STING in a list bat immune or non-immune cells. **Results and Conclusions:** We found some of the viral DNA sensors are under faster evolution, implying a change of function. Further experimental data also confirmed the dampening of viral DNA sensing, more specifically STING- dependent IFN production pathway. We then identified a ubiquitous key point mutation in all bat species tested, which hugely

decreased the cGAS-STING sensing ability (80%) by gain-of-function studies. Lastly, we restored the functionality of STING and STING-dependent viral DNA sensing pathway by changing this site to human. We conclude that bat naturally own a dampened STING-dependent IFN production, probably to avoid over responses to virus. This observation provides a model of how bats tolerance thus long-term hosting these viruses.

Regulation of immune activation and dampened inflammation in Pteropid bats
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Objective: Natural reservoir hosts can maintain low-level infection of pathogens without succumbing to severe disease. Several bat species host viruses such as Ebola, SARS, Nipah, Hendra, and other pathogenic viruses and while these same infections cause mass-inflammation in humans and other animals they are mostly asymptomatic in the bat. As such, bats are a unique model for studying the host control of systemic inflammation. **Methods:** We utilised bat cell lines, primary cells and tissue with qPCR, Western Blot, FACS analysis, NGS transcriptomics and cellular proteomics to profile pathways and characterise signalling mechanisms. **Results:** Through studying immune activation to flaviviruses, influenza and reovirus, along with natural stimulants of innate immunity such as TLR and RLR ligands we are beginning to characterize key differences to their human counterparts for PRRs.. There appears to be differences also in the kinetics and activation signals required for Interferon activation also. In addition, our data, from investigation of primary bat immune cells and studying bat homologs, suggests that inflammasome activation pathways may be altered with dampened activation of downstream inflammation. **Conclusion:** Along with fundamental differences to cell biology, this may indicate an evolutionary adaptation that while supporting flight, may cause susceptibility to infection yet maintain a symbiotic state with several pathogens. Initial observations show several key mutations, altered kinetics and a decrease in sensitivity to induce signaling all appear to be involved. From this we can gain understanding into a mechanism for controlling excess inflammation in humans.

Delineating the phenotype and function of the B cell population in the fruit-eating bat, Pteropus Alecto.
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Objective: The unique ability of bats to act as reservoir for viruses that are highly pathogenic to humans suggests unique properties and functional characteristics of their immune system. However, the lack of bat specific reagents, in particular antibodies, has limited our knowledge of bat's immunity.
Methods: Here, using cross-reactive antibodies, we report the phenotypic and functional characterization of B cells based on anti-mouse I-Ab (MHC-II) and anti-bat IgG. **Results**: Using flow cytometry, we show their distribution amongst the major lymphoid organs and scanned electron micrographs of these sorted population reveal that they are morphologically similar to human and murine B cells. In addition, a large population of these cells test positive for CD19 mRNA, tested using SmartFlare RNA probes, and anti-human CD19 antibody. Uniquely, these cells are able to show an increase in calcium uptake upon cross-linking of their B cell receptor with the addition of secondary donkey anti-goat antibody, which is specific for the goat anti-bat IgG. We also demonstrate T cells and myeloid cells do not release calcium in the presence of IgG and secondary antibody. Furthermore, we also demonstrate that injecting LPS for 5 hrs show an increase in MHC-II$^+$IgG$^+$ B cell population in the spleen and blood. This demonstrates a T-independent B cell activation amongst the B cell population. In addition, this population of cells do not respond to Poly (I:C) stimulation. We also performed single cell RNA sequencing on sorted MHC-II$^+$IgG$^+$CD19$^+$ positive cells to identify various B cell subsets based on their gene signature. Initial analysis reveal that these cells show increased expression of CD19 and do not express CD3, CD8 and CD11b. **Conclusions**: Here, we demonstrate for the first time the phenotype and function of B cells in *Pteropus Alecto.* This provides us with a platform to isolate and further elucidate the role of these cells in infectious models.

Integrative measures for assessing "health" in free-ranging bats – zoonotic and conservation implications from a One Health perspective

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Objectives: Risks of zoonotic spillover are likely related to the overall health of the animal host. For bat hosts of viral zoonotic diseases, the relationship between health and spillover risk is complex, with poor health possibly favoring transmission by increasing viral load and shedding but also decreasing animal mobility and human-host contact. Unfortunately, determining the health status of free-ranging bats is fraught with difficulty. Challenges exist not only in deciding which diagnostic measures to use, but also in interpreting the results of these measures. Furthermore, without the ability to measure fitness in these long-lived mammals, our understanding of the consequences of "good" or "bad" health for a free-ranging bat is poor. Our objective is to provide a framework for defining bat health that will facilitate bat studies and will enhance our understanding of spillover risk, ecosystem health, and human health. **Methods:** We combined an extensive literature review of health metrics in free-range wildlife, including bats, with our own long-term field studies and experiences studying bat physiology and disease. **Results:** Literature review and our past work point to several findings: (1) a number of measures commonly used in other vertebrate taxa and in other mammals have not been fully deployed for bats – sometimes owing to methodological hurdles; (2) due to a lack of tools, and often small sample volumes, most bat studies have relied on too-few measures, such as BMI (which suffers from allometric problems and is often surprisingly uninformative), the ubiquitous neutrophil-to-lymphocyte (N/L) ratio, ectoparasite load, and highly variable immune metrics such as hemmaglutination assays; (3) newer molecular methods, such as transcriptomic approaches hold promise for improving our understanding of bat health, especially when integrated with other measures such as infection status. We will present preliminary data from our recent field studies of African fruit bats in which we have deployed 20+ field diagnostic measures in combination with infection status and a transcriptomic approach. **Conclusions:** We recommend the development of integrative health metric(s), which will allow for the determination of the most informative measures for future studies. We also implore researchers to document normative physiological measures for more species of bats, analyzed with regards to life history, ecology, and phylogeny.

Host-pathogen interactions during white-nose syndrome

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Objectives: We have employed a dual RNA-Seq approach to study gene expression of both host and pathogen during the fungal infection that causes white-nose syndrome (WNS) in bats. **Results**: We have found that when *Pseudogymnoascus destructans* is causing WNS, the most significant differentially expressed genes in the pathogen were involved in heat shock responses, cell wall remodeling, and micronutrient acquisition. These results demonstrate that this fungal pathogen responds to host-pathogen interactions by regulating gene expression in ways that may contribute to evasion of host responses. We have also found that host responses vary between susceptible and resistant species of bats in ways that may indicate that host responses contribute more to pathogenesis than to protection. This may be because, during hibernation, host immune responses are too costly and lead to premature depletion of energy reserves. We have also determined which host transcriptomic responses to fungal infection can occur during torpor and which require arousal to euthermy. We found relatively few host transcripts that showed significant changes in expression levels due to fungal infection in torpid bats compared to euthermic bats. **Conclusions**: These results support the view that torpor is a period of relative dormancy and suggest that periodic euthermic arousals exist to provide an opportunity for host responses to pathogens.

Resistance or Tolerance – How do European bats cope with *Pseudogymnoascus destructans*?
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Objectives: *Pseudogymnoascus destructans* (*Pd*), the causing agent of the White-nose disease, colonizes bats during hibernation. The cold-loving fungus affects the snout and all the hairless skin membranes of torpid bats where it causes lesions. The spreading epidemic in North America (so called White-nose syndrome) is characterized by mass mortalities and regional extinctions of certain bat populations. In Europe, *Pd* has been recorded since several decades as a widespread pathogen, yet it does not cause mass mortalities. Several studies confirm that *Pd* is native to Europe and appeared as a new pathogen in North America in 2006. If and how European bats adapted to the disease and why North American bats cannot cope with the fungus remains unclear. **Methods**: We analysed data from over 300 hibernacula across Europe to test for factors influencing mortality, including *Pd* infections on bats. **Results**: Our results show an overall low mortality rate of bats in Europe with no evidence of *Pd*-associated mortalities. Physiological data and blood samples from infected and non-infected European bats were analysed to investigate, if bats suffer from White-nose disease and how the immune systems reacts to fungal infections during hibernation. **Conclusions**: Our ecological, physiological and immunological results suggest resistance and tolerance of European bats towards *Pd*.

Modeling the impact of White-nose syndrome on two western bat species
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Objectives: The rapid westward spread of white nose-syndrome (WNS) through North America has become a critical conservation issue for endemic hibernating bat species with many Eastern populations experiencing steep declines over the last ~10 years. The continued spread of the psychrophilic fungus *Pseudogymnoascus destructans* into Western states over the last two years has the potential to impact many hibernating species. Disease outcome varies widely between species, with infection of some species (namely European and Asian species) being largely benign. The identification of species that may be threatened is paramount to development of effective conservation strategies. **Methods:** Using field obtained morphometric data in conjunction with experimentally obtained estimations of key metabolic parameters we applied a modified hibernation model that includes fungal growth dynamics for two currently unaffected North American bat species: *Myotis californicus* and *Myotis yumanensis*. **Results:** Infection of *P. destructans* would likely reduce the maximal time spent in hibernation for both Western *Myotis* species. Reductions of maximal time spent in torpor were predicted to be the most drastic in microclimates with relative humidity approaching saturation and temperatures between ~5 °C and 10 °C. Despite the increased rate of overwinter energy consumption, fat reserves were still predicted to be sufficient to overwinter throughout the majority of their distribution. **Conclusions:** *M. californicus* and *M. yumanensis* are predicted not to experience distribution wide population declines like those witnessed for *M. lucifugus* and *M. septentrionalis* in eastern North America. Continuing field studies will provide data on important model parameter estimations, more species, realized hibernacula microclimate selection, and providing data to empirically validate model predictions.

Variable behaviors influence species susceptibility to disease – surviving white-nose syndrome.
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White-nose syndrome (WNS) continues to spread through populations of hibernating bats in North America, causing unprecedented mortality in several species occurring in eastern parts of the continent. Despite this devastation, other bat species that come into contact with the causative fungus, *Pseudogymnoascus destructans*, somehow survive. We still do not understand factors influencing species and continental differences in bat

susceptibility to WNS, but variability of innate behaviors among taxa and regions may help explain disease survival. This talk focuses on evidence suggesting infected bats can exploit 'survival habitats' (e.g., hibernacula with palliative microclimates) and 'survival behaviors' (e.g., palliative ways of regulating body temperature during winter). Our search for survival habitats and behaviors in WNS bats illustrates the challenges of understanding how microorganisms influence their cryptic hosts, how unknown host behaviors can obscure understanding of disease, and how new bat research methods may help overcome some of these challenges.

Emerging Insights into the Geographic Distribution, Genetic Diversity and Evolutionary Origin of Bat-borne Hantaviruses

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Objective: The recent discovery of genetically distinct hantaviruses in multiple species of shrews and moles (order Eulipotyphla) prompted a further exploration of their geographic distribution, genetic diversity and evolutionary relationships by analyzing tissues and feces from bats (order Chiroptera). **Methods:** Total RNA, extracted from frozen, ethanol-fixed or RNAlater®-preserved archival tissues (lung, liver, kidney, intestine, intercostal muscle) and rectal swab/feces of 1,890 bats, representing 10 families (Emballonuridae, Molossidae, Mormoopidae, Nycteridae, Phyllostomidae, Vespertilionidae in the Yangochiroptera suborder, and Pteropodidae, Hipposideridae, Megadermatidae, Rhinopholidae in the Yinpterochiroptera suborder), collected in Asia (China, Korea, Malaysia, Mongolia, Myanmar, Philippines, Republic of Georgia, Vietnam), Africa (Côte d'Ivoire, Guinea, Liberia) and the Americas (Bolivia, Brazil, Guyana, USA) during 1981–2015, were analyzed for hantavirus RNA by nested RT-PCR. Phylogenetic analysis was performed using maximum likelihood and Bayesian methods. **Results**: Hantavirus RNAs were detected in 2 of 12 *Neoromicia nanus* from Côte d'Ivoire (Mouyassué virus, MOYV), 6 of 49 *Hipposideros pomona* and 1 of 5 *Hipposideros cineraceus* from Vietnam (Xuan Son virus, XSV), 1 of 12 *Aselliscus stoliczkanus* from Vietnam (Dakrong virus, DKGV), 2 of 13 *Taphozous melanopogon* from Myanmar (Laibin virus, LBV), and 1 of 15 *Rousettus amplexicaudatus* from the Philippines (Quezon virus, QZN). Multiple attempts to acquire whole genomes of the newfound hantaviruses were unsuccessful, except for DKGV and QZNV. Phylogenetic analyses indicated incongruent topologies for each genomic segment, presumably because of the limited sequences available for most of the hantaviruses harbored by bats, shrews and moles. However, in both the S- and L-segment trees, QZNV appeared to share a common ancestry with XSV and LBV. Based on the host cytochrome *b* sequences, the phylogenetic positions of bats in the Yinpterochiroptera and Yangochiroptera suborders were consistent with the phylogenetic relationships among the bat-borne hantaviruses. **Conclusions:** Other research teams have reported Magboi virus in *Nycteris hispida* from Sierra Leone, Makokou virus in *Hipposideros ruber* from Gabon, Huangpi virus in *Pipistrellus abramus* from China, Longquan virus in *Rhinolophus affinis, Rhinolophus monoceros* and *Rhinolophus sinica* from China, Laibin virus in *Taphozous melanopogon* from China, and Brno virus in *Nyctalus noctula* from the Czech Republic, bringing to 11 the number of bat-borne hantaviruses to date. As in shrews, moles and rodents, the same hantavirus species was occasionally found in more than one bat species, and the same bat host species occasionally harbored more than one hantavirus species, suggesting that the formerly held conventional view of one hantavirus species and one host species is no longer tenable. Moreover, the basal position of the chiropteran-borne hantaviruses in phylogenetic trees and the demonstration that bat species in both suborders harbor hantaviruses suggest that primordial hantaviruses may have emerged in an early common ancestor of bats or other members of the Laurasiatheria superorder, that includes shrews and moles.

Neotropical Bats that Co-habit with Humans Function as Dead-End Hosts for Dengue Virus

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Objective: Several studies have shown Dengue Virus (DENV) nucleic acids and/or antibodies present in Neotropical wildlife including bats, suggesting that some bat species may be susceptible to DENV infection. Here we aim to elucidate the role of house-roosting bats in the DENV transmission cycle. **Methods**: Bats were sampled in households located in high and low dengue incidence regions during rainy and dry seasons in Costa Rica. We captured 318 bats from 12 different species in 29 households. Necropsies were performed in 205 bats to analyze virus presence in heart, lung, spleen, liver, intestine, kidney, and brain tissue. **Results**: Histopathology studies from all organs showed no significant findings of disease or infection. Sera were analyzed by $PRNT_{90}$ for a seroprevalence of 21.2% (51/241), and by PCR for 8.8% (28/318) positive bats for DENV RNA. From these 28 bats, 11 intestine samples were analyzed by RT-PCR. Two intestines were DENV RNA positive for the same dengue serotype detected in blood. Viral isolation from all positive organs or blood was unsuccessful. Additionally, viral load analyses in positive blood samples by qRT-PCR showed virus concentrations under the minimal dose required for mosquito infection. Simultaneously, 651 mosquitoes were collected using EVS-CO_2 traps and analyzed for DENV and feeding preferences (bat cytochrome b). Only three mosquitoes were found DENV positive and none was positive for bat cytochrome b. Our results suggest an accidental presence of DENV in bats probably caused from oral ingestion of infected mosquitoes. Phylogenetic analyses suggest also a spillover event from humans to bats. **Conclusion**: Therefore, we conclude that bats in these urban environments do not sustain DENV amplification, they do not have a role as reservoirs, but function as epidemiological dead end hosts for this virus.

Novel Gammaherpesvirus in Bats: discerning the secrets of these oncogenic viruses

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Objectives: *Gammaherpesvirinae* is a subfamily of herpesviruses which often cause lymphoproliferative diseases and have been linked to two human lymphoid cancers – Burkitt's lymphoma and Kaposi's sarcoma. Anecdotal evidence suggests that bats have lower rates of cancer than other mammalian species. This phenomenon may be because bats have evolved efficient mechanisms for detecting and repairing damaged DNA as a by-product of flight. How such a mechanism affects the interaction of Gammaherpesviruses (which cause cancer) with their bat, hosts is largely unknown. **Methods and Results:** We have isolated a novel Gammaherpesvirus (*Eptesicus fuscus* herpesvirus – EfHV) from a North-American Big Brown bat (*Eptesicus fuscus*). We have used a big brown bat cell line to study the growth kinetics of the virus. We have also performed electron microscopy and PCR to confirm that the virus belongs to the herpesvirus family. To determine the sequence of the herpesvirus, we have performed next generation sequencing (NGS) using Illumina mi-seq. Using the sequence obtained, we have performed phylogenetic analysis from which we found that although the EfHV belongs to the sub-family of Gammaherpesvirus, it forms a distinct branch within the sub-family. In addition to that we have identified the different proteins present in the virion by performing mass spectroscopy and have found that the virion components are similar to other herpesviruses. We have also infected cells of different species with the EfHV to understand the spectrum of different species that this virus is capable of infecting and we have found that it is able to infect human, monkey, porcine and feline cell lines apart from the bat cell line. **Conclusions:** The phylogenetic analysis shows that EfHV is a distant relative of all other gammaherpesviruses known so far. It might have evolved together with the big brown bat. Further studies looking at the interaction of EfHV and big brown bat might help us understand more about the persistent infection in bats and their unique was of resisting cancer.
Funding Source: NSERC

Experimental Infection of Jamaican Fruit Bats (*Artibeus jamaicensis)* with Zika Virus

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Objectives: Zika virus (ZIKV) emerged in the New World with the 2014 outbreak in Brazil. It has spread to much of South America, Central America, Mexico and the Caribbean, with hundreds of thousands of cases. While disease presentation may be subclinical to mild and include symptoms of maculopapular rash, conjunctivitis, and arthralgia, infection of pregnant women can lead to fetal microcephaly. Additionally ZIKV infection can induce Guillain-Barre syndrome. In the 1950s and 1960s bat species were investigated as possible reservoirs for ZIKV. In total, five different species of bats were found to be susceptible to the virus. Bats seroconverted, had viremia,

and, in one experimental infection study bats developed fatal neurological disease. This warranted further investigation of ZIKV in bats to determine their use as an animal-model, and to better understand the potential role of bats in viral ecology. **Methods:** Nine Jamaican fruit bats (*Artibeus jamaicensis*) were subcutaneously inoculated with $7.5x10^5$ pfu of ZIKV strain PRVABC59 and monitored over the course of 28 days, during which there were no conspicuous signs of disease. Bats were euthanized at 2, 5, 10 and 28 days post-inoculation to assess the course of infection and antibody responses. **Results:** Bats seroconverted by day 28 by ELISA with ZIKV-infected, fixed Vero E6 cells. Low levels of viral RNA were detected in one brain and one urine sample. IHC detected ZIKV antigen in lung and testes of one bat, and brains and salivary gland of two others. Pathology was consistently observed in the lungs, heart, testes and brain. Pneumonia was observed in four bats, cardiomyocyte necrosis in three bats, degeneration and lymphocyte infiltration in the testes of two bats, and neuronal degeneration in the hypothalamus and cerebellum in three bats. **Conclusions:** These results provide evidence that Jamaican fruit bats are susceptible to ZIKV and may serve as an animal model to study neurological components and sexual transmission of the virus. Low viral load in urine and tissues suggests the role of bats in viral ecology may be minimal.

Long-term monitoring of *Bartonella* bacteria in a captive colony of fruit bats and experimental evidence of bat flies as vectors of bartonella

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Objectives: Few experimental studies have monitored long-term infection dynamics in bat populations. This is especially true for vector-borne bacteria, where there can be significant challenges in maintaining both host and vector populations in controlled settings. In order to understand the importance of vector populations in the long-term maintenance of infection prevalence and bacterial diversity, we advocate for the use of semi-natural, long-term experiments capable of detecting changes in infection dynamics linked to the force of infection by vectors. **Methods:** Using blood samples taken from a captive colony of ~100 fruit bats (*Eidolon helvum*) in Accra, Ghana from July 2009 - March 2012, we monitored the dynamics of *Bartonella* spp. infection in the bat population using molecular techniques. Over this period, the bat fly population (*Cyclopodia greefi*) infesting the captive bats declined, but was then supplemented with additional flies from wild *E. helvum* in January 2012. We hypothesized that prevalence and species diversity of *Bartonella* infections in the colony will vary with changes in the bat fly population. **Results:** *Bartonella* prevalence and diversity peaked in March 2010 with 77% of bats infected and 8 *Bartonella* spp. present, then began to decline until July 2011 with only 15% of bats infected and 4 *Bartonella* spp. present. After the reintroduction of flies in January 2012, prevalence increased to 43% in March 2012 with 6 species present. Bats that received flies were equally likely to become positive after January 2012 as bats that did not receive flies, which may be attributable to dispersal of flies among bats after reintroduction. Additionally, changes in relative *Bartonella* spp. abundances showed that the species lost over time were uncommon in bats, but some of these uncommon species became more abundant after the reintroduction of flies. **Conclusions:** This experiment indicates that *C. greefi* bat flies are likely vectors of bartonella in *E. helvum* and play an important role in the maintenance of bacterial diversity in bats. Ongoing occupancy modeling work will explore the influence of within-host processes (including bacterial interactions and host resistance to infection) and alternative transmission routes on the long-term infection dynamics in individual bats.

Posters

1. Predicting the epizootiology of temperate bat disease: Is it all about the bats?James N. Aegerter[1], Ashley C. Banyard[2], Anthony R. Fooks[2], Graham C. Smith[1]

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Predicting the dynamics of disease in wild bats, their epizootiology, and the risks these pose to people, the economy or other biodiversity is complicated. Bats may be the evolved hosts for disease, effective maintenance hosts, or accidental spill-over hosts (we cannot always distinguish which), whilst their unique life-style permits the exceptional natural movement of disease, as well as an exceptional potential to vector disease into homes, farms or other sensitive sites. These diseases may pose social or economic concerns (i.e. to public or livestock health), or produce conservation concerns. Further, diseases may well also be endemic, exotic or newly emerging, and importantly their dynamics today occur in the contexts of rapid land-use change and climate change. With decision-makers relying on the quality of epizootiological predictions, and substantial uncertainty about the pathogen, its pathology in wild bats, a changing environment, and the abstraction of these into mathematical form, it is surprising that little effort has been made to construct and validate mechanistically realistic models of bat populations to act as the solid foundation for higher-level disease modelling. Here we aim to produce a generic tool to provide some evidence based predictions of bat disease epizootiology, founded on a coherent representation of bat ecology and behaviour deployed through an IBM (Individual Bat Model). Importantly, this is founded on an independently validated understanding of their ecology and population dynamics, both of which need to emerge as model behaviour before disease is added. We recognise at least two divergent life-history strategies and lifestyles; ‘slow’ bats, typified by cave hibernators, include a seasonal hierarchical spatial and population structure; ‘fast’ bats show larger but less structured communities. Both accommodate the emerging understanding of bats as social animals as well as assuming that spatial heterogeneity drives some form of meta-population process. Early work has illustrated the surprising variation/instability in demographic structure driven by environmental variation close to range edges (many British bats are at their cold edge in the UK), as well as highlighting basic gaps in knowledge which are pivotal in robust predictions of disease dynamics (males in summer – Where? When? And how much?).

2. **Comparative loss of function screens highlight common cellular pathways required by mumps virus for replication in bats and humans**
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Objectives: Bats have been implicated as an important source of new and emerging paramyxoviruses. The identification of bat-borne paramyxoviruses closely related to mammalian paramyxoviruses suggests a possible risk of zoonotic transmission of these paramyxoviruses. Mumps virus (MuV) a contagious virus of the genus *Rubulavirus*, was thought to be an exclusive human pathogen with no animal reservoir. Recently, the complete genomic sequence of a mumps-like rubulavirus was obtained from an African bat. In order to ascertain if bat and human cells are capable of supporting the replication of MuV, and to identify cellular proteins involved in the viral life cycle, we performed comparative genome scale siRNA screens using a human and novel bat siRNA library. **Methods**: Comparative genome scale siRNA screens with MuV were performed. The human MuV siRNA screen (Qiagen) was previously performed in our lab using A549 cells, a human lung adenocarcinoma cell line. A custom bat siRNA library was designed to target 18,328 genes of the *Pteropus alecto* genome. The bat siRNA screen was performed in PaKi cells, a *Pteropus alecto* kidney cell line. **Results**: The coatomer complex I, a known dependency factor was identified as required for MuV replication in both human and bat cells. Eukaryotic initiation factor 3 (eIF3) is a multiprotein complex that functions during the initiation phase of eukaryotic translation was also identified as a host factor. Interestingly, ABCE1, identified as a pan-paramyxovirus host factor, was not required for MuV replication in bat cells. **Conclusions**: This study is the first to utilize a bat genome scale siRNA screen and provides a novel overview of cellular proteins and pathways that impact this important pathogen.

3. **Implementation of a RT-PCR Assay to Detect Henipaviruses in Trinidad Bats**
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Objectives: Since the emergence of Hendra in Australia, and Nipah in Malaysia and Bangladesh, evidence of henipaviruses in bats has been reported in Thailand, Cambodia, India, Papau New Guinea, China, and Madagascar. Cedar virus, a novel henipavirus, has been isolated from bats in Australia. There has been evidence of seropositivity among humans and *Eidolon helvum* (Straw-coloured fruit bat) bats in Cameroon, as well the publishing of the genome sequence of a henipa-like virus from a bat sample in Ghana. More recently, sequences related to henipaviruses were identified in New World bats, and Brazilian bats were found to have antibodies against henipa-like viruses, though no viral isolate has yet been obtained. This suggests that henipaviruses are likely to exist in other regions, including the Western hemisphere, presenting a need to investigate host populations. The goal of this study is to design a PCR assay to screen bat samples from Trinidad to detect novel henipa or henipa-like viruses.
Methods: Using published primer sets from Tong, et al, and van Boheemen, et al, PCR assays were developed to screen various tissue samples collected from bats in Trinidad. Both primer sets will be evaluated for their ability to detect henipaviruses using viral RNA standards for Hendra, Nipah Bangladesh, and Nipah Malaysia. The 132 samples are from 30 bats, including the species *Saccopteryx bilineata* (greater sac-winged bat), *Carollia perspicillata* (Seba's short-tailed bat), and *Artibeus planirostris* (Flat-faced fruit-eating bat) (sensu Larsen, 2007). Tissues harvested include brain, kidney, liver, spleen, lung, and fetal tissue.
Results: The PCR assay is able to detect viral RNA standards of Hendra, Nipah Bangladesh, and Nipah Malaysia. The assay will be further optimized to screen tissue samples. Samples that screen positive by this assay will be sequencinged.
Conclusions: To our knowledge, no henipaviruses have yet been detected or isolated from New world bats, though studies suggest their presence. Thus, screening for novel henipaviruses in Trinidad bats will help elucidate the full geographic range of these viruses, allowing a better understanding of risks of emergence and outbreaks in humans.

4. **Genomic characterization and pathogenic potential of a novel evolutionarily-divergent alphacoronavirus isolated from *M. lucifigus* bats in Alaska.**
Jonathan C. Rupp[1], Maegan Lange[1], Megan Howard[2], Anitha Sundarajan[3], Jonny Sena[3], Faye D. Schilkey[3], Molly Murphy[4], Douglas Causey[1], Eric Bortz[1].

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4- Dept. of Veterinary Medicine, University of Alaska Fairbanks

Objectives: Coronaviruses (CoV) are zoonotic pathogens with the potential to cross species barriers from bats into other mammals, including marine mammals, swine and humans. Novel bat-origin coronaviruses have been responsible respiratory disease in humans, notably betacoronaviruses (OC43, HKU-1, SARS and MERS) and alphacoronaviruses (229E and NL63). Thus, it is important to identify the reservoirs of CoV in bats and their potential for transmission, and pathogenicity, in other mammalian species. We sought to analyze the virome of the most common bat species in Alaska, *Myotis lucifugus,* the little brown bat.

Methods: Swabs, tissue, and fecal samples were collected from habitats in close proximity to barns, farm buildings, and human habitations in southcentral Alaska. Total RNA extracts were screened by RT-PCR with coronavirus primers matching CoV ORF1a, and amplicon sequencing. Complete genomes of novel viruses were sequenced by next-generation sequencing (NGS) RNA-seq.

Results: Sanger sequencing of amplicons confirmed the presence of an alphacoronavirus phylogentically related to persistent alphacoronaviruses detected in bats in Colorado and the Rocky Mountains. Primary RNA samples were used in library preparation for short-read, paired-end next generation sequencing on an Illumina HiSeq platform. Aligning to a reference *M. lucifigus* virus from Colorado, bat alphacoronavirus CDPHE15/USA/2006, we assembled a full-length genome (28,515nt) identifying the novel alphacoronavirus/bat/Alaska/s7/2014. A high

degree of thermodynamically stable stem-loop RNA structures are predicted by Mfold within 700nt of 5' and 3' termini of genome**.** While nucleotide conservation to the Colorado virus was 96%, notable amino acid differences were identified in coronavirus proteins. The major CoV surface spike (S) protein exhibited 26 amino acid changes, including 14 in the globular head containing the putative receptor-binding domain, suggesting divergence based on immune evasion or receptor-specificity. Another 6 amino acids were altered in the fusion hinge. Protease cleavage sites were not conserved. Nucleoprotein (N) and ORF3 also exhibited amino acid differences.

Conclusions: Understanding the evolution and pathogenicity of this novel evolutionarily-divergent alphacoronavirus provides insight into the role of bats in virus transmission, and ecological assessment of bat-borne virus reservoirs in North American ecosystems.

5. Preliminary Evidence of Secondary Acquisition of Tymoviridae and Partitiviridae in Little Brown Bats (*Myotis lucifugus*) in Southcentral Alaska.

Douglas Causey[1] , Jonathan C. Rupp[1], Maegan Lange[1], Megan Howard[2], Anitha Sundarajan[3], Jonny Sena[3], Faye D. Schilkey[3], Molly Murphy[4], Eric Bortz[1]

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We sought to analyze the virome of the most common bat species in Alaska, *Myotis lucifugus,* the little brown bat. Swabs, tissue, and fecal samples were collected from habitats in close proximity to barns, farm buildings, and human habitations in southcentral Alaska. Total RNA extracts were screened by RT-PCR and CoV ORF1a, and primary RNA samples were used in library preparation for short-read, paired-end next generation sequencing on an Illumina HiSeq platform. Sanger sequencing of amplicons confirmed the presence of an alphacoronavirus phylogenetically related to persistent alphacoronaviruses detected in bats in Colorado and the Rocky Mountains. In two distinct bat samples, preliminary results indicate the likely presence of tymovirus (eg. Dulcama mottle virus) probably acquired through ingestion of insects feeding on infected plants. In addition, initial results indicate presence of β-partitivirus closely aligned to *Rosellina*-type associated with spruce/alder and other partitivirus-like sequences. Secondary acquisition of virus obtained by feeding or incidental infection by fungi (eg. γ-partitivirus associated with *P. destructans*) has been previously described for bats collected from similar ecological settings (eg. Thapa *et al.* 2016). We continue to further refine these initial for better resolution of the virome of Alaska bats.

6. Molecular Screening of Zika and Dengue Viruses in Bats (*Artibeus jamaicensis, Glossophaga longirostris* and *Molossus molossus*) from Grenada, West Indies.

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Background: In recent years Zika virus (ZikV) has changed from an uncommon and poorly documented infection to a global public health concern. Dengue virus (DenV) has long-standing human health concerns worldwide, including Grenada, and has been detected in bats from other tropical countries. **Objective**: To determine if Grenada bats are infected with ZikV and DenV and thus possible reservoir hosts for these viruses. **Methods**: Forty-nine bats from 3 different genera and feeding behaviours (frugivorous, nectivorous and insectivorous) were trapped and humanly euthanized. ZikV RT-PCR was performed on serum, testes, spleen and brain samples, and a DenV RT-PCR multiplex was performed on serum. Amplicons of the expected sizes were sequenced for confirmation. **Results**: Physical exams prior to euthanasia and sample collection indicated all bats were clinically healthy. All 3 bat species collected tested positive for both viruses. Sera from 27 bats out of 41 tested were positive for ZikV (65.9%) and sera from 12 bats out of 19 tested were positive for DenV (63.2%). All DenV positive bats were infected with serotype 2, with one of these bats testing positive for both DenV serotype 2 and 4. Brains from 22 bats out of 48 tested were positive for ZikV (45.9%). Testes from 2 bats out of 12 tested were ZikV positive (16.7%) and a spleen from one bat out of 22 tested was ZikV positive (4.5%). **Conclusions**: The results demonstrate that frugivorous, nectivorous and insectivorous bats in Grenada are infected with both ZikV and DenV. Of interest is that despite many bats testing positive for ZikV in the brain, all bats appeared clinically healthy with no signs of neurologic dysfunction. Histopathology and immunohistochemistry are pending to

determine if infection is associated with lesions. Virus quantification is currently underway to determine if the level of viremia for either ZikV or DenV is high enough to consider the different bat species as potential reservoir hosts.

7. Serologic evaluation of Alphavirus and Flavivirus exposure in bats in Grenada

Diana Stone[1], Christine Cornish[1], Amy C. Lyons[2], Yan-Jang S. Huang[2], Dana L. Vanlandingham[2], Stephen Higgs[2], Bradley Blitvich[3], Abiodun A. Adesiyun[4], Sharlene Santana[5], Leith Leiser-Miller[5], Sonia Cheetham[1].

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Objective: Determine exposure to Alphaviruses and Flaviviruses in bats in Grenada. **Methods:** Fifty bats were trapped in August, 2015 in Grenada. Sera from all bats were tested for antibodies to flaviviruses: West Nile virus, Japanese Encephalitis virus, St. Louis Encephalitis virus, Bussuquara virus and dengue virus serotypes 1-4 (DENV-1,2,3,4) using the plaque reduction neutralization test (PRNT). Forty three of the 50 samples were tested for antibody to alphaviruses: Western Equine Encephalitis virus, Venezuelan Equine Encephalitis virus and Eastern Equine Encephalitis virus using epitope-blocking ELISA and 42 samples were tested for antibody to the alphavirus Chikungunya (CHIKV) using PRNT. **Results and Conclusions:** Two species of fruit bats were sampled, *Artibeus jamaicensis*, (48), and *A. lituratus*, (2). Fifteen of the 42 tested positive for neutralizing antibodies to CHIKV at $PRNT_{50}$ with titers 1:10 to 1:640. All 43 bats tested negative for epitope blocking antibody to the other alphaviruses except one positive for Venezuelan Equine Encephalitis virus. All 50 bats tested negative for neutralizing antibody to flaviviruses except one which had a Bussuquara virus $PRNT_{80}$ titer of 20. **Discussion:** Historically, DENV has been endemic in Grenada. CHIKV was introduced to the island in 2014. Bats for this study were trapped a year after the peak human CHIKV epidemic. Of interest is that in a separate study molecular detection confirmed the presence of both DENV and CHIKV RNA in bats serologically tested in this study. Of the 15 CHIKV seropositive bats, one was positive for CHIKV RNA. Of the 50 DENV seronegative bats, 6 showed detection of flavivirus RNA with a band compatible with DEN3. Thus, the negative DENV serology is unanticipated, but may reflect lack of neutralizing antibody responses developed for DENV. Future studies will characterize the humoral immune response to DENV in naturally exposed Grenada bats and determine whether non-neutralizing antibody responses are present. The type of immune response to DENV in bats may promote persistent infection and high-titer viremia and thus contribute to viral maintenance. Our results and those of the molecular study confirm that Grenada fruit bats are exposed to CHIKV and DENV, but their role in the epidemiology of these viruses is currently unknown.

8. **Isolation and molecular characterization of Bukakata orbivirus, a novel virus from a Ugandan bat, and associated pathology in experimentally infected Jamaican fruit bats (*Artibeus jamaicensis*)**

Fagre AC, Kityo R, Lee J, Mossel E, Crabtree, M, Nalikka B, Nakayiki T, Kerbis J, Gilbert, A, Bergren, N, Nyakarahuka L, Lutwama J, Stenglein M, Byas A, Malmlov A, Bergren N, Rice L, Miller B, Schountz T & Kading, RC.

Objectives: In 2013, a novel orbivirus (*Reoviridae: Orbivirus*) was isolated from an Egyptian fruit bat (*Rousettus aegyptiacus*) in Uganda. Preliminarily named "Bukatata orbivirus" after the region where the infected bat was captured, this virus is the fourth identified orbivirus of bats. The genomes of all four bat orbiviruses (Bukakata, Ife, Fomede, and Japanaut viruses) were sequenced to assess their phylogenetic placement within the genus *Orbivirus*, and develop hypotheses regarding virus-vector associations. **Methods:** Whole genomes of all four viruses were sequenced using an Illumina platform and assembled *de novo*. To begin studying the effect of infection with Bukakata orbivirus on a bat host, three male Jamaican fruit bats (*Artibeus jamaicensis*) were inoculated intraperitoneally with 5.3 $\log_{10}$ pfu Bukakata orbivirus and monitored daily for signs of clinical disease. **Results:** Phylogenetic analysis placed Fomede and Bukakata orbiviruses in the tick-borne clade, and Japanaut and Ife in the mosquito/*Culicoides* clade. On day 12, all three bats were diffusely hyperemic and tachypneic and, thus, were humanely euthanized. Histopathologic lesions of perivascular inflammation, hemorrhage and edema were present in varying degree of severity in the liver, lung and kidney of all three bats. Additional lesions included meningeal hemorrhage in two of the bats and evidence suggestive of early hepatic vasculitis in the other. Eosinophilic and suppurative gastroenteritis affected all bats with one containing intraluminal bacilli, suggesting secondary bacterial infection. **Conclusions:** Immunohistochemistry and qPCR will be performed to assess

relative abundance of virus in various organ systems to optimize future analyses. Future experimental infections will be performed to monitor temperature, physiological and immune parameters, virus shedding and viremia throughout the course of infection. These preliminary data are critical in the assessment of the potential role of bats as reservoirs for arboviruses.

9. **Using GIS to Guide Ebola Virus Disease Ecology Field Investigations**

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Objectives: In the health field GIS is being used to track epidemics in real time and to create predictive models of outbreak potential. We have investigated the feasibility of using a maximum entropy model (Maxent) to assist in determining the target species and optimum locations and times to direct field sampling efforts. **Methods:** We developed an ecological niche model of Ebola virus (EBOV) using the location of Ebola virus disease (EVD) outbreak index cases as presence points we developed an ecological niche model to predict geographic locations that had environmental conditions similar to those of known outbreaks. To determine which environmental parameters were important in constructing the model, a correlation matrix was constructed using ArcGIS and highly correlative parameters were eliminated and the model reconstructed. Additionally, home ranges of African mammals were overlaid on a map and compared to the model to determine which species inhabit the geographical regions predicted to be suitable for a spillover event. **Results:** The model was used to highlight environmental factors common to the location of the EVD index cases from 19 environmental parameters and altitude that were used to construct the model. A list of 66 mammals including 26 bat species with home ranges that overlap the modeled range of EBOV was produced. **Conclusions:** While there is no conclusive evidence that bats serve as the reservoir for Ebola virus (EBOV) i.e. there is no wild EBOV bat isolate, there is evidence that they may play a role in maintaining the virus in nature. Combining what is known about the natural histories of bat species and animal species known to be susceptible to EVD such as great apes, duikers and forest hogs coupled with environmental factors predicted to be important, we can further prediction when and where spillover events may occur and tailor our sampling efforts to target these conditions. Additionally, as there is a dearth of knowledge on the natural history of deep forest fruit bats we are planning to monitor the short term daily movements of *Hypsignathus monstrosus* with the aim of being able to predict where the movements of the bats and susceptible species may commonly intersect.

10. **Bat - infection interactions: Signals of evolution, ecology, immunity and deforestation**

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Objectives: Bats are ecologically diverse and these ecological differences may lead to differences in infection prevalence and identity. We sought to discover the evolutionary and ecological signatures of differences in bat behavior and environment on bat-infection patterns, as well as to understand how these patterns are impacted by human activity. Regions where a high diversity of hosts occur with prevalent deforestation, human habitation and livestock rearing are of great concern for potential spillover. Accordingly, we aimed to characterize infections of potential spillover importance in an altered landscape. **Methods**: Using a combination of genomics, targeted sequence capture and tests of positive selection, we screened 60 species of bats distributed globally for evidence of selection in response to viruses. Additionally, we screened the speciose and ecologically diverse bat fauna of an agricultural landscape in Costa Rica for eight viral groups (Herpesviridae, Astroviridae, Adenoviridae, Paramyxoviridae, Coronaviridae, *Lyssavirus*, Filoviridae, Influenza A), *Bartonella* bacteria and ectoparasites to detect pathogen sharing, immunological and behavioral patterns of infection and the impact of humans on these relationships. **Results**: Evolutionarily, viral sharing has been important for shaping bat immune evolution. However, ecologically most infections are host specific and regulated by host immunity with species that are more frequently exposed less likely to yield detectable pathogen nucleic acids. In deforested areas, these patterns shift in a sex-specific manner, disproportionately impacting females with potential for population stability. **Conclusions**: This study yields evolutionary insights into the unique relationship between bats and viruses, identifying the environmental factors that are driving adaptation. Additionally, it represents one of the broadest infection screening studies in the Neotropics, which has the highest density of bat diversity but is less frequently screened than the Old World. Our data suggest that there are few pathogens of spillover concern circulating in this landscape, but that humans may be having a detrimental impact on bat health.

Daytime behavior of *Pteropus vampyrus* and *Acerodon jubatus* in the natural habitats: a cue of viral transmission

11. Yupadee Hengjan[1], Didik Pramono[2], Hitoshi Takemae[1], Ryosuke Kobayashi[1], Karla Cristine Doysabas[1], Keisuke Iida[1], Takeshi Ando[5], Supratikno[2], Chaerul Basri[2], Yuli Sulistya Fitriana[4], Eko M.Z. Arifin[6], Yasushige Ohmori[1], Ken Maeda[3], Srihadi Agungpriyono[2] and Eiichi Hondo[1]

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Objectives: The large flying fox (*Pteropus vampyrus*) are well-recognized host of Nipah virus. Base on serologic studies, the golden-crowned flying fox (*Acerodon jubatus*) are infected with Ebola Reston virus. To estimate the risk of disease emergence, it is important to understand the behavior of flying foxes. This study aimed to clarify diurnal behavior of *P. vampyrus* in Leuweung Sancang conservation area, Indonesia (7º 43′ 45.12″ S, 107º 54′ 10.08″ E), and *A. jubatus* in the Subic Bay Freeport, the Philippines (14º 46′ 31.54″ N, 120º 19′ 14.90″ E). **Methods:** Quantitative behavioral data were collected using instantaneous scan sampling and all occurrence focal sampling methods. **Results:** Unexpectedly, many flying foxes were awake during daytime (*P. vampyrus*: 46.9 ± 10.6%, *A. jubatus*: 23.7 ± 3.1% of scanned bats), and showed various activities. The commonly observed behavior were wing flapping and self-grooming behaviors. Males engaged in sexual activity more than females (*P. vampyrus*: 6.5 ± 1.6 % in males and 0.2 ± 0.1 in females, *A. jubatus*: 1.6 ± 0.5 % in males, 0% in females), sometimes accompanying with aggression behaviors between males and females. There was no significant difference in negative social behaviors (fighting and wing spreading) between males and females of *P. vampyrus*, whereas, the difference was found in *A. jubatus* (2.6 ± 0.7 % in males, 0.1 ± 0.04 % in females). The positive social behaviors (maternal care, mutual grooming and playing) were rarely found in *P. vampyrus*, but never in *A. jubatus*. Physical communications, not only among flying foxes, but also direct and/or indirect contacts between *P. vampyrus* and non-human primate (*Trachypithecus auratus*) were observed (3.3 ± 0.5 times per day). Specifically, periodic disturbance by tourists and unidentified aerial predators like raptors was observed at the roosting site of *A. jubatus*. *A. jubatus* shared the same roosting site with *P. vampyrus*, this enables the contacts between the two species of flying foxes, an average 25.4 ± 6.3 times per day. **Conclusions:** These observations would provide a cue to know how viral transmissions among flying foxes, other wildlife and humans in South-East Asia.

12. The study of whole spike gene of bat coronavirus from Thailand using Next Generation Sequencing

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Objectives Bats have been recognized as the natural reservoirs of a vast variety of viruses, including as host to Coronaviruses – a viral family of public health importance. Bat coronaviruses have been intensively studied since the discovery of Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) and have expanded even more after the emergence of Middle East Respiratory Syndrome Coronavirus (MERS-CoV), both of which are purposed to have originated from bats. Since spike protein is correlated with host cell receptor binding and membrane fusion, a better understanding of sequence diversity for this gene will help determine the potential for host-switching and zoonotic potential of CoVs. The aim of our study was to characterize the spike gene of bat coronaviruses from Thailand. **Methods** we PCR amplify about 4 kb of whole spike gene from seven PCR positive coronavirus of *M. magneter* and *R. shameli* bats from northern part of Thailand and sequencing using Next Generation Sequencing (NGS). Phylogenetic tree of the full alignment of whole spike gene sequences was estimated by maximum likelihood method. **Results** The average of 1,306,845 sequences of spike gene per sample was obtained from NGS. Phylogenetic tree of all seven spike sequences are grouped into the same clade in the alpha Coronavirus (α CoV) and mostly related to the Bat Coronavirus-1A (BatCoV-1A). **Conclusions** Even though seven spike genes of coronaviruses in this study showed sequence different from emerging disease beta coronavirus group B and C (β CoV B and β CoV C); nevertheless, more positive bat coronaviruses should be investigated including whole genome sequencing of bat coronaviruses that may useful for more understanding host-viral evolution and potential for host switching or spillover.

13. **Assessment of the cross-species potential of two emerging coronaviruses, SARS-CoV and MERS-CoV, by Protein-Protein Molecular Docking analyses**
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Objectives: Coronaviruses are a virus family with broad host range, and have spilled over from their natural reservoirs into various mammalian species, including humans. For humans, four of them cause common cold and circulate exclusively in the human population. In addition, SARS-CoV and MERS-CoV, recently emerged in the human population and are associated with severe respiratory illness. Where do these zoonotic viruses come from, and how did they cross the species barrier? These questions are generally difficult to address. The critical residues at interaction interface of host receptors (DPP4 for MERS-CoV and ACE2 for SARS-CoV) are believed to impact the binding ability of the receptors with viruses' surface-located spike. The diversity of available protein sequences limits our understanding of the receptor-mediated pathogen-host interactions for bat coronaviruses. Computational molecular docking is a bioinformatics tool, which allows us to explore the potential receptor-spike interactions in silico. The aim of this study is to analyze the diversity of SARS-CoV and MERS-CoV receptors from different mammalian hosts, to predict the host range using modeling and molecular docking. **Methods:** Up to 109 DPP4 and 94 ACE2 sequences from mammalian hosts were downloaded from genbank or acquired by sequencing, covering 60 and 51 different families respectively. The putative crystal structures were homologically modeled, and protein-protein docking was performed using Autodock Vina on NIH HPC Biowulf cluster. **Results:** Both of DPP4 and ACE2 receptors sequences from the hosts have relative high diversity. The docking results point out wide but family specific of host range of MERS-CoV and SARS-CoV. Virtual mutagenesis studies explored the impact of each critical residue of DPP4 on binding interaction for *Homo sapiens*, *Mesocricetus auratus*, *Desmodus rotundus*, *Canis lupus familiaris* and *Felis catus*. **Conclusions:** Although currently in silico analysis of spike-receptor interactions utilizing molecular docking methods still are in its early stages of development, the generated results could be utilized to perform large screens of potential virus reservoir, and intermediate hosts associated with emerging coronaviruses, and could potentially be utilized to estimate the distribution of MERS-CoV and SARS-CoV in ecosystems.

14. **Hendra virus phylogeography in eastern Australia**
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Objectives: Hendra virus (HeV) is an emerging zoonotic paramyxovirus that causes sporadic fatal disease in horses and humans in mainland Australia. Australian flying foxes (*Pteropus* spp. fruit bats), the endemic host, are gregarious, semi-migratory species that occupy the tropical and subtropical forests of coastal Australia. Despite the vast range of flying foxes, current outbreaks of Hendra virus have been restricted to a narrow band in southeast Queensland and northern New South Wales. Transmission dynamics of HeV between flying foxes is poorly understood, which limits our ability to identify potential points for management and spillover prevention. We used a phylogeographic framework to explore the spatial structure of HeV over eastern Australia, and to investigate factors that contribute to maintenance and spread of HeV in flying foxes. **Methods:** A three-year surveillance field study was initiated to improve understanding of Hendra virus diversity and disease dynamics in wild flying foxes, generating partial sequences from 26 colonies across eastern Australia. We incorporated sequenced isolates from spillover events in horses, and applied discrete and continuous Bayesian phylogenetic approaches to explore patterns in the dynamics and spatial spread of Hendra virus. Analysis was performed on a 2015 bp intergenic region between the nucleoprotein and phosphoprotein genes. **Results**: Preliminary analysis indicates a broad spatial structure, with lineages clustering loosely in space and time. However, we also find that multiple variants co-circulate in one colony at any given time, and that identical variants may co-circulate in geographically disparate colonies. Our ongoing approach is to identify drivers in the spatial spread and diversity of Hendra virus by examining the role species composition, roost structure, and migratory behavior play in shaping the geneology of Hendra virus. **Conclusions**: These data suggest that host factors (e.g., species composition within roosts) and/or environmental factors may play a role in HeV circulation within and between bat colonies. This work represents a novel approach to understanding the transmission dynamics and evolution of Hendra virus, as well as the functional connectivity of flying fox populations in eastern Australia.

15. **Viral Zoonosis in Georgian Bats**

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Objectives: Bats are reservoir-hosts of viral agents (lyssaviruses, paramyxoviruses, coronaviruses, and filoviruses), which are transmittable to humans and other animals. There are few bat virus detection studies linked to the Caucasus region. In Georgia, bat *Lyssavirus* (Rabies virus) is listed as a priority pathogen, and West Caucasian Bat Virus (WCBV) is the most genetically different member of the *Lyssavirus* genus. The goal of our study was to find WCBV and the newly discovered bat Coronavirus (bat-CoV) in Georgian bats. **Methods:** Bats that were used for sampling were collected in 2012 from four different regions in Georgia. Bat brains (n=236) were sampled and tested for the presence of lyssavirus antigen by the direct fluorescent antibody (DFA) test. A total of 186 bats of 11 different species were sampled for CoV confirmation. RT-PCR amplification assay targeting the 180 bp fragment within the RNA-dependent RNA polymerase RdRp gene and sequencing of the amplified product was used to confirm the presence of coronaviruses in bat specimens. The PCR product was sequenced on an ABI 3130 Automatic Sequencer. **Results:** None of the bats had detectable antigen consistent with an active infection of related *Lyssavirus* or WCBV. We found an outstanding diversity of CoV strains in Georgia; 54 bats tested positive for CoV. Sequence analysis demonstrated 97- 99% identity to five different types of CoV available at NCBI database. Most CoV positive bats were collected from Imereti, which is located in western Georgia. Bats with a higher prevalence of CoV were *Myotis blhytii* and *Rhinolophus ferrumequinum.* **Conclusions:** Our study revealed that we need additional research for excluding the existence of WCBV in Georgian bats. Future work will include determining the prevalence of rabies virus in these bat samples. To do this, we will perform rabies virus neutralization “Rabies Vaccine Response End-Point Titer (RFFIT)” assays. This was the first study addressing the genetic diversity of bat-CoV in this region. Further analyses and interpretation of the phylogenetic results for CoV will be a benefit for surveillance, system control, and response measures of emerging pathogens in Georgia.

16. Forestalling Future Outbreaks: Enhancing Capacity for Surveillance of Viral Hemorrhagic Fever Viruses in Sierra Leone

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Objectives: The first outbreak of Ebola virus disease in Sierra Leone exposed the limited in-country capacity for effective disease surveillance. Heavy reliance was placed on international support for human, technical and material resources. While the source of the outbreak has not been confirmed, human interactions with wildlife and their habitats continue unabated, raising fears of future outbreaks of zoonotic diseases. Building national level capacity, especially in research universities, would enhance Sierra Leone’s capability to forestall future outbreaks involving viral pathogens of public health concern. **Methods:** Through a collaborative agreement with the Viral Special Pathogens Branch at the Centers for Disease Control & Prevention, staff and students at Njala University have received field and laboratory training in ecological surveillance and molecular diagnosis of hemorrhagic fever viruses in bat populations. **Results:** Training in safe capture techniques, collection of blood/serum samples, necropsy techniques and the safe processing and storage of tissues specimens have been achieved over a period of 18 months for 12 Njala University staff and students. Further, three additional staff and students have been trained in molecular diagnostics using robotic nucleic acid extraction and qRT-PCR methods. These trainings, coupled with the acquisition of laboratory and field equipment and renovations of laboratory space on the Njala University campus and its field research station, are resulting in the inclusion of ecological surveillance and molecular diagnostics of viral pathogens in wildlife populations in the curriculum of Njala University in Sierra Leone. **Conclusions:** Strengthening technical and human capacity for disease surveillance in bats through long-term partnerships with research institutions could lay the foundation for preventing future outbreaks of global concerns.

17. Ecological aspects of bats in a cave frequented by members of the local community in Kaptum Cave in eastern Uganda.

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Few studies have addressed the ecology of cave bats in Uganda. This study assessed the diversity, roosting and feeding ecology, of micro bats (order *chiroptera*) as well as influence and frequency of human disturbance, in Kaptum cave of Eastern Uganda. Field observations were conducted between July/Augst 2016 and October/ November 2016 to document aspects of roost utilisation by the bats, their feeding choices and human influences on the cave in which 6 species of microchiropteran bats roosted. We used Mist nets and a Harp trap to capture individuals for examination and identification of species present. Infrared Trail trap Cameras were used to monitor roosting habits and activity patterns of the bats in the cave. A portable whether station was used to record the microclimatic conditions in the different sections of the cave in which the bats roosted to evaluate if there was any influence on choice roost. Kaptum cave has 6 species of insectivorous bats which seemed to prefer different sections of the cave. From evidence of insect remains in the roost, the diet of the bats in Kaptum cave consisted of eight insect orders (*Lepidoptera, Coleoptera, Orthoptera, Dictyoptera, Heymenoptera, Isopteran, Hemiptera, and Odonata*) with the order *Lepidoptera* constituting the bulk of insects preyed upon. At the moment we cannot separate the diet of the different species, since most insect remains were recovered in a section the cave we refer to as the Nycteris corner, because it was most used by these bats, but other species of Rhinolophids and Hipposiderids also frequented this corner in any 24hr period. We believe that the continued human presence in the cave could have implications for roost stability, but also could predispose the humans to potentially harmful aerosols associated with bats and bat guano.

18. **Middle East respiratory syndrome coronavirus spike plasticity in the context of the common vampire bat (*Desmodus rotundus*) DPP4 receptor.**

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Objectives: In 2012, a novel coronavirus, Middle East respiratory syndrome coronavirus (MERS-CoV), was discovered in humans and dromedary camels, although genetic evidence supports a bat ancestor. This range of animal hosts lead us to hypothesize that MERS-CoV can readily adapt to new hosts. The receptor for MERS-CoV, dipeptidyl peptidase 4 (DPP4) has previously been shown to act as a species barrier. By passing the virus over time on cells stably expressing the common vampire bat (*Desmodus rotundus*) DPP4 receptor, which MERS-CoV binds inefficiently, we will determine how potential adaptation in the spike glycoprotein may influence species tropism. **Methods:** We have compared the growth kinetics of MERS-CoV over 72hrs between different bat DPP4 receptors transfected on baby hamster kidney (BHK) cells, which are naturally unsusceptible to MERS-CoV. We then generated BHK cell lines stably expressing the *D. rotundus* DPP4 receptor. By passing MERS-CoV on these cells over time, we hope to observe adaptations in the viral spike protein that allow more efficient viral growth kinetics. Viral genomes containing the relevant mutations can be created through a reverse genetics system and tested for binding affinity and growth potential. **Results:** We show here that MERS-CoV can use DPP4 from different animal hosts, including a variety of bat species. Notably, MERS-CoV can bind and replicate using the *D. rotundus* DPP4 but very inefficiently compared to human DPP4, leading to delayed growth. We observed that MERS-CoV growth on cells stably expressing D. rotundus DPP4 displays a similar inefficient growth pattern as seen previously using a transfection method. **Conclusions:** Our data demonstrates that MERS-CoV can use a diverse set of host species receptors. Although we have successfully generated BHK cells stably expressing *D. rotundus* DPP4, sequencing of the MERS-CoV spike over many passages is needed to identify relevant mutations. The ability of the MERS-CoV spike to adapt to diverse host species receptors may play a significant role in cross-species transmission.

19. **Viral community dynamics of Australian Flying foxes**

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Objectives: Bats are reservoirs for a disproportionate number of zoonotic viruses, with spillover to people and domestic animals resulting in significant public health implications globally. In Australia, bat viral research has largely focused on Hendra virus, yet a diverse viral community has been detected in Australian Pteropid fruit bats (flying-foxes)[1,2]. Additionally, while the four Australian flying fox are capable of being infected with Hendra virus, not all species appear to be equally competent hosts[3,4]. In this context, interactions among co-infecting viruses and the dynamical consequences of these interactions are under- studied. We aimed to gain further insight into bat viral transmission dynamics by exploring dynamics within a multi-host-multi-pathogen framework. **Methods:** To characterise existing knowledge of the bat viral-host community in Australian flying foxes, a systematic literature review of published studies was undertaken and then complimented with additional unpublished data. Using urine samples collected from three of the four Australian flying-fox species in a related field study[6], we utilised a novel high-throughput multiplex PCR[5] to simultaneously detect up to 11 known bat paramyxoviruses. Within a Bayesian framework, we then modelled the monthly presence of different virus species at the roost level in relation to environmental drivers and the co-occurrence of other virus species. **Results:** Results support synchronous shedding pulses of multiple viruses, with significant co-circulation associations between certain virus species. **Conclusions:** Natural host-virus systems comprise complex communities, and our study explores how moving beyond single-pathogen-single host studies of bat pathogen dynamics towards broader consideration of the biotic interactions within viral and reservoir communities could progress our understanding of transmission and spillover of bat pathogens.

20. **The glycoprotein of Nipah virus in Thai bats associated with Nipah virus in Bangladesh**

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Objectives Bats have been recognised as a natural reservoirs of a large number of viruses including Nipah virus (NiV) and are associated with human activities which plays important role in the transmission of pathogens from bats to human. Study the glycoprotein NiV protein which plays important role in virus entry into host cells is a crucial in order to know the virus transmission. **Methods** Bat urine were collected from Luang Phrommawat temple, Chonburi province and screened for NiV nucleocapsid by using hemi-nested RT-PCR. The NiV positive urine samples were amplified the whole glycoprotein gene (1.8 kb). The whole sequences of nucleotide and amino acid of NiV glycoprotein were compared with sequences from both Malaysian and Bangladeshi strains from bats and humans. The phylogenetic tree was constructed by comparing amino acid sequence between NiV from Thai bat and NiV Bangladeshi patient. **Results** NiV glycoprotein sequence from Thai bats were homologous with Bangladeshi strain compared to the Malaysian strain. Furthermore, it shared 99.2-100% and 99.2-99.5% identity with nucleotide sequence of NiV glycoprotein from Bangladeshi bats and Bangladeshi patients, respectively. Amino acid sequence of NiV glycoprotein from Thai bats shared 99.8-100% and 99.5-99.7% identity with Bangladeshi bats and Bangladeshi patients, respectively. While, nucleotide sequence of NiV glycoprotein in Thai bats shared only 93.0-93.3% and 93.2% identity with Malaysian bats and Malaysian patients, respectively. Like nucleotide sequence, the amino acid sequence of NiV Thai bats shared only 95.7-96.0% and 95.7% identity with Malaysian bats and Malaysian patients. Phylogenetic analysis of NiV glycoprotein amino acid revealed that the NiV glycoprotein in Thai bats belonged to Bangladeshi patients. **Conclusions** This is the first step to understand the mechanism of NiV entry to the host. The results may indicates that NiV Thai bat strain has the potential to cause infection in humans. NiV glycoprotein and host receptors should be further investigated in order to understand the viral entry mechanism, host range, including intra- and cross-species transmission. Understanding the transmission of NiV from bats to humans is crucial in order to predict and prevent NiV outbreaks.

21. **Genomic characterization and pathogenic potential of a novel evolutionarily-divergent alphacoronavirus isolated from *M. lucifigus* bats in Alaska.**

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Coronaviruses (CoV) are zoonotic pathogens with the potential to cross species barriers from bats into other mammals, including marine mammals, swine and humans. Novel bat-origin coronaviruses have been responsible respiratory disease in humans, notably betacoronaviruses (OC43, HKU-1, SARS and MERS) and alphacoronaviruses (229E and NL63). Thus, it is important to identify the reservoirs of CoV in bats and their potential for transmission, and pathogenicity, in other mammalian species. We sought to analyze the virome of the most common bat species in Alaska, *Myotis lucifugus,* the little brown bat. Swabs, tissue, and fecal samples were collected from habitats in close proximity to barns, farm buildings, and human habitations in southcentral Alaska. Total RNA extracts were screened by RT-PCR with coronavirus primers matching CoV ORF1a, and Sanger sequencing of amplicons confirmed the presence of an alphacoronavirus phylogentically related to persistent alphacoronaviruses detected in bats in Colorado and the Rocky Mountains. Primary RNA samples were used in library preparation for short-read, paired-end next generation sequencing on an Illumina HiSeq platform. Aligning to a reference *M. lucifigus* virus from Colorado, bat alphacoronavirus CDPHE15/USA/2006, we assembled a full-length genome (28,515nt) identifying the novel alphacoronavirus/bat/Alaska/s7/2014. A high degree of thermodynamically stable stem-loop RNA structures are predicted by Mfold within 700nt of 5' and 3' termini of genome**.** While nucleotide conservation to the Colorado virus was 96%, notable amino acid differences were identified in coronavirus proteins. The major CoV surface spike (S) protein exhibited 26 amino acid changes, including 14 in the globular head containing the putative receptor-binding domain, suggesting divergence based on immune evasion or receptor-specificity. Another 6 amino acids were altered in the fusion hinge. Protease cleavage sites were not conserved. Nucleoprotein (N) and ORF3 also exhibited amino acid differences. Understanding the evolution and pathogenicity of this novel alphacoronavirus provides insight into the role of bats in virus transmission, and ecological assessment of bat-borne virus reservoirs in North American ecosystems.

22. **Spatial pattern of genetic diversity and selection in the MHC class II DRB of three Neotropical bat species**

Salmier A., de Thoisy B., Crouau-Roy B., Lacoste V. and Lavergne A.

Host–pathogen interactions—greatly influenced by environmental characteristics—are a major determinant of the extensive polymorphism of the Major histocompatibility complex (MHC) genes that play an important role in both resistance and susceptibility to diseases. Amazonia encompasses the greatest bat richness, as well as great landscape diversity. However, there are few studies regarding adaptation to infectious diseases of bats and even less in contrasting environmental conditions. We analyzed the genetic variability and positive selection signatures of the expressed MHC class II *DRB* exon 2 in three sympatric Amazonian bat species, *Carollia perspicillata*, *Desmodus rotundus*, and *Molossus molossus* inhabiting different environments (*e.g.*, forests, edge habitats, and urban areas). The role of the environment on the allelic composition and distribution of the *DRB* gene, as well as the effects of pathogen-mediated selection, recombination, gene conversion, demographic history and population structure on the MHC diversity were investigated. Overall, we identified 23 *DRB* alleles in 19 *C. perspicillata*, 30 *DRB* alleles in 35 *D. rotundus* and 20 *DRB* alleles in 28 *M. molossus*. We found clear evidence of at least two functional *DRB* loci as well as a trans-species mode of evolution within the Phyllostomidae family. Bats inhabiting forest environments presented higher number of alleles, revealing a heterozygote advantage likely associated with higher diversity of microorganisms in forest environments due to greater host species richness and better transmission-promoting parameters compared to disturbed environments. The *DRB* polymorphism was high in all sampling sites and for all species but different signatures of positive selection were detected depending on the environment, suggesting a local adaptation characteristic driven by an area-limited pathogen-mediated selection. The patterns of *DRB* diversity were similar to those of neutral markers for *C. perspicillata* and *M. molossus* while these patterns were different for *D. rotundus* for which a geographical structure was highlighted. These results supported that demographic process acts as an additional force in shaping *DRB* diversity. However, in structured populations, environmental constraints associated with characteristic pathogen pressures are the main drivers of MHC diversity.

23. Establishing a field collection scheme to investigate the role of African fruit bats as the natural reservoir of ebolaviruses

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Objectives: Filoviruses are among the most well-known and well-studied zoonotic pathogens, yet we know little about filovirus populations in their natural reservoirs. Phylogeographic and population genetic studies of filoviruses isolated from their natural reservoirs would shed light on the population structure and evolutionary history of these important zoonotic pathogens. African fruit bats including *Hypsignathus monstrosus* and *Epomops franqueti*, are the candidate natural reservoirs for filoviruses in the *Ebolavirus* genus; however, there have been no successful attempts to sequence or isolate *Ebolavirus sp.* from PCR-positive bats due to low viral copy numbers in the bats and difficulty associated with sampling from wild bat populations. We sought to increase the likelihood of acquiring live virus and viral whole genome sequences through extensive sampling from wild bat species in the Odzala-Kokoua National Park, Republic of Congo, within the geographical area of previous Zaire ebolavirus outbreaks. **Methods:** Multiple capture-release studies were performed to sample fruit bats over a period of four years. Bats were captured by mist netting near an *H. monstrosus* lekking tree and sampled for whole blood in addition to collecting nasal, urogenital, and rectal swabs. **Results:** In total, samples were taken from 456 *H. monstrosus* bats and 43 *E. franqueti* bats across four years of sampling. An additional 57 samples were taken from other bat species. Preliminary serological work shows 4.9% seroprevalence against Zaire ebolavirus in a subset of the *H. monstrosus* bats. **Conclusions:** The field collection efforts have yielded a large number of bats sampled which show a history of Zaire ebolavirus exposure. Future work will focus on detecting active infection with ebolavirus and isolation of live ebolavirus for whole genome sequencing.

24. **Co-infection in Georgian Bats**

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Objectives: Bats have been recognized as natural reservoirs for a variety of zoonotic pathogens. The prevalence of different pathogens in bats could be associated with colony size and migration patterns. In this study, bats were collected from four different Georgian regions (Kakheti, Imereti-Tskhaltubo, Samegrelo, Kvemo Kartli) and were tested for different pathogens that are endemic to Georgia. **Methods**: In total, 218 bats (*Eptesicus serotinus*-20, *Miniopterus shrebersii*-27, *Myotis blythii*-67, *Myotis emarginatus*-38, *Pipistrellus pygmaeus*-12, *Rhinolopus Euriale*-26, and *Rhinolopus ferrumequinum*-22) were tested for four bacterial agents (*Bartonella, Brucella, Leptospira,* and *Yersinia*). Bat kidneys were dissected, and their DNA was tested for *Bartonella*, and *Leptospira*. Spleen DNA was tested for *Brucella* and *Yersinia*, and the intestine DNA was tested for *Yersinia*. Triplex Real-Time PCR (rtPCR) Assay was performed to detect *Brucella* (IS711), *Bartonella* (tmRNA), and *Yersinia* (pal). Singleplex rtPCR was used to identify *Leptospira* (LipL32). Targeting the 16S rRNA gene, conventional PCR was performed to detect multiple bacterial strains. Cultured *Bartonella* isolates of the *gltA* gene were sequenced. **Results:** A total of 113 (51%) were positive for at least one of the four pathogens. Co-infection was detected in different bat species from Tskhaltubo and Kakheti. One Tskhaltubo bat was positive for *Bartonella*, *Brucella*, and *Leptospira*. Two bats from Kakheti were co-infected with *Bartonella* and *Brucella*: (*Myotisblythii* (n=1), and *Miniopterusschreibersii* (n=1). Eighteen bats were co-infected with *Bartonella* and *Leptospira*: *Myotisblythii* (n=15), and *Miniopterusschreibersii* (n=3). Sequencing analysis confirmed a co-infection with two different *Bartonella* sequences from 16 different bats: *Myotisblythii blythii* (n=3), *Miniopterusschreibersii schreibersii* (n=7), *Myotisblythii emarginatus* (n=1), *Rhinolophus euryale* (n=2), and *Rhinolophus ferrumequinum* (n=3). All bats were negative for *Yersinia*. **Conclusions:** Our results indicate that bat colonies in Tskhaltubo have the highest prevalence of infection and co-infection; since these bats are in enclosed, small spaces such as caves, this may be a reason we see a mixture of pathogens and mutation. In the past couple of years', Georgian caves have become a popular tourist attraction; from a public health standpoint, it is important to know what types of pathogens exists in these local bats.

25. Caves of Myanmar: a high-risk human-wildlife interface for zoonotic disease
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The Southeast Asian country of Myanmar has been deemed a “hotspot,” both in terms of its biodiversity and disease emergence potential. Despite this recognition, there is a paucity of data and limited surveillance on emerging infectious diseases in Myanmar, due in part to almost five decades of political isolation. Recent changes in the government have expanded economic development, strengthening trade with neighboring countries and opening border access to tourists and investors, further contributing to potential underlying drivers of disease emergence. Of particular import and concern are zoonotic diseases arising from human-animal contact. The vast cave and karst system of Myanmar presents an understudied interface between humans and wildlife, such as bats, rodents, and non-human primates. Caves, particularly where intricate Buddhist shrines have been installed, are popular destinations for local, national, and international visitors despite high-contact potential with animals and their excrement. This poster underscores the growing risk of bat-borne pathogen exposure in relation to cave utilization in Myanmar, exemplified by the popular tourist destination town, Hpa-An.

26. **Prevalence Patterns of Coronaviruses in Lyle's flying fox (*Pteropus lylei*) in Thailand**
Supaporn Wacharapluesadee[1], Prateep Duengkae[2], Aingorn Chaiyes[2], Sangchai Yinsakmongkon[3], Pattarapol Maneeorn[4], Patcharakiti Phengsakul[2], Wachirapon Khumbucha[2], Thongchai Kaewpom[1], Apaporn Rodpan[1], Thiravat Hemachudha[1]

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Objectives Coronavirus (CoV) surveillance in Lyle’s flying fox (*Pteropus lylei*); a medium-sized flying fox which forms large colonies high up in trees in areas close to humans and other animals, was conducted to characterize strain of CoV and determine prevalence patterns in Chonburi province, Thailand. **Methods** *P. lylei* bats were captured monthly during January - December 2012 for detection of CoV at three closed areas in Chonburi province, two human dwellings which were 0.6 (S1) and 5.5 km (S2) away from the bat roost, and a bat roosting site (S3). Two nested RT-PCR of RNA-dependent RNA polymerase (RdRp) from rectal swabs were used for CoV detection. The strain of CoV was confirmed by sequencing and phylogenetic analysis. **Results** From 390 *P. lylei* bats, 239 were male and 151 were female, while 101 were juvenile (forearm length ≤136 mm) and 289 were adult. CoVs were detected in 68 bats, 17.4% using family-wide CoV PCR but not by group C betacoronavirus assay. The positive samples were found in eight months in the year that the study was conducted, the highest in June 2012. Ten mother–pup pairs were captured. Samples from 10 mothers were negative. Rectal swabs from 9 unweaned pups were available for CoV PCR assays and three of them were positive. PCR positive pup was identified with a PCR negative mother. Phylogenetic analysis of conserved RdRp gene revealed that the detected CoVs belonged to group D betacoronavirus (n=64) and alphacoronavirus (n=4). **Conclusions** Younger bats appeared to play a more significant epidemiological role in harbouring CoV. Young age but not sex or gravidity, correlated significantly with CoV detection. CoV was found in unweaned pups whose mothers tested negative for CoV. One possible conclusion is transient shedding from mother during peri-partum to the young, may maintain the virus transmission within the population. The immune status of young and adult bats against CoV, in terms of susceptibility to infection, needs to be studied to explore this. Further study into the association of CoVs with natural hosts is necessary to understand their prevalence and maintenance patterns, to evaluate its zoonotic potential.

27. Genetically Diverse Filoviruses in *Rousettus* and *Eonycteris* spp. Bats, China, 2009 and 2015
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Bats have been implicated as natural reservoirs for filoviruses based on serological or nucleotide evidence from 19 bat species in 8 countries across Asia, Africa, and Europe. Previously, we discovered filovirus antibodies in several bat species in China. Here we report genetically divergent novel filoviruses are circulating in the *Rousettus* and *Eonycteris* bats from China. The 310-bp L-gene sequences exhibited 65–99% nucleotide (nt) identity among themselves and 61–78% nt identity with known filoviruses. Phylogenetic analysis of these sequences suggests that at least 3 distinct groups of filovirus are circulating in these bats. Q-PCR results showed these filoviruses were mainly located in the lung, with genome copy number varying from 29 to 523,582/mg of tissue. Thus, these filoviruses may have the potential to be transmitted through the respiratory tract. Co-infection with four different filoviruses was found in a single bat. ELISA and Western Blot showed the antibodies reacting more strongly to EBOV NP than RESTV NP in some filovirus RNA negative bats. One of the viruses named BtFilo9447 were tried to amplify the whole genome. The GP gene of BtFilo9447 shared 34-39% similarity on aa level and 35-53% similarity on nt level with known filoviruses. Our results demonstrate that fruit bats may are important reservoirs of filoviruses. Considering their feeding habitats, fruit bats are often in close contact with domestic animals and human populations. It is therefore necessary to establish long-term and proactive surveillance of these viruses and related diseases.

28. **Development of a monoclonal antibody to Jamaican fruit bat CD3γ**
Miles Eckley, Ann Hawkinson, Tyler Sherman, Tony Schountz, Corey L Campbell

[1]Arthropod-borne and Infectious Diseases Laboratory, Colorado State University and [2]Department of Biology, University of Northern Colorado.

Objective: T cells have critical immunomodulatory roles in the innate immune response to infection. The CD3 cell-surface protein complex is required for T cell activation, and thus treating bats with therapeutic Aj-anti-CD3 IgG antibodies may have immunosuppressive effects. Monoclonal antibodies are of particular interest for this application because of their ability to bind to the Fc receptor of phagocytic and cytotoxic cells and label a pathogen for destruction. Our goal is to investigate the biological mechanisms by which T cells may induce immunopathology in response to viral infection. **Methods**: BALB/c mice were immunized and boosted with a KLH-conjugated 30mer peptide from Jamaican fruit bat CD3γ. Hybridoma cells were produced from the fusion of splenocytes with Sp2/0-Ag14 myeloma cells. Hybridoma cells were selected and cloned on methylcellulose plates, transferred to 24 well plates and supernatants screened. Candidates were identified by ELISA to 30mer peptide conjugated to BSA first, followed by flow cytometry of bat splenocytes. Antibodies were purified from supernatants by affinity chromatography using a protein A/G agarose resin bed. Isotype determination was done by ELISA using HRP labeled mouse anti-IgM, IgG2a, IgG1 and biotin labeled rat anti- IGg2b, IgA and IgG3 primary antibodies. **Results**: Three hybridoma clones for Aj-anti-CD3 IgG were purified from the cell culture supernatants and stored for later use. Each of the three hybridoma clones are expected to have produced a different isotype based on flow cytometry data. **Conclusions**: In future work, we will use Aj-anti-CD3 antibody labelling of T cells in vivo to deplete T cells and determine whether immunopathology to Tacaribe virus, which normally causes fatal infection, will be ameliorated.

29. **Bats and Immunity: Anti-Viral IFNγ Responses Differ Among Hosts**
C. Cotter, T. Schountz, C.L. Campbell

Arthropod-borne and Infectious Diseases Laboratory, Colorado State University

Anti-viral responses in bats (order Chiroptera) is largely unknown to researchers. Although bats account for 20% of all mammal species, they are relatively understudied in the scientific community (Baker et al., 2013). Bats are reservoir hosts for zoonotic diseases such as severe acute respiratory syndrome (SARs), rabies virus, and Ebola virus (Mandl et al., 2015). Reservoir hosts, generally, do not show pathogenic signs or succumb to disease when infected with such viruses. Current efforts by Kuzmin et al to better understand anti-viral responses in Egyptian rousette bat (*Rousettus aegyptiacus*) and human cells include a comparative study of host innate immune response to infection with Ebola virus or Marburg virus. They focused on the interferon (IFN) response. Kuzmin et al. demonstrated that bat IFNγ (type II IFN response) decreased viral replication in cell culture, whereas the human IFNγ produced by the human cells did not. Additionally, IFNγ stimulated the type I IFN (IFNα/β) response Kuzmin et al., 2017). My research focuses on Jamaican fruit bat (*Artibeus jamaicensis*—Aj) IFNg and its role in an anti-viral response to New World mammarenavirus Tacaribe (TCRV). *A. jamaicensis*, when infected with

TCRV, suffer fatal infections (Cogswell-Hawkinson, 2012). Most arenaviruses, TCRV excluded, produce a nuclear protein (NP) that blocks the type I IFN response at interferon response factor-3 (IRF-3) (Martinez-Sobrido et al., 2007). Pathogenesis of TCRV is still unknown; however I hypothesize that it interferes with the IFN response pathway by a different mechanism. Therefore, introduction of therapeutic Aj IFNγ to TCRV infected A. jamaicensis should be able to stimulate an appropriate, anti-viral innate immune response to rescue them from death. My project focuses on cloning, expressing, and purifying Aj IFNγ in order to synthesize a recombinant antibody for Aj IFNγ.

30. **Virome analysis of neotropical bats on the Caribbean island of Trinidad**

Janine F.R. Seetahal[1], Orchid M. Allicock[1,2], Stephen C. Sameroff[2], Christopher Oura[3], Vernie Ramkissoon[1], W. Ian Lipkin[2], Christine V.F. Carrington[1]

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Objectives: Bats are recognized as reservoirs for a number of important zoonotic viruses. The Caribbean island of Trinidad is richly diverse in bat fauna with 68 species recognized. Viruses detected in Trinidad bats include Rabies virus, Tacaribe virus, Rio Bravo virus, Tamana bat virus and more recently a bat coronavirus. The objective of this study was to identify and characterize known and novel viruses in Trinidad bat species. **Methods:** During the period 2012- 2016, bats were sampled from 19 locations in Trinidad. The novel virome capture sequencing platform for vertebrate viruses (VirCapSeq-VERT) was employed to sequence faecal swab samples from 73 bats belonging to seven neotropical species (*Desmodus rotundus, Carollia perspicillita, Uroderma bilobatum, Molossus molossus, Molossus rufus, Pteronotus parnellii* and *Artibeus spp*). Sequence reads were processed using the bioinformatics pipeline at Center for Infection and Immunity to remove host background and assemble contigs that were then subjected to homology search using MegaBlast against the GenBank nucleotide database. Sequences that showed poor or no homology at the nucleotide level were searched against the GenBank viral protein database using BLASTx. The bat fecal samples were also screened by consensus PCR for 8 viral families (*Arenaviridae*, *Herpesviridae*, *Coronaviridae*, *Orthomyxoviridae*, *Alphaviridae*, *Flaviviridae*, *Rhabdoviridae*, *Picornaviridae*) using broadly reactive degenerate primers as outlined in the laboratory protocol for the PREDICT II surveillance project. All PCR products were confirmed by sequencing. **Results:** Consensus PCR detected sequences of Herpesviridae (bat herpesviruses) and Coronaviridae (bat coronaviruses). Preliminary analysis of VirCapSeq-VERT data provided evidence of both known and potentially novel viruses, the majority of which belonged to the families *Anelloviridae*, *Herpesviridae*, *Coronaviridae*, *Orthomyxoviridae*, *Parvoviridae*, *Rhabdoviridae* and *Retroviridae*. The *Anelloviridae* and *Herpesviridae* were detected primarily in fruit bats. The *Orthomyxoviridae* family included Influenza A viruses and were identified in *Desmodus* and *Molossus* species. *Parvoviridae* were overwhelmingly from *Desmodus* and *Artibeus* bats from one trapping site within the same year. *Rhaboviridae* viruses were detected in Desmodus bats sampled from various locations throughout the sampling period. The Retroviridae were primarily previously described bat endogenous retroviruses. **Conclusions:** Our results indicate the presence of a wide range of both known and novel viruses in faeces from Trinidad bats. The limited identification of viruses by consensus PCR as compared to the deep sequencing technique implies that viral detection is more efficient by targeted deep sequencing. Further analysis including targeted PCR and sequencing to assemble full genomes is required to further characterise the viruses detected. Analysis of other tissues will be required to distinguish between bat viral infections and viruses associated with animal prey.

31. **Delineating the phenotype and function of major lymphocyte populations in the fruit-eating bat, Pteropus Alecto.**

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Objective: The unique ability of bats to act as reservoir for viruses that are highly pathogenic to humans suggests unique properties and functional characteristics of their immune system. However, the lack of bat specific reagents, in particular antibodies, has limited our knowledge of bat's immunity. **Methods and Results**: Here, using cross-reactive antibodies, we report the phenotypic and functional characterization of CD3+ T cell subsets, CD19+ B and NK1.1+ NK cells in the fruit-eating bat Pteropus alecto. Our findings indicate the predominance of CD8+ T cells in the spleen from wild-caught bats that may reflect either the presence of viruses in this organ or predominance of these cells at steady state. In addition, bone marrow of the bat contains over 30% T lymphocytes. This is significantly greater when compared to the T cell percentages in human and mouse bone marrow which ranges between 4% and 8%. Uniquely, a significant proportion of CD3+ T cells in bat spleen constitutively express IL-17A, IL-22 and TGF- at the mRNA level. Hence, the spleen may contain a substantial population of naïve T cells that are programmed to readily differentiate into TH17 cells or Tregs. Furthermore, mitogenic stimulation induced proliferation of bat immune cells and production of cytolytic molecules granzyme and perforin, and cytokines IL-2, IL-10, TNF and IFN. Additionally, we also demonstrate B cell function via calcium flux assay. **Conclusions**: This work paves the way towards a better understanding of bat's immunity that may offer new perspectives of therapeutic interventions for humans.

32. **Seasonal serological signals in viral infections for Madagascar fruit bats**

Cara E. Brook[1], Hafaliana C. Ranaivoson[2], Christopher C. Broder[3], Andrew A. Cunningham[4], Andrea L. Graham[1], Jean-Michel Héraud[2], Louise Wong[4], James L.N. Wood[5], Andrew P. Dobson[1*], C. Jessica E. Metcalf[1*]

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Objectives: Considerable evidence supports a seasonal driver of bat-borne zoonoses, with most spillover events aligned with the synchronous reproductive season of the bat host in question. Previous modeling work proposes three possible mechanisms which could underpin such seasonality: classic Susceptible-Infectious-Recovered (SIR) dynamics with a seasonal influx of naïve juveniles, Susceptible-Infected-Recovered-Susceptible (SIRS) dynamics with periodic, waning immunity, and Susceptible-Infectious-Latent-Infectious (SILI) dynamics, by which hosts maintain virus persistently but shed seasonally. We fit variations on these contrasting dynamic models to age-seroprevalence data for henipavirus infections in Madagascar fruit bats in order to test these hypotheses. **Methods:** We live-captured, serum-sampled, and extracted lower premolar teeth (under anesthesia) from 340 Madagascan fruit bats (Eidolon dupreanum) over an eighteen-month seasonal trajectory. Serum samples were subjected to Luminex assay for henipavirus antibodies, and teeth underwent histological processing to quantify bat age, resulting in the construction of age-serprevalence curves for heniapivrus exposure in E. dupreanum. We fit variations on SI, SIR, SIS, and SIRS compartmental models to these data and used generalized additive models (GAMs) to investigate seasonal variation in antibody titers for both sexes, including several individuals recaptured across our time series. **Results:** Seroprevalence to henipavirus increased with age across the early years of life in our dataset, then declined to zero in later life. Field data were best fit by either frequency-dependent transmission models incorporating infection-induced mortality or by density-dependent transmission models, allowing for rapid waning of immunity. GAM analysis of seasonal trends showed significant seasonality in an animal's serostatus, corresponding to the nutritional calendar for male bats and the reproductive calendar for female bats. Recaptured individuals demonstrated considerable dynamism in antibody titers, changing serostatus in both directions across our time series. **Conclusions:** Our analyses suggest that henipavirus infections in E. dupreanum fruit bats are governed by highly dynamic transmission mechanisms, involving rapidly waning immunity and seasonal peaks and troughs in infection status. We reject a classic SIR model in favor of a more flexible SIRS or SILI model underpinning viral transmission among bat hosts in our system. More fine-scale field data will be needed to further parse remaining hypotheses.

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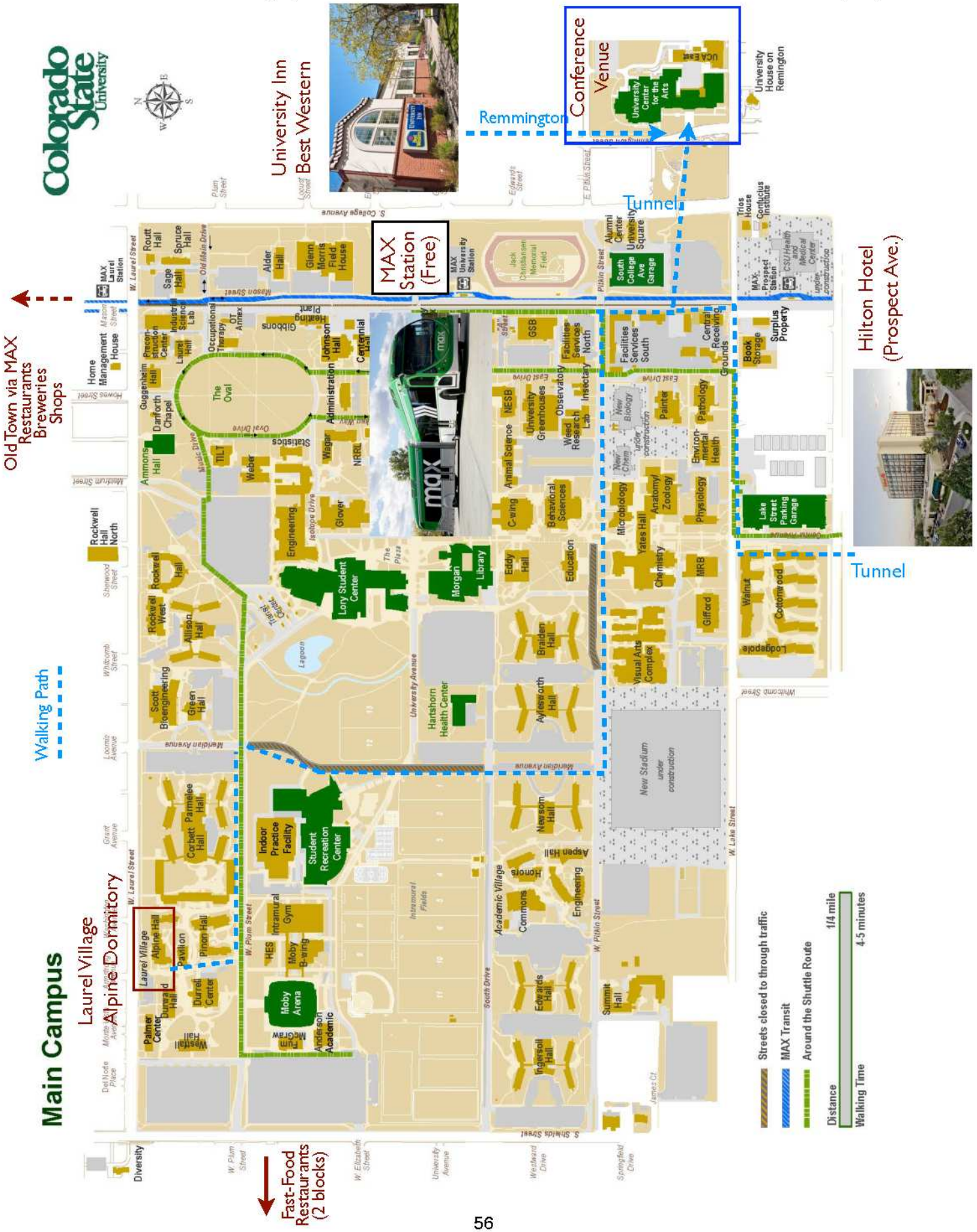
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Mrs	Stefania	Leopardi		Italy	Istituto Zooprofilattico Sperimentale delle Venezie
Dr	Jun	Li		Montana	NIH/Rocky Mountain Lab
Dr.	Holly	Lutz		IL	Field Museum of Natural History, University of Chicago
Dr.	Wenjun	Ma		KS	Kansas State University
Dr.	Joanne	Maki		Georgia/USA	Boehringer Ingleheim Animal Health
Dr.	Fedelino	Malbas Jr.		Philippines	Research Institute for Tropical Medicine (RITM)
Prof	Wanda	Markotter		South Africa	University of Pretoria
Mr.	Benard	Matovu		Uganda	Makerere University
Prof	Hamish	McCallum		Queensland/ Australia	Griffith University
Mr	Stewart	McCulloch		South Africa	Centre for Viral Zoonoses, University of Pretoria
Mr.	Clifton	McKee		CO	Colorado State University
Ms	Rebekah	McMinn		Montana	NIH/Rocky Mountain Lab
Dr	Ian	Mendenhall		TX	Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore
Dr	Solomon Gebre	Michael		Houston	NAHDIC, Ethiopia
Dr	Vikram	Misra		Saskatchewan	University of Saskatchewan
Mrs	Marinda	Motlock		South Africa	Centre for Viral Zoonoses, University of Pretoria
Dr	Vincent	Munster		Montana	NIH/Rocky Mountain Lab
Ms.	Betty	Nalikka		Uganda	Makerere University
Dr.	Sarah	Olson		MT	Wildlife Conservation Society
Dr	EunChung	Park		MD	NIH
Dr	Alison	Peel		QLD	Griffith University
DR	PRAVIN	PERIASAMY		SINGAPORE	National University of Singapore
Dr.	Kendra	Phelps		Texas	Texas Tech University
Dr	Raina	Plowright		United States	Montana State University
Dr.	Abhishek	Prasad		Texas	University of Texas Medical Branch
Prof	Wolfgang	Preiser		South Africa	University of Stellenbosch
Dr.	DeeAnn	Reeder		PA/USA	Bucknell University
Dr.	Patricia	Repik		MD, USA	NIH/NIAID
Dr.	Arielle	Salmier		French Guiana/ France	Institut Pasteur de la Guyane
Ms.	Cecilia	Sanchez		GA	University of Georgia, Odum School of Ecology
Dr.	Will	Sander		VA	CTR A&AS Support / Booz Allen Hamilton
Dr	Sarkis	Sarkis		French Guiana/ France	Institut Pasteur de la Guyane
DR	Tony	Schountz		USA	Colorado State University
Dr.	Amy	Schuh		GA	Centers for Disease Control and Prevention
Dr.	Martin	Schwemmle		Germany	University Freiburg
Dr.	Janine	Seetahal		Trinidad and Tobago	The University of the West Indies
Dr	Stephanie	Seifert		Montana	NIH/Rocky Mountain Lab
Prof	Zhengli	Shi		China	Wuhan Institute of Virology, CAS
Dr	Marty	Stokes		VA	Cooperative Biological Engagement Program
Dr.	Sonu	Subudhi		Saskatchewan	University of Saskatchewan
Dr	Edit	Szalai		Colorado	Colorado State University
Dr.	Jonathan	Towner		GA	Centers for Disease Control and Prevention
Ms	Nil	Unal		Turkey	Ministry of Food, Agriculture
Ms.	Lela	Urushadze		Georgia	National Center for Disease Control
Ms.	Megan	Vodzak		DC	Smithsonian Conservation Biology Institute
Dr	Able	Wade		TX	LANAVET Annex Yaounde
Prof	Patrick CY	Woo		China	The University of Hong Kong
Dr.	Tracy	Woodall		Colorado	Colorado Department of Public Health and Environment
Mrs	Lisa	Worledge		United Kingdom	Bat Conservation Trust
Dr.	Richard	Yanagihara		Hawaii/USA	University of Hawaii at Manoa
Dr.	Peng	Zhou		China	Wuhan Institute of Virology, CAS

From: Schountz,Tony
Sent: Tuesday, April 11, 2017 9:37 PM EDT
To: 胡犇 <huben
Subject: Re: Re: Requesting invitation letter for visa application

You're very welcome, Ben. I look forward to meeting all of you at the symposium.

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: 胡犇 <huben
Sent: Tuesday, April 11, 2017 7:34 PM
To: Schountz,Tony
Subject: Re: Re: Requesting invitation letter for visa application

Dear Dr. Schountz:
Thank you so much for your kind help!
Sincerely
Ben

-----原始邮件-----
发件人: "Schountz,Tony" <
发送时间: 2017年4月11日 星期二
收件人: "胡犇" <huben >
抄送:
主题: Re: Requesting invitation letter for visa application

Ben, I have attached a Word file that you can edit with the names and addresses of the four participants. So, just make a copy for each one and use them.

Thank you,

Tony

> On Apr 11, 2017, at 3:56 AM, 鏖 $ 妵 <huben wrote:
>
> Dear Dr.Schountz:
> I am a researcher at Wuhan Institute of Virology, Chinese Academy of Sciences. My colleagues and I are studying bat viruses and we have submitted four abstracts to the 2nd International Symposium on Infectious Diseases of Bats which is going to be held in Fort Collins in June.
> The title for the 4 abstracts are:
> 1) SARS coronavirus may have originated from frequent recombination events betwwen SARS-like coronaviruses in a single horseshoe bat habitat (oral)
> 2) Dampening of STING-dependent IFN production: an implication of virus tolerance in bats? (oral) 锛嶲 noticed from the web that this abstract has already been confirmed as oral presentation)
> 3) Genomic characterization of diverse BatCoV HKU10 and three novel alphacoronaviruses (poster)
> 4) Genetically diverse filoviruses in Rousettus and Eonycteris spp. bats, China, 2009 and 2015. (poster)
> As it is a unique conference specializing on our research area, we are very eager to attend. However, it usually takes at least two months for us to get the US visa due to the complicated procedure of applying for travel permit to Chinese Academy of Sciences and then one month of administrative processing by US embassy. So in order we can make our visit to Colorado in late June, we have to start the process of travel permit and visa application now.
> To apply for a travel permit, we are required to submit an invitation letter from the conference organizer. I know for the bat-borne disease meeting, we will know the results of the acceptance of the abstract by May. But it will be late for us to apply for the travel permit and US visa.
> Could you please kindly provides four invitation letters to us indicating we will attend the meeting and give presentations? (oral or posters)

It does not matter whether the abstracts will be finally selected as he invitation letters are only for visa application.
We deeply appreciate your understanding and assistance.
Thank you very much!
Best regards

Ben Hu Ph.D
Research Assistant
Wuhan Institute of Virology, CAS

欤?/div>
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony
Sent: Monday, October 22, 2018 2:42 AM EDT
To: 胡犇 <huben >
Subject: Re: Re:Re: Final Program of the 8th International Symposium on Emerging Viral Diseases
Attachment(s): "Boarding passes.pdf"

Thank you, Ben. My boarding passes are attached as a single PDF (two passes).

Will I need to pay the driver? If so, can it be done with my credit card? If not, I will need to get currency exchange and need to know how much it will cost.

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: 胡犇 <huben
Sent: Monday, October 22, 2018 12:24 AM
To: Schountz,Tony
Subject: Re:Re: Final Program of the 8th International Symposium on Emerging Viral Diseases

Hi Dr Schountz,

Your flight will be on tomorrow morning at 9:35?

I will be at th hotel at 6:30. I will meet you at the hotel lobby then and ask a vehicle to send you to the airport.

Please also send me your boarding pass and I will print it for you and give you tomorrow morning.

Best

Ben

在 2018-10-22 11:44:15，"Schountz,Tony" 写道：

>Hi Ben
>
>
>Do I need to schedule a ride to the airport tomorrow? Also do you know if I can print my boarding passes here at the hotel?
>
>
>Thanks
>
>
>Tony
>
>
>Sent from my iPhone
>
>On Oct 18, 2018, at 10:16 PM, 胡犇 <huben wrote:
>
>
>
>
> Dear Dr.Schountz:
>
>
> I have an app via which I can follow the status of any flight.

>
>
> So I can arrange with flexibility.
>
>
> But hope everything will be fine.
>
> Sincerely
>
> Ben
>
>
>-----原始邮件-----
>发件人:"Schountz,Tony" >
>发送时间:2018-10-18 21:59:58 (星期四)
>收件人: "胡犇" <huben
>抄送:
>主题: Re: Re:Re: Final Program of the 8th International Symposium on Emerging Viral Diseases
>
>
>
>Hi Ben,
>
>
>
>
>It looks like heavy thunderstorms for my arrival in Tokyo. Hopefully, they will not delay my connection to Wuhan. If I miss the flight to Wuhan, I will email you so that you can let the driver know. Otherwise, I should see him/her in about 24 hours!
>
>
>
>
>Thanks,
>
>
>
>
>Tony
>
>
>
>
>—
>Tony Schountz, PhD
>Associate Professor
>Arthropod-borne and Infectious Disease Laboratory
>Department of Microbiology, Immunology and Pathology
>College of Veterinary Medicine
>Colorado State University

>
>
>
>From: 胡犇 <huben >
>Sent: Wednesday, October 17, 2018 9:54 AM
>To: Schountz,Tony
>Subject: Re:Re: Final Program of the 8th International Symposium on Emerging Viral Diseases
>
>
>
>Yes Dr.Schountz.
>
>The pick-up from the airport to the hotel will be arranged.
>
>Safe journey and see you soon.
>
>Best
>
>Ben

>
>在 2018-10-17 23:41:10，"Schountz,Tony" > 写道：
>
>>Hi Ben,
>>
>>
>>I just want to verify a driver will pick me up at the airport upon my arrival and take me to the hotel.
>>
>>
>>Thank you,
>>
>>
>>Tony
>

BOARDING PASS

ANA | A STAR ALLIANCE MEMBER

SCHOUNTZ/WILLIAM ANTONE

DATE	23OCT2018
FROM	WUHAN
TO	TOKYO(NARITA)
DEP TIME	09:35

ECONOMY CLASS

Y

UA*S
GYH13508 accepted

FLIGHT	GATE	BOARDING TIME	SEAT
NH 0938		09:00	24A

API ETKT 01671124838503 022

Note: Please confirm the latest information on boarding gates and times at the departure airport.

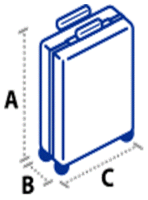
[Information for an ANA-operated flight]

[If Checking In Baggage]
Please arrive at the check-in counter at least one hour before the departure time (or at least 40 minutes before the departure time for an international flight from Haneda Airport).
When connecting to an international flight from a Japan domestic flight, please arrive at the domestic check-in counter at least 30 minutes before the departure time of the domestic flight.

[Boarding]
Please arrive at the gate at least 10 minutes before the departure time.There is a possibility that passengers who do not arrive at the gate by this time may not be able to board the flight.
When boarding a Japan domestic flight, please pass through the airport security check at least 15 minutes before the departure time.

[Required Travel Documents]
Passengers must have valid passports, visas, and other applicable travel documents ready. Travel documents will be checked at the check-in counter and boarding gate.

[Carry-on Baggage]
For international flights, each passenger may bring on board one piece of carry-on baggage in addition to one personal item.
Carry-on baggage must weigh 10 kg or less and be within the following dimensions: 55 cm x 40 cm x 25 cm (total linear dimensions cannot exceed 115 cm).
(Size restrictions may vary depending on the type of aircraft that the flight is operated with.)



A+B+C ≦ 115cm(45inch)

Note: Check-in guidelines may vary for codeshare flights. For details, please contact the operating carrier directly.

For staff use
SCHOUNTZ/WILLIAM ANTONE
NH 0938 23OCT2018
GYH13508
ETKT 01671124838503

SEAT 24A

SEC 022

BOARDING PASS

ANA | A STAR ALLIANCE MEMBER

SCHOUNTZ/WILLIAM ANTONE

DATE	23OCT2018
FROM	TOKYO(NARITA)
TO	DENVER
DEP TIME	17:15

Y

UA*S
GYH13508 accepted

FLIGHT	GATE	BOARDING TIME	SEAT
UA 0142		16:25	23L

API ETKT 01671124838504 004

Note: Please confirm the latest information on boarding gates and times at the departure airport.

[Information for an ANA-operated flight]

[If Checking In Baggage]
Please arrive at the check-in counter at least one hour before the departure time (or at least 40 minutes before the departure time for an international flight from Haneda Airport).
When connecting to an international flight from a Japan domestic flight, please arrive at the domestic check-in counter at least 30 minutes before the departure time of the domestic flight.

[Boarding]
Please arrive at the gate at least 10 minutes before the departure time.There is a possibility that passengers who do not arrive at the gate by this time may not be able to board the flight.
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For international flights, each passenger may bring on board one piece of carry-on baggage in addition to one personal item.
Carry-on baggage must weigh 10 kg or less and be within the following dimensions: 55 cm x 40 cm x 25 cm (total linear dimensions cannot exceed 115 cm).
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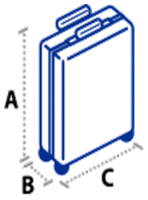

A+B+C ≦ 115cm(45inch)

Note: Check-in guidelines may vary for codeshare flights. For details, please contact the operating carrier directly.

For staff use
SCHOUNTZ/WILLIAM ANTONE
UA 0142 23OCT2018
GYH13508
ETKT 01671124838504

SEAT 23L

SEC 004

From: Schountz,Tony
Sent: Thursday, October 18, 2018 9:59 AM EDT
To: 胡犇 <huben
Subject: Re: Re:Re: Final Program of the 8th International Symposium on Emerging Viral Diseases

Hi Ben,

It looks like heavy thunderstorms for my arrival in Tokyo. Hopefully, they will not delay my connection to Wuhan. If I miss the flight to Wuhan, I will email you so that you can let the driver know. Otherwise, I should see him/her in about 24 hours!

Thanks,

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: 胡犇 <huben
Sent: Wednesday, October 17, 2018 9:54 AM
To: Schountz,Tony
Subject: Re:Re: Final Program of the 8th International Symposium on Emerging Viral Diseases

Yes Dr.Schountz.

The pick-up from the airport to the hotel will be arranged.

Safe journey and see you soon.

Best

Ben

在 2018-10-17 23:41:10，"Schountz,Tony" 写道：

>Hi Ben,
>
>
>I just want to verify a driver will pick me up at the airport upon my arrival and take me to the hotel.
>
>
>Thank you,
>
>
>Tony

From: Schountz,Tony
Sent: Friday, August 03, 2018 11:38 AM EDT
To: 胡犇 <huben >
Subject: Re: Re:Re: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

Hi Ben,

I'm sorry I'm late on the abstract. I will get it to you on Monday.

Thanks for your understanding.

Tony

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: 胡犇 <huben
Sent: Saturday, May 12, 2018 9:37 AM
To: Schountz,Tony
Subject: Re:Re: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases

No need, Dr.Schountz. For invited speakers the rooms will be reserved by the conference.

Ben

在 2018-05-12 23:15:20，"Schountz,Tony" > 写道：

>Thank you, Ben. Should I make my own reservation?
>
>
>
>
>Tony
>
>
>
>
>—
>Tony Schountz, PhD
>Associate Professor
>Arthropod-borne and Infectious Disease Laboratory
>Department of Microbiology, Immunology and Pathology
>College of Veterinary Medicine
>Colorado State University

>
>
>
>From: 胡犇 <huben
>Sent: Friday, May 11, 2018 6:47 PM
>To: Schountz,Tony
>Cc: 石正丽; 周鹏
>Subject: Re: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases
>
>
>
>
>

> Dear Dr.Schountz:
>
> Here is the hotel information:
>
> name: Optics Valley Kingdom Plaza Hotel Wuhan,
>
> address: No.1 Wu Jia Wan, Hongshan District, Wuhan, Hubei Province, China.
>
>
>
> Best
>
> Ben
>
>
>
>
>-----原始邮件-----
>发件人:"Schountz,Tony"
>发送时间:2018-05-12 00:01:20 (星期六)
>收件人: "胡犇" <huben >
>抄送: "Schountz,Tony" , "石正丽" <zlshi >, "周鹏" <peng.zhou
>主题: Re: Invitation to the 8th International Symposium on Emerging Viral Diseases
>
>Hi Ben,
>
>
>I have my flight booked and will arrive in Wuhan at 10:00 PM on October 19 (All Nippon Airways NH 937). Can you tell me the name and address of the hotel? I will need it for my visa and for my university administrators.
>
>
>Thank you,
>
>
>Tony
>
>
>On Apr 9, 2018, at 8:06 AM, 胡犇 <huben > wrote:
>
>
>
>Dear Dr.Schountz:
>
>
>
>The 8th International Symposium on Emerging Viral Diseases will be held in October 20-22, 2018, in Wuhan, China. The biennial symposium is organized by Wuhan Institute of Virology, Chinese Academy of Sciences and has become an important event for leading Chinese and international virologists to discuss cutting-edge science on emerging viruses as well as to foster global collaborations.
>
>
>Prof Zhengli Shi and Dr.Peng Zhou had a nice experience last year in Colorado when attending the symposium on bat-borne infectious diseases, and we know you have made great contributions to bat virus researches. We sincerely hope that you can attend the symposium. Please find enthe formal invitation letter for the meeting.
>
>
>If you have any question regarding the conference, please contact me.
>
>
>Thank you!
>
>
>Best regards
>
>
>
>
>Ben Hu Ph.D
>
>
>Research Assistant
>

>
>Secretary of the 8th International Symposium on Emerging Viral Diseases
>
>
>Wuhan Institute of Virology, Chinese Academy of Sciences
>Wuhan 430071, P.R. China
>
><Invitation letter Tony Schountz.pdf>
>
>
>—
>Tony Schountz, PhD
>Associate Professor
>Arthropod-borne and Infectious Disease Laboratory
>Department of Microbiology, Immunology and Pathology
>College of Veterinary Medicine
>Colorado State University

>

From: Tony Schountz on behalf of Schountz,Tony
Sent: Tuesday, September 01, 2020 4:26 PM EDT
To: Aleksei Chmura < ecohealthalliance.org>
CC: Schountz,Tony < >; Peter Daszak < ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Re: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

Yes, that would work. Talk to you soon. I'm at the number below.

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

> On Sep 1, 2020, at 2:22 PM, Aleksei Chmura ecohealthalliance.org> wrote:
>
> Thanks, Tony!
>
> That is good to read. Would 3pm Colorado (5pm NYC) today work for you - in approximately 40 mins?
>
> If not, then what about tomorrow or Thursday at the same time?
>
> Cheers,
>
> -Aleksei
>
> > On Sep 1, 2020, at 16:20, Schountz,Tony wrote:
> >
> > Hi Aleksei,
> >
> > I think a phone call would be better. I think she'd make a great addition to your team.
> >
> > I'm available most of this week.
> >
> > Tony
> > —
> > Tony Schountz, PhD
> > Associate Professor
> > Arthropod-borne and Infectious Disease Laboratory
> > Department of Microbiology, Immunology and Pathology
> > College of Veterinary Medicine
> > Colorado State University
> >
> > > On Aug 30, 2020, at 4:26 PM, Aleksei Chmura ecohealthalliance.org> wrote:
> > >
> > > Dear Dr. Schountz,
> > >
> > > We just interviewed Anna Fagre for a position here at EcoHealth Alliance as a Research Scientist and Project Manager. Our hiring committee thought she was terrific with the right background and attitude for our team. Anna listed you as a reference. If you would be

willing to send some comments about Anna, that would be terrific!

I have attached our position advertisement, so you may know more about the position - though based on her skillset, the specifics would evolve a bit. This position would focus primarily on our emerging infectious disease projects based in Southeast Asia including our recently awarded, NIAID funded EID-SEARCH program:

- https://www.ecohealthalliance.org/program/south-east-asia-research-collaboration-hub

I look forward to your reply and should a phone call be more convenient, we could do that as well.

On behalf of our whole committee, I sincerely appreciate your time.

-Aleksei

Aleksei Chmura, PhD
Chief of Staff

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-4182

)
www.ecohealthalliance.org

<2020 Research Scientist and Project Manager Job Ad.pdf>

From: Tony Schountz > on behalf of Schountz,Tony <
Sent: Tuesday, September 01, 2020 4:20 PM EDT
To: Aleksei Chmura ecohealthalliance.org>
CC: Schountz,Tony < >; Peter Daszak ecohealthalliance.org>; Hongying Li ecohealthalliance.org>
Subject: Re: Reference for Anna Fagre for EID-Search Research Scientist & Project Manager at EcoHealth Alliance

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Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

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-Aleksei

Aleksei Chmura, PhD
Chief of Staff

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-4182

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

<2020 Research Scientist and Project Manager Job Ad.pdf>

From: Schountz,Tony on behalf of Schountz,Tony
Sent: Tuesday, April 11, 2017 11:28 AM EDT
To: 胡犇 <huben >
Subject: Re: Requesting invitation letter for visa application
Attachment(s): "letter of invitation.doc"

Ben, I have attached a Word file that you can edit with the names and addresses of the four participants. So, just make a copy for each one and use them.

Thank you,

Tony

On Apr 11, 2017, at 3:56 AM, 鏖 $ 妵 <huben > wrote:

Dear Dr.Schountz:

I am a researcher at Wuhan Institute of Virology, Chinese Academy of Sciences. My colleagues and I are studying bat viruses and we have submitted four abstracts to the 2nd International Symposium on Infectious Diseases of Bats which is going to be held in Fort Collins in June.

The title for the 4 abstracts are:

1) SARS coronavirus may have originated from frequent recombination events betwwen SARS-like coronaviruses in a single horseshoe bat habitat (oral)

2) Dampening of STING-dependent IFN production: an implication of virus tolerance in bats? (oral) 镅圛 noticed from the web that this abstract has already been confirmed as oral presentation)

3) Genomic characterization of diverse BatCoV HKU10 and three novel alphacoronaviruses (poster)

4) Genetically diverse filoviruses in Rousettus and Eonycteris spp. bats, China, 2009 and 2015. (poster)

As it is a unique conference specializing on our research area, we are very eager to attend. However, it usually takes at least two months for us to get the US visa due to the complicated procedure of applying for travel permit to Chinese Academy of Sciences and then one month of administrative processing by US embassy. So in order we can make our visit to Colorado in late June, we have to start the process of travel permit and visa application now.

To apply for a travel permit, we are required to submit an invitation letter from the conference organizer. I know for the bat-borne disease meeting, we will know the results of the acceptance of the abstract by May. But it will be late for us to apply for the travel permit and US visa.

Could you please kindly provides four invitation letters to us indicating we will attend the meeting and give presentations? (oral or posters)
It does not matter whether the abstracts will be finally selected as he invitation letters are only for visa application.

We deeply appreciate your understanding and assistance.

Thank you very much!

Best regards

Ben Hu Ph.D

Research Assistant

Wuhan Institute of Virology, CAS

Arthropod-borne and Infectious Diseases Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine and Biomedical Sciences
3185 Rampart Road
Fort Collins, CO 80523-1692

April 11, 2017

Ben Hu, Ph.D
Research Assistant
Wuhan Institute of Virology
Chinese Academy of Sciences
Wuhan 430071, China

Dear Dr. Hu,

On behalf of the selection committee, I am pleased to inform you that your abstract submission, *Genomic characterization of diverse BatCoV HKU10 and three novel alphacoronaviruses*, has been accepted for a presentation at the **2nd International Symposium on the Infectious Diseases of Bats**, to be held at Colorado State University June 29 to July 1, 2017. We invite you to participate and present your findings at the symposium. If you have any questions, please do not hesitate to contact me.

Sincerely,

Tony Schountz, Ph.D.
Associate Professor of Microbiology
Organizing Committee Chair
2nd International Symposium on the Infectious Diseases of Bats
Department of Microbiology, Immunology and Pathology
Colorado State University
Fort Collins, CO 80523 USA

From: Schountz,Tony
Sent: Tuesday, April 11, 2017 8:25 AM EDT
To: 胡犇 <huben >
Subject: Re: Requesting invitation letter for visa application

Hi Ben,

I am happy to provide the letters. Can you help me by providing the names and address(es) of the four individuals? I'm not in my office today so that would be very helpful for me. Something like this for each of you:

Ben Hu, Ph.D
Research Assistant
Wuhan Institute of Virology
Chinese Academy of Science
Xiao Hong Shan No.44,Wu Han,P.R.China.
Postcode:430071

If you provide this information for all four attendees then I can copy and paste them into each of the four letters that I will email to you.

Thanks,

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: 胡犇 <huben >
Sent: Tuesday, April 11, 2017 3:56 AM
To: Schountz,Tony
Subject: Requesting invitation letter for visa application

Dear Dr.Schountz:
I am a researcher at Wuhan Institute of Virology, Chinese Academy of Sciences. My colleagues and I are studying bat viruses and we have submitted four abstracts to the 2nd International Symposium on Infectious Diseases of Bats which is going to be held in Fort Collins in June.
The title for the 4 abstracts are:
1) SARS coronavirus may have originated from frequent recombination events betwwen SARS-like coronaviruses in a single horseshoe bat habitat (oral)
2) Dampening of STING-dependent IFN production: an implication of virus tolerance in bats? (oral) （I noticed from the web that this abstract has already been confirmed as oral presentation)
3) Genomic characterization of diverse BatCoV HKU10 and three novel alphacoronaviruses (poster)
4) Genetically diverse filoviruses in Rousettus and Eonycteris spp. bats, China, 2009 and 2015. (poster)
As it is a unique conference specializing on our research area, we are very eager to attend. However, it usually takes at least two months for us to get the US visa due to the complicated procedure of applying for travel permit to Chinese Academy of Sciences and then one month of administrative processing by US embassy. So in order we can make our visit to Colorado in late June, we have to start the process of travel permit and visa application now.
To apply for a travel permit, we are required to submit an invitation letter from the conference organizer. I know for the bat-borne disease meeting, we will know the results of the acceptance of the abstract by May. But it will be late for us to apply for the travel permit and US visa.
Could you please kindly provides four invitation letters to us indicating we will attend the meeting and give presentations? (oral or posters)
It does not matter whether the abstracts will be finally selected as he invitation letters are only for visa application.
We deeply appreciate your understanding and assistance.
Thank you very much!
Best regards

Ben Hu Ph.D
Research Assistant
Wuhan Institute of Virology, CAS

From: Schountz,Tony > on behalf of Schountz,Tony
Sent: Thursday, June 22, 2017 5:34 PM EDT
To: Kevin Olival, PhD ecohealthalliance.org>
Subject: Re: Sorry, will get u an abstract soon...

Kevin, try to keep it under 350. Tomorrow morning is fine.

Thanks,

Tony

> On Jun 22, 2017, at 12:46 PM, Kevin Olival, PhD @ecohealthalliance.org> wrote:
>
> Word limit? Last possible deadline time??

—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Tony Schountz on behalf of Schountz,Tony
Sent: Wednesday, April 01, 2020 10:34 AM EDT
To: epstein ecohealthalliance.org>
CC: Schountz,Tony >; Ebel,Greg
Subject: Re: still working on bat section
Attachment(s): "C06 Update 2020.docx"

Jon, I've added a few paragraphs. Hopefully, some of them are on target. Feel free to edit/delete/add as you think is best.

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

On Mar 31, 2020, at 11:04 PM, Ebel,Greg wrote:

Hi Jon,

Thanks for the update. I'm working on the part of the document that is the pivot from the original C06 to the new scope. I'm attaching it in draft form in case you're interested in looking at it. Comments are welcome as always.

Greg

From: Jon Epstein ecohealthalliance.org>
Sent: Tuesday, March 31, 2020 11:02 PM
To: Ebel,Greg >; Schountz,Tony >
Subject: still working on bat section

Greg and Tony,
I wasn't able to work on this much tonight. I'll pick it up tomorrow afternoon and will have you something by the end of the day.

I did get a letter of support from Vincent - just waiting for a signed copy.

Cheers,
Jon

--
Jonathan H. Epstein DVM, MPH, PhD
Vice President for Science and Outreach
EcoHealth Alliance
460 West 34th Street, Ste. 1701
New York, NY 10001

)

web: ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

<C06 Update 2020.docx>

Pathogens transmitted by bat and arthropod vectors continue to burden the health of humans around the world. Bat-associated pathogens, such as the currently circulating SARS-CoV-2, ebolaviruses, Nipah virus, rabies virus and others are among the most impactful and dreaded infections known. Malaria is perhaps the most deadly infection in the tropics. West Nile, chikungunya and Zika viruses have emerged as major global pathogens. Tick-transmitted infections such as Lyme disease and Powassan virus continue to emerge in temperate regions. Agents vectored by bat and/or arthropod vectors thus constitute some of the most feared, difficult and persistent problems affecting human health.

Therefore, Colorado State University (CSU) established the Arthropod-borne and Infectious Disease Laboratory (AIDL) in 1984 to counter these emerging threats. One of the many unique aspects of AIDL includes housing one of the only captive breeding colonies of bats for use in infectious disease research, and BSL2 and BSL3 insectaries. The pandemic spread of SARS-CoV-2 highlights the national need for this unique resource, and the central role that CSU now occupies in the ability of the US to study and design countermeasures against emerging viral threats of this type.

Commented [S1]: This seems out of place in the context of bats (before) and SARS-CoV-2 (after).

To support research into emerging diseases, CSU committed $22M in 2019 to construct a new building, the Center for Vector-Borne Infectious Diseases (CVID), to replace aging AIDL infrastructure. CVID construction is ongoing and we anticipate moving in in late 2020.

While CSU's commitment of $22M is laudable, it is insufficient to provide adequate housing for the additional bat colonies needed to address the urgent need for research into the biology and emergence of SARS-CoV-2. Further, additional infrastructure within the CVID is required in order to ensure that research focusing on bat-borne diseases is paired with adequate BSL2 lab, tissue culture and other support space.

This proposal, reviewed highly favorably in 2019 but not selected for funding, represents a unique opportunity to rapidly increase US capacity for housing, breeding and using bats in research. In particular, we propose to:

Current Bat Research at CSU

Colorado State University has a breeding colony of Jamaican fruit bats (*Artibeus jamaicensis*), one of the most common and largest bats in the New World. This colony was established in 2005 with funds from the NIAID Emerging Virus Disease Unit contract (AI25489) after it was determined that SARS-CoV was a bat-borne virus. Currently funded bat projects are to study SARS-CoV (CSU VPR funding), MERS-CoV (AI140442), bat influenza A viruses (AI134768), henipaviruses (DARPA G228-19-W7329) and rabies virus (DOE B634747). Our long-term goal for this colony is to make it the "bat version" of the laboratory mouse so that we can conduct experimental infections for other researchers, or provide bats to those who may need them for experiments at their institutions.

We have determined the species is susceptible to several viruses, including Zika virus (30716104), H18N11 bat influenza A virus (31527796), Middle East respiratory coronavirus (MERS-CoV) (26899616), Cedar henipavirus (unpublished), Tacaribe virus (22379103) and Bukakata virus (unpublished), the last two of which cause fatal diseases in the bats. We have also established primary cell lines from the species that are susceptible to MERS-CoV

(26899616), Zaire ebolavirus (27354372), and Nipah, Hendra and Cedar henipaviruses (unpublished). We have generated a number of reagents, including monoclonal antibodies and recombinant cytokines, virological and immunological methods, large transcriptome data sets (23166587, 28959737), basic physiological parameters (32164795) and we have demonstrated that it can serve as a surrogate bat model organism for the study of bat-borne viruses. Importantly, a genome assembly to 30x coverage is available (NCBI PVKR01).

SARS-CoV Project. We performed an initial susceptibility study of three Jamaican fruit bats and found that all had low levels of viral RNA in oral swabs within a few days after intranasal inoculation. By day 14, all three bats had seroconverted by ELISA to recombinant SARS-CoV-2 nucleoprotein and by day 24 the titers had increased at least 4-fold for each bat. Thus we are confident that we have established a surrogate bat model for the study of SARS-CoV-2 in bats. We currently have 27 bats enrolled in a challenge and transmission study and are performing serial euthanasia to determine virus kinetics, tissue tropism, host response and transmission dynamics.

From: Schountz,Tony on behalf of Schountz,Tony < >
Sent: Wednesday, November 15, 2017 1:13 PM EST
To: Schountz,Tony >
BCC:

Subject: Tenure track position at Wadsworth Center
Attachment(s): "Wadsworth Center Recuitment ad.docx"

Dear colleagues,

Please find attached a new position at the Wadsworth Center that may be relevant to you or your students. Please pass along to anyone who may be interested.

Thanks,

Tony

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine

NEW YORK STATE | Department of Health | Wadsworth Center

Tenure-Track Position at the Wadsworth Center

Host Response to Zoonotic and Vector-borne Diseases

The Wadsworth Center is seeking an outstanding scientist at the Assistant or Associate Professor level to establish a competitive, grant-funded research program in the area of the host response to Vector-Borne Zoonotic Diseases. Areas of particular interest include responses to tick- or mosquito-borne pathogens. The focus may include innate recognition of such pathogens, elucidating the protective mechanisms of the immune response and/or development of novel diagnostics and vaccines. Candidates using a systems biology approach are also encouraged to apply.

The Wadsworth Center located in Albany, NY, is the country's most comprehensive state public health laboratory, with a staff of 700, that includes over 100 doctoral level scientists. The Center provides a dynamic research atmosphere focused on infectious, genetic, and environmental diseases and their impact on human health.

The incumbent will join a vibrant group of research scientists and epidemiologists that participate in the Center's Zoonotic and Vector-borne Diseases research focus area. Established research programs include immune evasion and pathogenesis of Lyme disease *Borreliae*, host and vector factors that determine competence of arboviruses, antibody-mediated protection against infectious agents and population genetics of *Anopheles*. Complementary Wadsworth Center research activities can be found at www.wadsworth.org.

Successful applicants will receive a competitive start-up package and access to the Center's outstanding scientific cores, a BSL2/3 insectary and AAALAC accredited BSL2/3 animal space. Teaching opportunities are available through faculty appointments in the Wadsworth Center Masters of Laboratory Science program and the University at Albany Department of Biomedical Sciences, School of Public Health.

Ph.D. degree or equivalent and relevant postdoctoral research experience required. Applicants should submit their curriculum vitae, research plan and contact information for at least three references to wcphgc@health.ny.gov referencing "Host Response" in the subject line. Applications will be accepted until December 15, 2017. AA/EOE.

From: Schountz,Tony on behalf of Schountz,Tony <
Sent: Tuesday, October 30, 2018 12:11 PM EDT
To: zlshi <zlshi
Subject: Thank you!

Dear Zhengli,

I want to thank you for the invitation to speak at the emerging infectious disease conference. It was a really great experience for me and I was pleased with the talks, posters and how well your team organized and ran the meeting. I hope I can return to the next meeting in two years as I am sure we will have much more data on bats and influenza virus, MERS-CoV and henipaviruses.

I was so struck by the work at the Wuhan Institute of Virology that I spoke briefly to Peng about how your institute and our Arthropod-borne and Infectious Disease Laboratory (AIDL, http://csu-cvmbs.colostate.edu/academics/mip/aidl/Pages/default.aspx) group have so many similarities. I wonder if you might have an interest in forming a loose association between our groups? I don't know how we could manage this, but one feature I envision would be collaboration on relevant projects (e.g., arboviruses and bat-borne viruses) and training of students. So, if you think there might be interest amongst your group, perhaps we can have further discussions about it.

Thank you very much!

Tony
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

From: Schountz,Tony < on behalf of Schountz,Tony
Sent: Monday, July 10, 2017 6:32 PM EDT
To: Jon Epstein ecohealthalliance.org>
Subject: The barn

Hi Jon,

Dick will contact you about the barn. If you don't hear from him by the end of the week, let me know and I'll bug him about it.

Nice to see you last week. Another good meeting, I think. Already on the calendar for 2020!

T.
—
Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University

Budget for Amendment 1 per email from Susan Rogers, 11/25/2019. Includes remainder of Year 1 and 60% of Year 2.

Amendment 1 Budget

	Remainder Yr 1	Yr 2 (60%)	Total
Schountz, Tony		$ 7,491	$ 7,491
Eckley, Miles	$ 5,451		$ 5,451
Schountz fringe		$ 2,142	$ 2,142
Eckley fringe	$ 1,564		$ 1,564
Materials	$ 660		$ 660
Bat Per Diem	$ 8,702	$ 5,880	$ 14,582
Bat Overnight Shipping	$ 1,000		$ 1,000
Hamilton Trip	$ 2,794		$ 2,794
Bozeman		$ 1,496	$ 1,496
Direct Total	**$ 20,172**	**$ 17,009**	**$ 37,181**
F&A	$ 10,489	$ 8,845	$ 19,334
Total	**$ 30,661**	**$ 25,854**	**$ 56,515**

MONTANA STATE UNIVERSITY

Federal Subaward Amendment 1 MSU ID G228-19-W7329

Pass-Through Entity (PTE)	Subrecipient
Name Montana State University Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470	Name Colorado State University Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins, CO 80523-2002 Duns 785979618 Colorado State University
PTE Principal Investigator: **Raina Plowright**	Principal Investigator: **Tony Schountz**
PTE Awarding Agency: **Defense Advanced Research Projects Agency**	PTE Awarding Agency ID: D18AC00031
PTE CFDA 12.910 Research and Technology Development	This subaward is subject to OMB Uniform Guidance PTE FAIN: D18AC00031

Subaward Title: Preventing emergence and spillover of bat pathogens in high-risk global hotspots

Subaward Period of Performance	Authorized Amount	**Subaward ID: G228-19-W7329**
Start **10/01/2018** End **09/30/2020** Incremental Funded Estimate End **09/30/2020**	**78,450.00** Incremental Estimated Total **85,686.09**	1. Cost Sharing is Not Required 2. This award is a Cost Reimbursable agreement 3. Project Reporting is Required (Attachments 4 and 4A)

Amendments to Original Agreement

The parties agree to amend the above referenced agreement as follows.

The Subaward Period of Performance is hereby extended to 09/30/2020.

The total consideration for this project is increased FIFTY-SIX THOUSAND FIVE HUNDRED FIFTEEN dollars AND 00/100 ($56,515.00) in accordance with the Revised Budget to a total of SEVENTY-EIGHT THOUSAND FOUR HUNDRED FIFTY dollars AND 00/100 ($78,450.00). See Attachment 5.

All other terms and conditions of the subaward remain the full force and effect. This amendment will become effective on the date of the last signature, although costs may be accrued prior to that date.

By an Authorized Official of Montana State University	By an Authorized Official of SUBRECIPIENT
Dale Huls Signature 12/16/2019 Date Dale Huls, Assistant Director Office of Sponsored Programs Montana State University OSP Ref W7329-G19-228	Ashley Stahle Signature Digitally signed by Ashley Stahle Date: 2019.12.10 09:08:24 -07'00' 12/10/19 Date Ashley Stahle, Assistant Director, OSP Printed Name and Title

MONTANA STATE UNIVERSITY

Attachment 3
Subaward Amendment 1 Contacts

MSU ID G228-19-W7329

Pass-Through Entity Contacts	Subrecipient Contacts
Institution/Organization ("Pass-through Entity") Name Montana State University Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470	**Institution/Organization ("Subrecipient")** Name Colorado State University Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Duns Number 785979618 Duns Name Colorado State University
Administrative Contact Name Leslie Schmidt Associate Vice President Research Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470 Phone Email subawards@montana.edu	**Administrative Contact** Name Ashley Stahle Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email
Principal Investigator Name Raina Plowright Address Lewis Hall 111 Montana State University PO Box 173610 Bozeman, MT 59717-3610 Phone Email	**Principal Investigator** Name Tony Schountz Address 1692 Campus Delivery Fort Collins,CO 80523-1692 Phone Email
Financial Contact Name Jennifer Hodges Address Montana State University PO Box 173520 Bozeman, MT 59717-3520 Phone Email	**Financial Contact** Name Kim Marrale Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email
Authorized Official Name Dale Huls Assistant Director Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470 Phone Email subawards@montana.edu	**Authorized Official** Name Julie Harvey Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email

MONTANA STATE UNIVERSITY

Attachment 5
Subaward Amendment 1 Budget

MSU ID G228-19-W7329

SUBAWARD EXPENSE BUDGET

COST REIMBURSABLE EXPENSES - NO PAYMENTS IN ADVANCE

	Previous Amount	Amendment Amount	Total
Salaries	10,058.00	12,942.00	23,000.00
Benefits	2,877.00	3,706.00	6,583.00
Sub Awards	0.00	0.00	0.00
Contracted Services	0.00	15,582.00	15,582.00
Supplies	0.00	660.00	660.00
Communication	0.00	0.00	0.00
Foreign Travel	0.00	0.00	0.00
Domestic Travel	1,496.00	4,291.00	5,787.00
Rent	0.00	0.00	0.00
Repair and Maint	0.00	0.00	0.00
Awards	0.00	0.00	0.00
Participant Support	0.00	0.00	0.00
Capital Equipment	0.00	0.00	0.00
Major Renovations	0.00	0.00	0.00
Facilities and Admin	7,504.00	19,334.00	26,838.00
TOTAL	**21,935.00**	**56,515.00**	**78,450.00**

Facilities and Admin (IDC) Basis: MTDC less equip, sub, part supp,awa Rate: 52% Base Amount: 51,612.00

MONTANA STATE UNIVERSITY

Federal Subaward Amendment 2 MSU ID G228-19-W7329

Pass-Through Entity (PTE)	Subrecipient
Name Montana State University Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470	Name Colorado State University Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins, CO 80523-2002 Duns 785979618 Colorado State University
PTE Principal Investigator: Raina Plowright	Principal Investigator: Tony Schountz
PTE Awarding Agency: Defense Advanced Research Projects Agency	PTE Awarding Agency ID: D18AC00031
PTE CFDA 12.910 Research and Technology Development	This subaward is subject to OMB Uniform Guidance PTE FAIN: D18AC00031

Subaward Title: Preventing emergence and spillover of bat pathogens in high-risk global hotspots

Subaward Period of Performance	Authorized Amount	**Subaward ID: G228-19-W7329**
Start **10/01/2018** End **03/31/2021** Incremental Funded Estimate End **03/31/2021**	**95,682.84** Incremental Estimated Total **95,682.84**	1. Cost Sharing is Not Required 2. This award is a Cost Reimbursable agreement 3. Project Reporting is Required (Attachments 4 and 4A)

Amendments to Original Agreement

The parties agree to amend the above referenced agreement as follows.

The Subaward Period of Performance is hereby extended to 03/31/2021.

The total consideration for this project is increased SEVENTEEN THOUSAND TWO HUNDRED THIRTY-TWO DOLLARS dollars AND 84/100 ($17,232.84) in accordance with the Revised Budget to a total of NINETY-FIVE THOUSAND SIX HUNDRED EIGHTY-TWO dollars AND 84/100 ($95,682.84). See Attachment 5.

All other terms and conditions of the subaward remain the full force and effect. This amendment will become effective on the date of the last signature, although costs may be accrued prior to that date.

By an Authorized Official of Montana State University	By an Authorized Official of SUBRECIPIENT
Dale Huls — Signature	Signature
10/8/2020 — Date	10/08/2020 — Date
Dale Huls, Assistant Director Office of Sponsored Programs Montana State University	Liz Grinstead, Senior Research Administrator
OSP Ref W7329-G19-228	Printed Name and Title

MONTANA STATE UNIVERSITY

Attachment 3
Subaward Amendment 2 Contacts

MSU ID G228-19-W7329

Pass-Through Entity Contacts	Subrecipient Contacts
Institution/Organization ("Pass-through Entity") Name Montana State University Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470	**Institution/Organization ("Subrecipient")** Name Colorado State University Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Duns Number 785979618 Duns Name Colorado State University
Administrative Contact Name Leslie Schmidt Associate Vice President Research Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470 Phone Email subawards@montana.edu	**Administrative Contact** Name Liz Grinstead Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email
Principal Investigator Name Raina Plowright Address Lewis Hall 111 Montana State University PO Box 173610 Bozeman, MT 59717-3610 Phone Email	**Principal Investigator** Name Tony Schountz Address 1692 Campus Delivery Fort Collins,CO 80523-1692 Phone Email
Financial Contact Name Jennifer Hodges Address Montana State University PO Box 173520 Bozeman, MT 59717-3520 Phone Email	**Financial Contact** Name Kim Marrale Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email
Authorized Official Name Dale Huls Assistant Director Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470 Phone Email subawards@montana.edu	**Authorized Official** Name Julie Harvey Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email

SUBAWARD EXPENSE BUDGET

COST REIMBURSABLE EXPENSES - NO PAYMENTS IN ADVANCE

	Previous Amount	Amendment Amount	Total
Salaries	23,000.00	1,338.32	24,338.32
Benefits	6,583.00	-337.01	6,245.99
Sub Awards	0.00	0.00	0.00
Contracted Services	15,582.00	0.00	15,582.00
Supplies	660.00	7,543.09	8,203.09
Communication	0.00	0.00	0.00
Foreign Travel	0.00	0.00	0.00
Domestic Travel	5,787.00	2,793.00	8,580.00
Rent	0.00	0.00	0.00
Repair and Maint	0.00	0.00	0.00
Awards	0.00	0.00	0.00
Participant Support	0.00	0.00	0.00
Capital Equipment	0.00	0.00	0.00
Major Renovations	0.00	0.00	0.00
Facilities and Admin	26,838.00	5,895.44	32,733.44
TOTAL	**78,450.00**	**17,232.84**	**95,682.84**

Facilities and Admin (IDC) Basis: MTDC less equip, sub, part supp,awa Rate: 52% Base Amount: 62,949.40

MONTANA STATE UNIVERSITY

Federal Subaward Agreement MSU ID G228-19-W7329

Pass-Through Entity (PTE)	Subrecipient
Name Montana State University Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470	Name Colorado State University Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins, CO 80523-2002 Duns 785979618 Colorado State University
PTE Principal Investigator: Raina Plowright	Principal Investigator: Tony Schountz
PTE Awarding Agency: Defense Advanced Research Projects Agency	PTE Awarding Agency ID: D18AC00031
PTE CFDA 12.910 Research and Technology Development	This subaward is subject to OMB Uniform Guidance PTE FAIN: D18AC00031

Subaward Title: Preventing emergence and spillover of bat pathogens in high-risk global hotspots

Subaward Period of Performance	Authorized Amount	**Subaward ID: G228-19-W7329**
Start **10/01/2018** End **09/30/2019**	**21,935.00**	1. Cost Sharing is Not Required 2. This award is a Cost Reimbursable agreement 3. Project Reporting is Required (Attachments 4 and 4A)

Terms and Conditions

1) PTE hereby awards a cost reimbursable subaward, as described above, to SUBRECIPIENT. The Budget and Scope of Work for this subaward are shown in Attachments 5 and 5A. In its performance of subaward work, SUBRECIPIENT shall be an independent entity and not an employee or agent of PTE.
2) PTE shall reimburse SUBRECIPIENT not more often than monthly for allowable costs.
3) All invoices shall be submitted using SUBRECIPIENT's standard invoice, but at a minimum shall include current and cumulative costs (including cost sharing), subaward number, and certification as to truth and accuracy of the invoice as required in 2 CFR 200.415 . Invoices that do not reference PTE's subaward number shall be returned to SUBRECIPIENT. Invoices and questions concerning invoice receipt or payment should be directed to the appropriate party's Financial Contact, as shown in Attachment 3 and detailed in Attachment 6.
4) A final statement of cumulative costs incurred, including cost sharing, marked "FINAL", must be submitted to PTE's Financial Contact NOT LATER THAN forty-five (45) days after subaward end date. The final statement of costs shall constitute SUBRECIPIENT's final financial report.
5) All payments shall be considered provisional and subject to adjustment within the total estimated cost in the event such adjustment is necessary as a result of an adverse audit finding against the SUBRECIPIENT.
6) PTE reserves the right to reject an invoice, in accordance with 2 CFR 200.305.
7) Matters concerning the technical performance of this subaward should be directed to the appropriate party's Principal Investigator, as shown in Attachment 3.
8) Matters concerning the request or negotiation of any changes in the terms, conditions, or amounts cited in this subaward agreement, and any changes requiring prior approval, should be directed to the appropriate party's Administrative Contact, as shown in Attachment 3. Any such changes made to this subaward agreement require the written approval of each party's Authorized Official, as shown in Attachment 3.
9) Substantive changes (for example, change in Scope of Work, Attachment 5A) made to this subaward agreement require the written approval of each party's Authorized Official as shown in Attachment 3. The PTE may issue non-substantive changes to the Period of Performance Bilaterally.
10) Each party shall be responsible for its negligent acts or omissions and the negligent acts or omissions of its employees, officers, or directors, to the extent allowed by law.
11) Either party may terminate this agreement with thirty (30) days written notice to the appropriate party's Administrative Contact, as shown in Attachment 3. PTE shall pay SUBRECIPIENT for termination costs as allowable under Uniform Guidance, 2 CFR 200, or 45 CFR Part 75 Appendix IX, "Principles for Determining Costs Applicable to Research & Development under Grants and Contracts with Hospitals," if applicable. If the PTE Awarding Agency suspends or terminates the prime award in whole or in part, PTE may suspend or terminate this subaward accordingly.
12) No-cost extensions require the approval of the PTE. Any requests for a no-cost extension should be addressed to and received by the Administrative Contact, as shown in Attachment 3, not less than thirty (30) days prior to the desired effective date of the requested change.
13) The subaward is subject to the terms and conditions of the PTE Award and other special terms and conditions, as identified in Attachment 2.
14) By signing below SUBRECIPIENT makes the certifications and assurances shown in Attachments 1 and 2.

By an Authorized Official of Montana State University		By an Authorized Official of SUBRECIPIENT	
Dale Huls Signature	5/30/2019 Date	Signature Ashley Stahle cn=Ashley Stahle, o=Colorado State University, ou=Sponsored Programs, email=ashley.stahle@colostate.edu, c=US 2019.05.30 15:03:14 -06'00'	Date
Dale Huls, Assistant Director Office of Sponsored Programs Montana State University		Ashley Stahle, Senior Research Administrator Printed Name and Title	
OSP Ref W7329-G19-228			

By signing the Subaward Agreement, the authorized official of SUBRECIPIENT certifies, to the best of his/her knowledge and belief, that:

Certification Regarding Lobbying

1) No Federal appropriated funds have been paid or will be paid, by or on behalf of the SUBRECIPIENT, to any person for influencing or attempting to influence an officer or employee of any agency, a Member of Congress, an officer or employee of Congress, or an employee of a Member of Congress in connection with the awarding of any Federal contract, the making of any Federal grant, the making of any Federal loan, the entering into of any cooperative agreement, and the extension, continuation, renewal, amendment, or modification of any Federal contract, grant, loan, or cooperative agreement.

2) If any funds other than Federal appropriated funds have been paid or will be paid to any person for influencing or intending to influence an officer or employee of any agency, a Member of Congress, an officer or employee of Congress, or an employee of a Member of Congress in connection with this Federal contract, grant, loan, or cooperative agreement, the SUBRECIPIENT shall complete and submit Standard Form -LLL, "Disclosure Form to Report Lobbying," to the PASS-THROUGH ENTITY.

3) The SUBRECIPIENT shall require that the language of this certification be included in the award documents for all subawards at all tiers (including subcontracts, subgrants, and contracts under grants, loans, and cooperative agreements) and that all subrecipients shall certify and disclose accordingly.

This certification is a material representation of fact upon which reliance was placed when this transaction was made or entered into. Submission of this certification is a prerequisite for making or entering into this transaction imposed by section 1352, title 31, U. S. Code. Any person who fails to file the required certification shall be subject to a civil penalty of not less than $10,000 and not more than $100,000 for each such failure.

Debarment, Suspension, and Other Responsibility Matters

SUBRECIPIENT certifies by signing this Subaward Agreement that neither it nor its principals are presently debarred, suspended, proposed for debarment, declared ineligible, or voluntarily excluded from participation in this transaction by any federal department or agency.

Audit and Access to Records

Subrecipient certifies by signing this Subaward Agreement that it complies with the Uniform Guidance, will provide notice of the completion of required audits and any adverse findings which impact this subaward as required by parts 200.501- 200.521, and will provide access to records as required by parts 200.336, 200.337, and 200.201 as applicable.

See Copy of Award Notice Attachment 2A.

Special Terms and Conditions:

1. Copyrights
   SUBRECIPIENT grants to PASS-THROUGH ENTITY (PTE) an irrevocable, royalty-free, nontransferable, non-exclusive right and license to use, reproduce, make derivative works, display, and perform publicly any copyrights or copyrighted material (including any computer software and its documentation and/or databases) first developed and delivered under this Agreement solely for the purpose of and only to the extent required to meet PTE's obligations to the Federal Government under its Prime Award.
2. Data Rights
   SUBRECIPIENT grants to PTE the right to use data created in the performance of this Agreement solely for the purpose of and only to the extent required to meet PTE's obligations to the Federal Government under its Prime Award.
3. Carry Forward
   Carry Forward requests must be sent to PTE's Authorized Official contact, as shown in Attachment 3.

Additional Special Terms: See Copy of Award Notice Attachment 2A.

DEPARTMENT OF THE INTERIOR
Interior Business Center
Acquisition Services Directorate, Division III
354 South Highway 92
Sierra Vista, AZ 85635

Agent for:
Defense Advanced Research Projects Agency (DARPA)

RESEARCH COOPERATIVE AGREEMENT SCHEDULE

1. **Agreement Number**: **D18AC00031**

2. **Recipient Name:** **Montana State University - Bozeman**
307 Montana Hall
Bozeman, MT 59717

3. **Identification Numbers**:

Tax Identification Number (TIN)**: 81-6010045**

Data Universal Numbering System (DUNS) Number**: 625447982**

Commercial and Government Entity (CAGE) Code**: 1KQE9**

Federal Interagency Code for Education (FICE)**: 002532**

Catalog of Federal Domestic Assistance (CFDA): **12.910 – Research and Technology Development**

ASAP Recipient Number: **3034514**

Defense Advanced Research Projects Agency (DARPA) MIPR Number(s)**: HR0011836358**

4. **Principal Investigator/Key Personnel**: Dr. Raina Plowright
111A Lewis Hall
P.O. Box 173520
Bozeman, MT 59717-3520

Telephone:
E-mail address:

5. **Statement of Work:** The research to be accomplished is identified in the Recipient's Statement of Work and is incorporated in full text as part of this agreement. The revised budget proposal entitled "Preventing emergence and spillover of bat pathogens in high-risk global hotspots" dated 07/18/2018 and revised technical proposal dated 07/17/2018, submitted in response to Broad Agency Announcement DARPA-BAA- HR001118S0017 are incorporated by reference herein.

6. Points of Contact:

a. Agreements Officer:

Department of the Interior
Interior Business Center
Acquisition Services Directorate, Division III
354 South Highway 92
Sierra Vista, AZ 85635

Attention: Doreen Vieira-Cross
Telephone:
FAX:
Email:

b. Cooperative Agreement Administrator:

Department of the Interior
Interior Business Center
Acquisition Services Directorate, Division III
354 South Highway 92
Sierra Vista, AZ 85635

Attention: Deborah Branham
Telephone:
FAX:
Email:

c. Agreements Officer's Representative:

J. Aura Gimm
Air Force Office of Scientific Research
875 N. Randolph Street
Arlington, VA 22203

Telephone:
Email:

d. DARPA Program Manager (PM):

Defense Sciences Office (BTO)
675 N. Randolph Street
Arlington, VA 22203-2114

Attention: Dr. James L. Gimlett
Telephone:
Email:

e. DARPA DSO Assistant Director, Program Management (ADPM)

Attention: Kristen Fuller
Email:

7. Delegation of Administrative Duties: Department of the Interior/Interior Business Center (DOI/IBC) and the Office of Naval Research (ONR). See Article 17 of Exhibit A for the administration duties delegated to ONR. The cognizant ONR office that will perform the delegated duties is identified below:

Office of Naval Research
300 Fifth Ave, Suite 710
Seattle, WA 98104-2398

Phone:
Email:

8. **Period of Performance Profile:**

a.	**Base Phase I (24 Months):**	**(10/01/2018 through 09/30/2020)**	**$6,296,068.00**
b.	**Optional Phase II (18 Months):**	**(10/01/2020 through 03/31/2022)**	**$1,943,433.00 (If funded)**
c.	**Total Award Amount:**		**$8,239,511.00**

9. **Funding:** The following funds are allotted to this cooperative agreement.

FY2018/2019:	$2,719,770.00 (MIPR# HR0011836358)
Total:	$2,719,770.00

10. **Appropriation Data:** Pursuant to this action:

MIPR# HR0011836358 $2,719,770.00
Account Assignment: K G/L Account: 6100.411C0
Business Area: D000 Commitment Item: 411C00
Cost Center: DS68694000 Functional Area:
DNPAQ0000.000000 Fund: XXXD4529NP Fund Center:
DS68694000 Project/WBS: DR.F3BN8.DPBX6358 PR Acct
Assign: 01

11. **Terms and Conditions:** This cooperative agreement is subject to General Terms and Conditions for Cooperative Agreements set forth in the attached Exhibit A and to any Special Terms and Conditions contained in Item 17 of this Research Cooperative Agreement Schedule.

12. **Acceptance of Cooperative Agreement:** Acceptance of this cooperative agreement is pursuant to Article 14 of Exhibit A. The Recipient is not required to countersign the Cooperative Agreement document; however, the Recipient agrees to the conditions specified in the Research Cooperative Agreement Schedule and the Articles herein unless notice of disagreement is furnished to the Agreements Officer within 15 calendar days after the date of the Agreements Officer's signature. In case of disagreement, the Recipient shall not assess the Cooperative Agreement of any costs of the research unless and until such disagreement(s) is/are resolved.

13. **Payments:** Payments will be made in accordance with Article 3 of Exhibit A.

14. **Reporting Requirements:** A final DD Form 882 is required to be filed listing all subject inventions or stating that there were none. In accordance with DARPA-BAA-HR001118S0017, the frequency of the reporting requirement differs from those commonly found in financial assistance agreements due to significant Government involvement throughout the duration of the research cycle. The following reports shall be submitted and will become due on the dates as shown below:

REPORT TYPE	DUE DATE	SUBMIT TO
Quarterly R&D Status Reports	Within 30 days of the end of each quarter	See Exhibit A Attachment 1
Monthly Financial Management Report	Within 30 days of the end of each month	See Exhibit A Attachment 2
Special Technical Report	Due as required	AOR, AO, PM, & DARPA Research Services
Annual Federal Financial Report (SF 425)	29 Dec 2019 29 Dec 2020	AOR, AO, PM, ONR & DARPA Research Services
Final Technical Report	29 Dec 2020	AOR, AO, PM, ONR, DTIC*, & DARPA Research Services
Final Financial Report (SF425)	29 Dec 2020	AOR, AO, PM, ONR, DTIC*, & DARPA Research Services
Final Invention Report (DD Form 882)	28 Jan 2021	See Exhibit A Article 8 - Intellectual Property Matters

*Defense Technical Information Center
ATTN: DTIC-O
8725 John J. Kingman Road
Ft. Belvoir, VA 22060-6218

If Optional Phase II is implemented - The following reports shall be submitted and will become due on the dates as shown below:

REPORT TYPE	DUE DATE	SUBMIT TO
Quarterly R&D Status Reports	Within 30 days of the end of each quarter	See Exhibit A Attachment 1
Monthly Financial Management Report	Within 30 days of the end of each month	See Exhibit A Attachment 2
Special Technical Reports	Due as required	AOR, AO, PM, & DARPA Research Services
Annual Federal Financial Report (SF 425)	29 Dec 2021	AOR, AO, PM, ONR, & DARPA Research Services
Final Technical Report	29 JUN 2022	AOR, AO, PM, ONR, DTIC*, & DARPA Research Services
Final Financial Report (SF425)	29 JUN 2022	AOR, AO, PM, ONR, DTIC*, & DARPA Research Services
Final Invention Report (DD Form 882)	29 JUL 2022	See Exhibit A Article 8 - Intellectual Property Matters

*Defense Technical Information Center
ATTN: DTIC-O
8725 John J. Kingman Road
Ft. Belvoir, VA 22060-6218

15. **Substantial Involvement:** Substantial involvement is expected between the U. S. Government and the Recipient when carrying out the activity contemplated in this Agreement.

    Substantial Government involvement will include:

    a. DARPA review and approval required after completion of one phase of the project to move on to the next phase

b. DARPA monitoring of the work with the potential of redirecting work because of interrelationships with other projects
c. DARPA review and collaboration in the development of research and analyses protocols necessary to complete the work

16. Funding Increments and Options: The Government's obligation to provide funding for increments and/or options is pursuant to Article 16 of Exhibit A.

17. Special Terms and Conditions:

a. Assurance by University to adhere to the Defense Advanced Research Agency's (DARPA) policy and communication on Dual Use of Research Concerns (DURC).

i. Definitions:

1. "Dual use research" is research conducted for legitimate purposes that generates knowledge, information, technologies, and/or products that can be utilized for benevolent or harmful purposes.
2. "Dual use research of concern," or "DURC," is life sciences research that, based on current understanding, can be reasonably anticipated to provide knowledge, information, products, or technologies that could be directly misapplied to pose a significant threat with broad potential consequences to public health and safety, agricultural crops and other plants, animals, the environment, materiel, or national security.

ii. DURC Policy: Any data with potential dual use of research concerns emerging from DARPA funded research shall be evaluated by the team, communicated to DARPA, and submitted for evaluation by team's Institutional Review Entity (IRE). If the IRE and DARPA determine that results or information obtained during the course of funded effort could be considered DURC, the IRE and DARPA will jointly determine an acceptable risk mitigation plan including a responsible publication strategy to determine appropriate venues and content that can and should be released to the public.

iii. Reporting Process: The principal investigator (PI) shall collect information about team's activities (including experiments, data collection, and data processing) on any emergent issues of relevance to DURC and GOF, and send a brief monthly report to DARPA (including negative responses). Within 15 days of a notification of a potential DURC issue the PI shall submit the findings to team's Institutional Review Entity (IRE). If the IRE determines that the findings in question are not of concern, the reported findings are not subject to additional review or oversight, but future activities must continue to be assessed by the PI in monthly reports. If IRE determines the findings could be considered DURC, the PI shall notify DARPA within 10 days of IRE's assessment along with a copy of the assessment.

b. This research **DOES NOT** require the use of Human Subjects.
c. This research **DOES** require the use of Animal Subjects. See Article 15 of Exhibit A. **No animal studies may be conducted using funds from this award until Institutional Animal Care and Use Committee (IACUC) and DARPA second level review approvals are received.**

IACUC Protocol #: Pending Approval — Expiration Date: Pending Approval
Second-level Review #: Pending Approval — Renewal due date: Pending Approval

d. This research **DOES NOT** have restricted data rights.

THIS ACTION IS MADE ON BEHALF OF A DoD CUSTOMER UTILIZING DoD FUNDS.

UNITED STATES OF AMERICA
Department of the Interior, Interior Business Center
Acquisition Services Directorate, Division III

DOREEN VIEIRA-CROSS
Digitally signed by DOREEN VIEIRA-CROSS
Date: 2018.09.21 15:32:40 -07'00'

Doreen Vieira-Cross
Agreements Officer

Exhibit A: General Terms and Conditions
Attachment 1: Quarterly Status Report Template
Attachment 2: Monthly Financial Detail Spreadsheet Example
Attachment 3: Revised Statement of Work, dated 17 Jul 2018

EXHIBIT A

JULY 2018
DARPA AGENCY SPECIFIC TERMS AND CONDITIONS

This award is subject to the DoD Research and Development (R&D) general terms and conditions, which can be found at https://www.onr.navy.mil/Contracts-Grants/submit-proposal/grants-proposal/grants-terms-conditions.aspx under the header "DoD Research and Development General Terms and Conditions," dated July, 2018 and are incorporated herein. The DARPA Agency Specific Terms and Conditions supplement the DoD Research and Development general terms and conditions. This document addresses agency-specific concerns in addition to the above referenced regulations. Award recipients (hereafter, recipient) are accountable for all applicable statutory and regulatory requirements that govern these awards, even if not specifically listed in this document or documents referenced herein.

ORDER OF PRECEDENCE

Any inconsistencies in the requirements of this award shall be resolved in the following order:

- Federal statutes
- Federal regulations
- 2 CFR part 200, as modified and supplemented by DoD's interim implementation found in 2 CFR part 1103
- Award-specific terms and conditions (DARPA Agency Specific terms and conditions)
- DoD Research and Development general terms and conditions

In case of disagreement with any requirements of this award, the Recipient shall contact the Agreements Officer listed in the award document in order to resolve the issue. The Recipient shall not assess any costs to the award or accept any payments until the issue is resolved.

1. Research Responsibility
2. Amendment of Cooperative Agreement
3. Payments
4. Prior Approvals
5. Reports
6. Public Release or Dissemination of Information
7. Acknowledgment of Sponsorship
8. Intellectual Property Matters
9. Activities Abroad
10. Security
11. Research Involving Recombinant DNA Molecules
12. Restrictions on Printing
13. Prohibition on Awarding to Entities that Require Certain Internal Confidentiality Agreements
14. Acceptance and Amendment of Cooperative Agreement
15. Live Organisms – Human and Animal Subjects
16. Funding Increments and/or Options
17. Delegation of Administrative Duties
18. Rights in Technical Data, Computer Software, and Copyright
19. Changes in Performance Period

1) Research Responsibility:

a) The Recipient has full responsibility for the conduct of the research activity supported by this Cooperative Agreement, in accordance with the Recipient's proposal, and the terms and conditions specified in this Cooperative Agreement. Recipients are encouraged to suggest or propose to discontinue or modify unpromising lines of investigation or to explore interesting leads which may appear during the development of the research. However, they must consult the Agreement Officer's Representative (AOR) through the Agreement Officer (AO) before significantly deviating from the objectives or overall program of the research originally proposed.

b) The Recipient shall immediately notify the Agreement Officer of developments that have a significant impact on the award-supported activities. Also, notification shall be given in the case of problems, delays, or adverse conditions which materially impair the ability to meet the objectives of the award. This notification shall include a statement of the action taken or contemplated, and any assistance needed to resolve the situation.

2) **Amendment of Cooperative Agreement:** The only method by which this Cooperative Agreement can be amended is by a formal, written amendment signed by the Agreements Officer. No other communications, whether oral or in writing, shall modify this Cooperative Agreement.

3) **Payments**:

a) Requests for payment for this effort shall be submitted through the Department of the Treasury's Automated Standard Application Payments System (ASAP). Once the Government has submitted a completed ASAP Participation Request forms to ASAP, Recipient will receive an e-mail with further instructions from ASAP.

The recipient organization can use on-line process to request payments. Payment requests are approved or rejected automatically unless placed on review or based on the amount of available funds in the ASAP account. The available balance for an ASAP account is displayed when initiating the payment request. Recipient organizations will receive immediate notification of approval or rejection for all on-line payment requests with the exception of those subject to review. The timing and amount of cash advances shall be as close as is administratively feasible to the Recipient's actual disbursements for direct program costs and the proportionate share of any allowable indirect costs.

b) The Recipient may be paid in advance, provided they comply with the requirements of 2CFR 200.305(b)(1).

c) Reimbursement is the preferred method when the requirements for advance payment cannot be met.

d) Liquidation. The Recipient shall liquidate all obligations incurred under the Cooperative Agreement no later than 90 days after the date of completion. The Recipient shall promptly refund any balances of unobligated cash that the Government has advanced or paid and that is not authorized to be retained by the Recipient for use in other projects. The Agreements Officer is authorized to make a settlement for any upward or downward adjustments to the Federal share of costs after closeout reports are received.

4) **Prior Approvals:** In addition to the prior approvals required by the DoD R&D general terms and conditions, prior written approval is required for the following actions:

The subaward, transfer, or contracting out of any work under this award, unless described in the Recipient's proposal and specifically approved and funded in the Cooperative Agreement Schedule. The Recipient's request for approval shall include the following supporting data:

(i) Basis for contractor selection;
(ii) Justification for lack of competition when competitive bids or offers are not obtained;
(iii) Basis for award cost or price, to include price or cost analysis performed by the Recipient; and
(iv) Approval of the AOR.

5) **Reports**: Reports shall be furnished as specified in the Cooperative Agreement. Report types & descriptions include:

a) Report Types

1) *Quarterly R&D Status Report* - This report is due within 30 calendar days of the end of the previous quarter and shall keep the Government informed of Recipient activity and progress toward accomplishment of Cooperative Agreement objectives and advancement in state-of-the-art on the research and development involved.

2) *Phase Completion Report* - This report is due within 30 calendar days of the end of each phase describing the progress made on the specific milestones as laid out in the SOW.

3) *Monthly Financial Management Report* - This report is due as specified in the Cooperative Agreement and shall be monthly expenditure report that documents cumulative spending and provides a schedule of tasks and events for each report period, with financial expenditures broken down by task.

4) *Annual Technical Report* - This report is due as specified in the Cooperative Agreement, shall document the results of the complete effort. It shall contain brief information on each of the following:

1. A comparison of actual accomplishments with the goals and objectives established for the Cooperative Agreement, the findings of the investigator, or both.
2. Reasons why established goals were not met, if appropriate.
3. Other pertinent information

5) *Special Technical Report* - This report, due as required, shall document the results of a significant task, test, event or symposium.

6) *Final Technical Report* - This report, due 90 days after expiration or termination of the Cooperative Agreement, shall document the results of the complete effort. It shall contain brief information on each of the following:

a) A comparison of actual accomplishments with the goals and objectives established for the Cooperative Agreement, the findings of the investigator, or both.

b) Reasons why established goals were not met, if appropriate.

c) Other pertinent information.

7) *Financial Status Repor*t- shall be submitted on a Standard Form 425 "Federal Financial Report (FFR)" as follows.

a) Interim Status Report – This report is due within 90 days of the end of the interim reporting period (annually). The report shall be on a cash or accrual basis, depending on how the Recipient's accounting records are normally kept.

b) Final Financial Status Report - This report is due 90 days after completion of the Cooperative Agreement. The report shall be on a cash or accrual basis, depending on how the Recipient's accounting records are normally kept.

8) *Report of Federal Cash Transactions [applicable only to advance payment Cooperative Agreements]* – This report, due 15 days following the end of each quarter, shall be submitted on a Standard Form 425. The Recipient shall provide forecasts of Federal cash requirements in the "Remarks" section of the report.

6) Public Release or Dissemination of Information:

a) At this time, DARPA expects the work performed under this Cooperative Agreement to be fundamental research, and it is, therefore, not subject to publication restrictions. Papers resulting from unclassified contracted fundamental research are exempt from prepublication controls and requirements, pursuant to DoD Instruction 5230.27 dated October 6, 1987.

b) All papers resulting from this Cooperative Agreement will include the following

distribution statement: "Approved for public release; distribution is unlimited."

c) Should the character of the research change during Cooperative Agreement performance so that the research is no longer considered fundamental, the Cooperative Agreement will be modified to impose the restrictions on public release and dissemination of information that apply to those research efforts that are not considered fundamental research.

7) Acknowledgment of Sponsorship:

a) The Recipient agrees that in the release of information relating to this Cooperative Agreement, such release shall include a statement to the effect that (1) the project or effort depicted was or is sponsored by the Defense Advanced Research Projects Agency, (2) the content of the information does not necessarily reflect the position or the policy of the Government, and (3) no official endorsement should be inferred.

b) For the purpose of this article, information includes news releases, articles, manuscripts, brochures, advertisements, still and motion pictures, speeches, trade association proceedings, symposia, etc.

c) Nothing in the foregoing shall affect compliance with the requirements of the clause entitled "Security."

8) Intellectual Property Matters: Questions regarding intellectual property matters should be referred to the Agreements Officer (AO). All patent reports (interim and final) shall be submitted using the i-Edison.gov reporting website (http://s-edison.info.nih.gov/iEdison). In the event the Recipient is unable to submit reports through i-Edison, the Recipient may utilize DD Form 882, Report of Inventions and Subcontracts, for submission of interim and final invention reports. The DD Form 882 and all invention disclosures shall be submitted to the AO for proper disposition no later than 120 days after the end of the period of performance.

9) Activities Abroad: The Recipient shall assure that project activities carried on outside the United States are coordinated as necessary with appropriate Government authorities and that appropriate licenses, permits, or approvals are obtained prior to undertaking proposed activities. The awarding agency does not assume responsibility for Recipient compliance with the laws and regulations of the country in which the activities are to be conducted.

10) Security: The Recipient may not be granted access to classified information under this Cooperative Agreement. If security restrictions should happen to apply to certain aspects of the proposed research, the Recipient will be so informed. In the event that the scientific work under this Cooperative Agreement may need classification, or involve access to or storage of any classified data, the Government shall make its decision on the need to classify, or require such access or storage, within 30 days after receipt of written notice from the Recipient. If the decision is affirmative, the Government shall invoke the clause in reference to the "Termination"

proceedings in the DoD R&D general terms and conditions.

11) Research Involving Recombinant DNA Molecules: Any Recipient performing research involving recombinant DNA molecules and/or organisms and viruses containing recombinant DNA molecules agrees, by acceptance of this award, to comply with the National Institutes of Health "Guidelines for Research Involving Recombinant DNA Molecules," July 5, 1994 (59 FR 34496) as amended, or such later revision of those guidelines as may be published in the Federal Register.

12) Restrictions on Printing: Unless otherwise authorized in writing by the AO, reports, data, or other written material produced using funds provided by this Cooperative Agreement and submitted hereunder shall be reproduced only by duplicating processes and shall not exceed 5,000 single page reports or a total of 25,000 pages of a multiple page report. These restrictions do not preclude the writing, editing, and preparation of manuscript or reproducible copy of related illustrative materials if required as a part of this Cooperative Agreement, or incidental printing such as forms or materials necessary to be used by the Recipient to respond to the terms of the Cooperative Agreement. To satisfy the requirements of the Defense Technical Information Center, at least one copy of each technical report submitted to the Defense Technical Information Center must be black typing or reproduction of black on white paper or suitable for reproduction by photographic techniques. Reprints of published technical articles are not within the scope of this paragraph.

In accordance with Executive Order 12873, dated October 20, 1993, as amended by Executive Order 12995, dated March 25, 1996, the Recipient is encouraged to submit paper documents, such as letters or reports, that are printed/copied double-sided on recycled paper that has at least 30 percent postconsumer material.

13) Prohibition on Awarding to Entities that Require Certain Internal Confidentiality Agreements:

a) The Recipient shall not require employees, contractors, or subrecipients seeking to report fraud, waste, or abuse to sign or comply with internal confidentiality agreements or statements prohibiting or otherwise restricting such employees or contractors from lawfully reporting such waste, fraud, or abuse to a designated investigative or law enforcement representative of a Federal department or agency authorized to receive such information.

b) The Recipient must notify its employees, contractors, or subrecipients that the prohibitions and restrictions of any internal confidentiality agreements inconsistent with paragraph (a) of this award provision are no longer in effect.

c) The prohibition in paragraph (a) of this award provision does not contravene requirements applicable to any form issued by a Federal department or agency governing the nondisclosure of classified information.

d) If the Government determines that the Recipient is not in compliance with this award provision, it:

1) Will prohibit the Recipient's use of any funds under this award, in accordance with Federal appropriations law; and

2) May pursue other remedies available for the Recipient's material failure to comply with award terms and conditions.

14) Acceptance and Amendment of Cooperative Agreement:

1) The only method by which this Cooperative Agreement can be amended is by a formal, written amendment signed by the Agreements Officer. No other communications, whether oral or in writing, are valid.

2) The Recipient is not required to countersign the Cooperative Agreement document; however, the Recipient agrees to the conditions specified in the Research Cooperative Agreement Schedule and the Articles herein unless notice of disagreement is furnished to the Agreements Officer within 15 calendar days after the date of the Agreements Officer's signature.

In case of disagreement, the Recipient shall not assess the Cooperative Agreement of any costs of the research unless and until such disagreement(s) is/are resolved.

15) Live Organisms – Human and Animal Subjects:

a) Human Subjects. Cooperative Agreement funds may NOT be used for research that uses uninformed or nonvoluntary humans as experimental subjects. The Recipient is responsible for the protection of the rights and welfare of any human subjects involved in research, development, and related activities supported by this Cooperative Agreement. The Recipient agrees to comply with the Common Federal Policy for the Protection of Human Subjects, codified by the Department of Health and Human Services at 45 CFR part 46 implemented by the Department of Defense at 32 CFR part 219.

Department of the Interior/Interior Business Center (DOI/IBC) collaborates with the Institutional Review Board (IRB) and the U. S. Army Medical Research and Materiel Command (USAMRMC) for DARPA's Second-Level review. No work can be performed on human subjects without a Second-Level review and approval.

b) Animal Welfare. The Recipient shall register its research, development, test, and evaluation or training facility with the Secretary of Agriculture in accordance with 7 U.S.C. 2136 and 9 CFR subpart C, and section 2.30, unless otherwise exempt from this requirement by meeting the conditions in 7 U.S.C. 2136 and 9 CFR parts 1 through 4 for the duration of the activity. The Contractor shall have its proposed animal use approved in accordance with Department of Defense Instruction (DoDI) 3216.01, Use of Animals in DoD Programs, by a DoD Component Headquarters Oversight Office. The Contractor shall furnish evidence of such registration and approval to the Contracting Officer before beginning work under this agreement."

DOI/IBC collaborates with Institutional Animal Care and Use Committee (IACUC) for DARPA's Second-Level review. No work can be performed on animal subjects without a Second-Level review and approval.

The Recipient shall make its animals, and all premises, facilities, vehicles, equipment, and records that support animal care available during business hours and at other times mutually agreeable to the Contractor and the United States Department of Agriculture Office of Animal and Plant Health Inspection Service (USDA/APHIS) representative, personnel representing the DoD component oversight offices, as well as the Contracting Officer, to ascertain that the Contractor is compliant with 7 U.S.C. 2131-2159 and 9 CFR parts 1 through 4.

(1) The Recipient shall acquire animals in accordance with DoDI 3216.01, current at time of award (http://www.dtic.mil/whs/directives/corres/pdf/321601p.pdf).

(2) The Recipient agrees that the care and use of animals will conform with the pertinent laws of the United States, regulations of the Department of Agriculture, and policies and procedures of the Department of Defense (see 7 U.S.C. 2131 et seq., and 9 CFR subchapter A, parts 1 through 4, DoDI 3216.01, Army Regulation 40-33/ SECNAVINST 3900.38C/AFMAN 40-401(I)/DARPAINST 18/USUHSINST 3203). The Contractor shall also comply with DoDI 1322.24, Medical Readiness Training, if this contract includes acquisition of training.

(3) The Agreements Officer may immediately suspend, in whole or in part, work and further payments under this contract for failure to comply with the requirements of paragraphs (a) through (c) of this clause.

(1) The suspension will stay in effect until the Recipient complies with the requirements.

(2) Failure to complete corrective action within the time specified by the Contracting Officer may result in termination of this contract and, if applicable, removal of the Contractor's name from the approved vendor list for live animals used in medical training.

The recipient may request registration of its facility by contacting USDA/APHIS/AC, 4700 River Road, Unit 84, Riverdale, MD 20737-1234, or via the APHIS Animal Care website at: http://www.aphis.usda.gov/wps/portal/aphis/ourfocus/animalwelfare.

The Recipient shall include the substance of this clause, including this paragraph in all subcontracts involving research, development, test, and evaluation or training that use live vertebrate animals.

c) In the event a revised technical proposal with human or animal subject research is incorporated under this Cooperative Agreement, Recipient shall obtain all reviews and approvals prior to beginning any testing on humans or animals.

d) This article shall be flowed down to subcontractors, suitably modified to ensure that the recipient fully complies with this article.

16) Funding Increments and/or Options: The Recipient is advised that the Government's obligation to provide funding for funding increments and/or options included in the Cooperative Agreement is contingent upon (i) satisfactory performance and (ii) the availability of funds. Accordingly, no legal liability on the part of the Government exists unless or until (i) funds are made available to the Government and notice of such availability is confirmed in writing to the Recipient and (ii) performance of the research is deemed satisfactory in the judgment of the Agreements Officer.

17) Delegation of Administrative Duties: The administrative duties listed below have been delegated to the Office of Naval Research (ONR) identified in Item 7 of the Cooperative Agreement Schedule:

a) During performance:

1) Perform government furnished property administration.

2) Receive interim technical, cost/financial and patent reports from Recipient.

3) Review and adjudicate audit findings after receipt of the audit report and ensure that the recipient takes appropriate and timely corrective action, if required.

b) Upon expiration of agreement:

1) Receive final technical, cost/financial and patent reports from Recipient.

2) Obtain final government property report. Perform plant clearance, if required.

3) Assist the awarding Agreements Officer in resolving any questioned costs. Order audit from Department of Health and Human Services (DHHS), if applicable.

4) Perform cost sharing adjustments, if applicable.

5) Assure that all refunds due the Government are received.

6) Complete and submit to the awarding Agreements Officer a Completion Statement for this award.

18) Rights in Technical Data, Computer Software, and Copyright:

(a) Technical Data and Computer Software. Rights are as specified in 2CFR 200.315(d).

(b) Copyright. Rights are as specified in 2CFR 200.315(b).

19) Changes in Performance Period:

Recipient may initiate a one-time extension of the period of performance by up to 12 months unless one or more of the conditions outlined in subparagraphs a.-c. below apply. For one-time extensions, the Recipient must notify the Federal awarding agency in writing with the supporting reasons and revised period of performance at least 30 calendar days before the end of the period of performance specified in the award. This one-time extension may not be exercised merely for the purpose of using unobligated balances.

Extensions require explicit prior Federal awarding agency approval when:

a) The terms and conditions of the award prohibit the extension.

b) The extension requires additional Federal funds.

c) The extension involves any change in the approved objectives or scope of the project.

Montana State University - Bozeman
PREEMPT Program – Cooperative Agreement D18AC00031
Quarterly R&D Status Report

Period Covered by the Report: [Date] through [Date]

Date of Report:

Project Title: Preventing emergence and spillover of bat pathogens in high-risk global hotspots
Total Dollar Value: $8,239,511.00
Program Manager: Dr. James Gimlett, DARPA

Submitted by:
[PI Name]
[Institution]
[Address]

Telephone:
Email:

Subcontractors: [Co-PI name(s) and institution(s)]

TABLE OF CONTENTS

General notes:

- **Contact the program manager and team to report any financial or technical issues** (i.e., please do not wait until a report is due to bring up major issues).
- Clearly indicate if funding from another federal agency (e.g., NIH) has been used to support any data presented.
- Clearly indicate if any content is pre-publication sensitive or proprietary.
- Delete all instructional text from this document before submitting your report.
- Support your claims with data, images, and other evidence.
- Please update the header of each report with the respective quarterly period.
- Please use the following naming convention for report filenames: QR – PI institution – period covered (e.g., QR – University of XYZ – 01OCT2018 to 31DEC2018).
- Quarterly reports are due within 30 days of the quarter end date. For example, if the period ends on March 31, the report must be submitted by April 30.
- Monthly progress updates via conference calls will be scheduled with the program manager and his team.

Definitions:

- **Functional block diagram:** describes the functions and interrelationships of a system in a flock-block diagram style so that one can easily and thoroughly understand the system and the relationship of each of the parts to the whole. If the hardware evolves throughout your project, please provide a block diagram for each evolution (example included).
- **Work Breakdown Structure (WBS):** a hierarchical and incremental decomposition of the project into phases, deliverables and work packages. It is a tree structure that shows the subdivision of effort required to achieve an objective (example included).
- **Deliverable:** a measurable and verifiable outcome or object that a project team must create and deliver according to the terms of an agreement. An intangible deliverable is a particular outcome that the team achieves. A tangible deliverable is a concrete or material object created by the team.
- **Milestone:** a milestone describes the status of the project as represented by an event or moment at which one or more project activities are complete. Milestones can represent the completion of key project tasks, conclusions reached, or questions answered that affect project schedule significantly.
- **Major finding:** data with significant impact (positive or negative).
- **Metrics update:** progress (including delays and issues) toward achieving pre-established metrics of success.
- **SETA:** Science, Engineering, and Technical Assistant (internal DARPA term for technical support staff).

1 Progress Summary

1.1 Major Findings

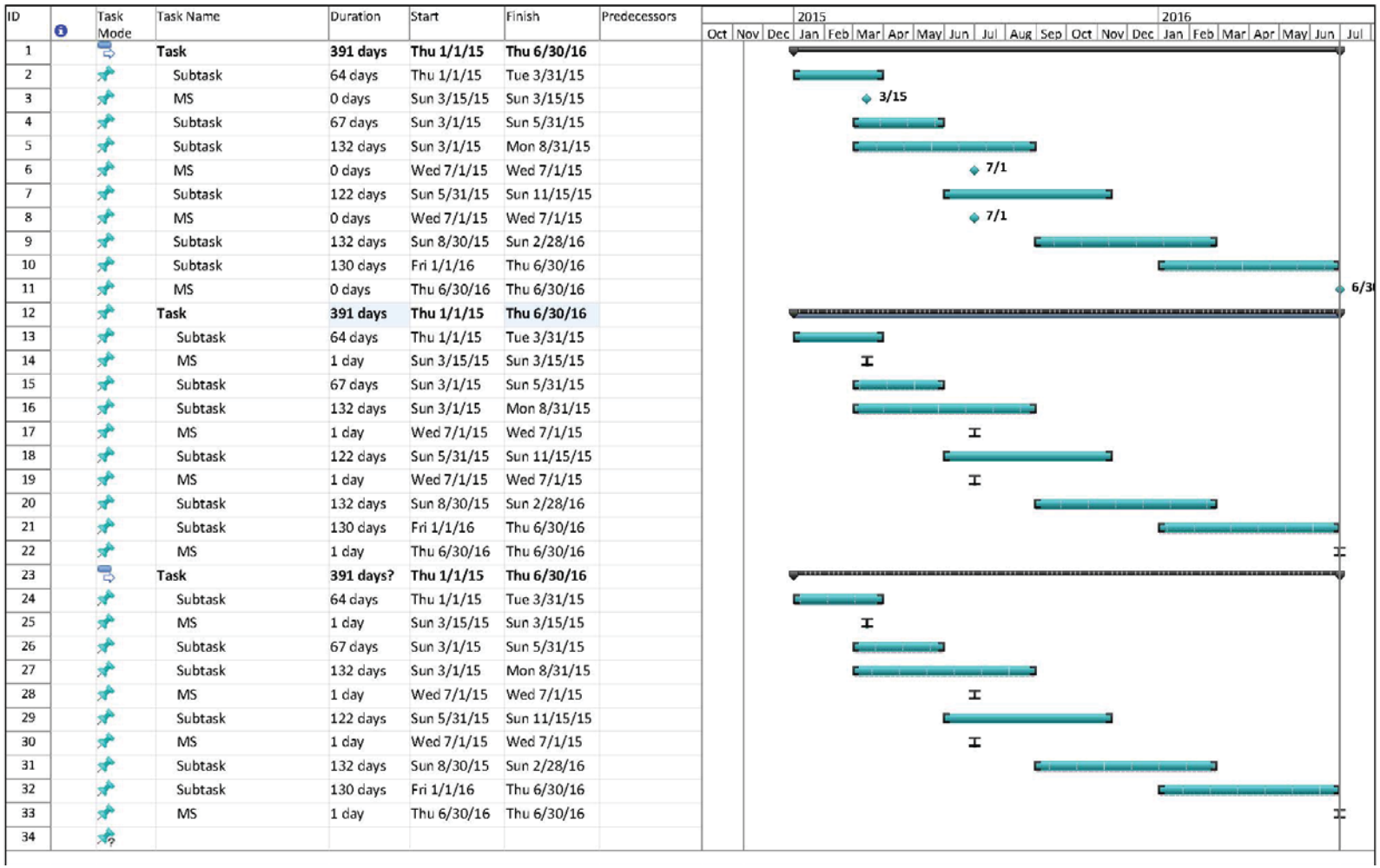
Briefly describe the most significant and salient accomplishment(s) achieved during the ***most recent quarter***. How has this compared to the original project plan?

1.2 Metrics Update

Accomplishment *Include associated task #*	**Month** *Planned vs. achieved*	**Update** *Provide current status, explain any schedule discrepancies, list next steps*

2 Schedule – Milestones and Deliverables

Provide a high-level Gantt chart for Phase I that includes all milestones and deliverables for each task. An example of an acceptable chart is shown below.



ID	Task Mode	Task Name	Duration	Start	Finish	Predecessors
1		**Task**	**391 days**	**Thu 1/1/15**	**Thu 6/30/16**	
2		Subtask	64 days	Thu 1/1/15	Tue 3/31/15	
3		MS	0 days	Sun 3/15/15	Sun 3/15/15	
4		Subtask	67 days	Sun 3/1/15	Sun 5/31/15	
5		Subtask	132 days	Sun 3/1/15	Mon 8/31/15	
6		MS	0 days	Wed 7/1/15	Wed 7/1/15	
7		Subtask	122 days	Sun 5/31/15	Sun 11/15/15	
8		MS	0 days	Wed 7/1/15	Wed 7/1/15	
9		Subtask	132 days	Sun 8/30/15	Sun 2/28/16	
10		Subtask	130 days	Fri 1/1/16	Thu 6/30/16	
11		MS	0 days	Thu 6/30/16	Thu 6/30/16	
12		**Task**	**391 days**	**Thu 1/1/15**	**Thu 6/30/16**	
13		Subtask	64 days	Thu 1/1/15	Tue 3/31/15	
14		MS	1 day	Sun 3/15/15	Sun 3/15/15	
15		Subtask	67 days	Sun 3/1/15	Sun 5/31/15	
16		Subtask	132 days	Sun 3/1/15	Mon 8/31/15	
17		MS	1 day	Wed 7/1/15	Wed 7/1/15	
18		Subtask	122 days	Sun 5/31/15	Sun 11/15/15	
19		MS	1 day	Wed 7/1/15	Wed 7/1/15	
20		Subtask	132 days	Sun 8/30/15	Sun 2/28/16	
21		Subtask	130 days	Fri 1/1/16	Thu 6/30/16	
22		MS	1 day	Thu 6/30/16	Thu 6/30/16	
23		**Task**	**391 days?**	**Thu 1/1/15**	**Thu 6/30/16**	
24		Subtask	64 days	Thu 1/1/15	Tue 3/31/15	
25		MS	1 day	Sun 3/15/15	Sun 3/15/15	
26		Subtask	67 days	Sun 3/1/15	Sun 5/31/15	
27		Subtask	132 days	Sun 3/1/15	Mon 8/31/15	
28		MS	1 day	Wed 7/1/15	Wed 7/1/15	
29		Subtask	122 days	Sun 5/31/15	Sun 11/15/15	
30		MS	1 day	Wed 7/1/15	Wed 7/1/15	
31		Subtask	132 days	Sun 8/30/15	Sun 2/28/16	
32		Subtask	130 days	Fri 1/1/16	Thu 6/30/16	
33		MS	1 day	Thu 6/30/16	Thu 6/30/16	
34						

Include a corresponding table that provides:

- Short text-identifier for each milestone/deliverable
- Team members associated with each
- Schedule status (provide explanation if behind schedule or significantly ahead of schedule)
- Description of how the milestone/deliverable is contingent or dependent on other parts of the effort (if applicable)

Milestone/ Deliverable	**Team member(s)**	**Due date**	**Date initiated**	**Date completed**	**Status**	**Dependencies** *Across tasks & team members*

3 Task Progress, Accomplishments, and Plans

*Please provide updates from the **most recent quarter**, not a cumulative discussion of the project to date. Support all claims with data. Highlight major accomplishments. Provide explanations and/or justifications for any deviation from the negotiated schedule and spending plan.*

Identify the following for each major task in your SOW; this section will form the bulk of your report:

- Task number (from SOW)
- High-level task description
- Completion status (e.g., ongoing, delayed, etc.)
- Funding associated with the task (spent to date vs. remaining to spend); explain any deviations from your original spend plan

Task #/Title	Brief Description	% Complete	Total $ for task	Spent	Remaining	Explain deviations from planned expenditures

- **Describe planned vs. actual progress towards the goals, milestones, and deliverables of the task; discuss why planned expectations were met, not met, or exceeded; highlight significant accomplishments**
- List next steps
- Support claims with data, images, or other evidence
- Identify and describe all significant challenges and risks encountered during work towards the goals of this task, including:
    - Critical dependencies across tasks and teams
    - Mitigation plan
    - Level of risk (high, medium, or low)
    - Changes in risk status since proposal or last report
    - Anticipated date risk will be resolved

4 Project Coordination, Dissemination, and Translation

4.1 Project Coordination

- Summarize key project planning and coordination over the quarter, including:
  - Meeting date(s), location, purpose
  - Attendees
  - Meeting outcomes, action items

4.2 Dissemination and Translation (if applicable)

- List any new partnerships, collaborators, users, etc.
- Describe potential commercialization pathways/partners

5 Publications and Presentations

Please provide a cumulative update on current and upcoming publications.

Title, Authors	Description/Type	Status
	Presentation to Conference Name	Published
	Paper, Name of Journal	Submitted
	Letter to the Editor, Scientific Organization	In preparation

6 Patents, Invention Disclosures, IDEs, etc…

Please provide a cumulative update of current or upcoming patents, inventions, Investigational Device Exemption (IDE), etc. Examples are listed in the table below.

Title, Authors	Description/Type	Status
	Patent; Name of Patent	Accepted
	FDA IDE	Filed/submitted
	Invention Disclosure	In preparation

Appendix I – Project Context

For future reports, only update this section if any information changes. Please indicate changes using red font.

Teaming and Personnel

Organizational Chart

Insert an organizational chart for your entire team

Contact Information

Please populate the following table with contact information for each team member. Please provide general area of expertise each will provide (e.g., microfluidics). In the last column, list tasks or otherwise briefly describe each individual's involvement in the effort.

Prime Team Members and Contact Information: [Institution]

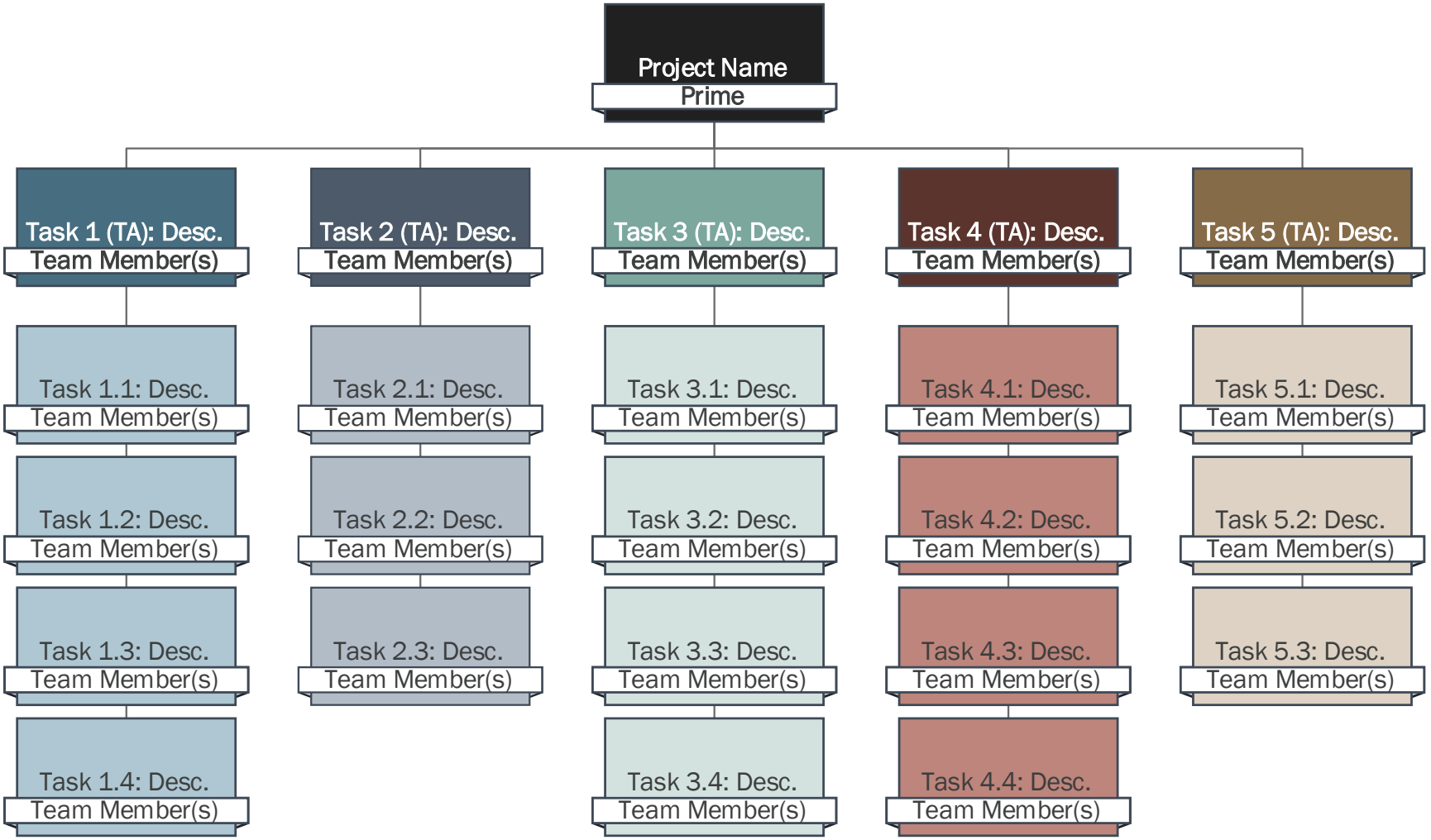
Role	Full name	Phone and email	Areas of Involvement
PI		(888) 888-8888 XXX@univ.edu	
Co-PI (expertise)		(888) 888-8888 XXX@univ.edu	
Postdoc (expertise)		(888) 888-8888 XXX@univ.edu	

Subcontract Team Members and Contact Information: [Institution]

Role	Full name	Phone and email	Areas of Involvement
PI (expertise)		(888) 888-8888 XXX@univ.edu	
Co-PI (expertise)		(888) 888-8888 XXX@univ.edu	
Postdoc (expertise)		(888) 888-8888 XXX@univ.edu	

Work Breakdown Structure

Provide breakdown of tasking and assigned team members as per the template shown below



Monthly Financial Report Template

LINK TO TEMPLATE (click here)

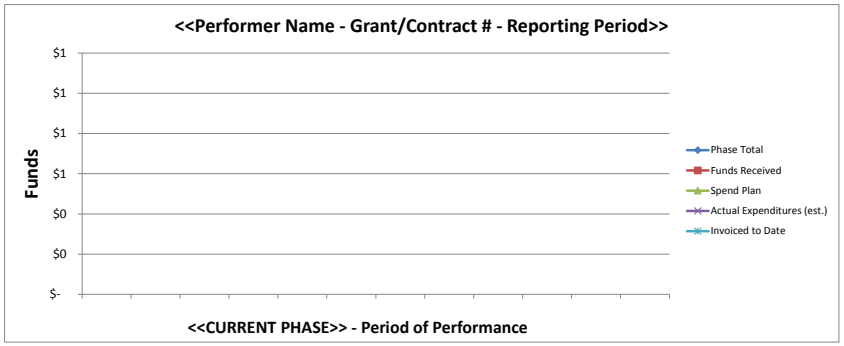
Please use this template to provide monthly financial updates to the PREEMPT team. As you input your data, the graph will automatically update. ***Please keep past reports in this file and create a new tab each month. We want to see all reports in the same file. Title tabs "Phase-Month-Year, " e.g., "Base - January - 2015"***

LINK TO EXAMPLE (click here)

An example of a completed template is also provided. The example graph illustrates a scenario where the performer is under spending. It is designed to show how this template will make it easy for INTERCEPT performers to clearly communicate the status of their effort to DARPA so that both can plan for and initiate contractual actions quickly and effectively.

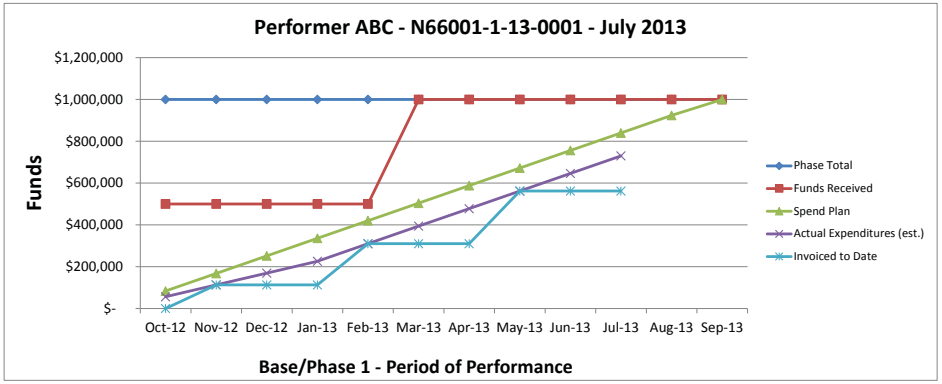
Spend Plan Data	
Period of Performance	The financial report will only cover the current phase (e.g., Base, Option 1, etc.). Use a format similar to "Sep-2013," not "Month 6." In order to plan for continuing resolution requests, DARPA may reach out to you separately to request your projected spend rate for future phases.
Phase Total	Total for current phase *(Example Graph - total is $1,000,000)* .
Funds Received	Funds awarded to date; most efforts are funded incrementally *(Example Graph - this effort received an increment for $500,000 in Oct-2012 to exercise the base, and received the remainder of their base period funding in Mar-2013 (remaining $500,000))* .
Spend Plan	Projected Expenditures must cover the entire phase.
Actual Expenditures (est.)	Actual Expenditures should not be solely based off of invoices you have submitted or received to date. Instead, it should be an accurate (to the extent that is possible) account of the expenses you have actually incurred to date. For example, if a subcontractor has incurred but hasn't invoiced $100,000 worth of work, include the $100,000 in your actual expenditures. Or a large amount of equipment valued at $50,000 that hasn't yet been invoiced should also be factored in to the actual expenditures.
Invoiced to Date	Report the invoices you have submitted to date *(Example Graph - the scenario used in the example graph submits invoices quarterly)* .
Issues/Updates Summary (if applicable)	
Use this section as an opportunity to bring issues, concerns, or updates to the attention of DARPA. For example, you can summarize reasons for over/under-spending, potential no-cost extension requests, invoicing problems, etc.	

***Amounts for Spend Plan, Actual expenditures, Invoiced to Date are cumulative.



Spend Plan Data												
Period of Performance (Current Phase Only)												
Phase Total												
Funds Received												
Spend Plan												
Actual Expenditures (est.)												
Invoiced to Date												

Issues/Updates Summary (if applicable)



Spend Plan Data												
Period of Performance (Current Phase Only)	Oct-12	Nov-12	Dec-12	Jan-13	Feb-13	Mar-13	Apr-13	May-13	Jun-13	Jul-13	Aug-13	Sep-13
Phase Total	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000
Funds Received	$ 500,000	$ 500,000	$ 500,000	$ 500,000	$ 500,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000
Spend Plan	$ 84,000	$ 168,000	$ 252,000	$ 336,000	$ 420,000	$ 504,000	$ 588,000	$ 672,000	$ 756,000	$ 840,000	$ 924,000	$ 1,000,000
Actual Expenditures (est.)	$ 56,500	$ 113,000	$ 169,550	$ 226,100	$ 310,100	$ 394,100	$ 478,100	$ 562,100	$ 646,100	$ 730,100		
Invoiced to Date	$ -	$ 113,000	$ 113,000	$ 113,000	$ 310,100	$ 310,100	$ 310,100	$ 562,100	$ 562,100	$ 562,100		

Issues/Updates Summary (if applicable)

We anticipate that we will need to request a four-month no cost extension (NCE). The NCE is necessary due to delays we experienced while getting Subcontractor #1 under contract. Although our effort's period of performance began in October 2012, the subcontract was finalized and fully-executed in February 2013, which resulted in a four-month delay from the intended start date. Subcontractor #1 is conducting a 12-month study, and cannot speed up their experiments. We would, however, like to begin work on Option 1. We intend to perform these tasks in parallel to the extended Base Period tasks (which are primarily performed by Subcontractor #1).

Preventing emergence and spillover of bat viruses in high-risk global hotspots

STATEMENT OF WORK

July 17th 2018

Milestones by Task

CIES: Cary Institute of Ecosystem Studies; **CSU**: Colorado State University; **Cornell**: Cornell University; **GU**: Griffith University; **JH**: Johns Hopkins University; **MSU: Montana State University**; **PSU**: Penn State University; **RML**: Rocky Mountain Laboratories; **TTU**: Texas Tech University; **UCB**: University of California, Berkeley; **UCLA**: University of California, Los Angeles; **Cambridge**: University of Cambridge.

Note that Rocky Mountain Laboratories (RML) is funded separately by DARPA via IAA/MIPR to NIAID.

TA1

COLLECT AND ANALYZE FIELD SAMPLES

Task 11.01, Data collection: longitudinal sampling of wild bat populations and a captive population. Cambridge, GU, JH, and UCB, with assistance from MSU and TTU, will sample multiple bat populations longitudinally in multiple locations and ship retrospective bat samples to RML or local laboratory for analyses (11.03).

Task 11.02, Data collection: retrospective analysis of bat samples. Cambridge, GU, JH, and UCB will identify, locate, and ship retrospective bat samples to RML or local laboratory for analyses (11.03).

Task 11.03, Lab: screening, metagenomics to identify virus and quasispecies. RML and Cambridge or local laboratory will screen and sequence samples from bats; create a list of sequences that have spilled over from bats to other species; and select sequences for genotype-phenotype modeling.

Task 11.12, Lab: screening retrospective samples from human/domestic livestock hosts. Cambridge, JH, and UCB will identify, locate, and ship retrospective human/livestock samples to RML or local laboratory for analysis; RML or local laboratory will screen samples and create a list of sequences that have spilled over from bats to other species.

Milestones

Australia (GU will do field collection and RML or local laboratory will do sequencing):

- Establish field sites and train field teams (6mths)
- Sample up to 40 bats in 4 bat colonies monthly for 2 years (12mths, 24mths)
- Respond to spillover events or viral pulses within the study area by sampling adaptively until prevalence decreases (12mths, 24mths)
- PCR on all samples for Hendra virus (30mths)
- Sequence all positive samples available (36mths)
- Analyze 1000 retrospective bat samples for henipaviruses (24mths).

Bangladesh (JH will do field collection and in-country PCR; RML will do sequencing):

- Sample up to 40 bats in 4 colonies monthly for 2 years (24mths)
- Respond to spillover events or viral pulses by sampling adaptively until prevalence decreases (24mths)
- PCR on samples for Nipah virus (30mths)
- Sequence all positive samples available (36mths)
- Analyze retrospective bat samples for henipaviruses (24mths).

Ghana (Cambridge will do field collection and laboratory analyses, with some help from RML):

- Locate retrospective human and animal samples suitable for testing and establish sequencing pipeline (6 months)
- Sample up to 120 bats per quarter in 3 colonies, perform PCR testing on the first batches and send positive sample for sequencing (12 months)
- Update sampling effort in bat colonies for year 2 based on 12 months result, for PCR and sequencing, with up to 500 bats to be caught in year 2 (24mths)
- Sample bats in the captive colony every 3 months (24mths)
- Sequence all positive samples available (36mths)

Madagascar (UCB will do field collection and PCR, and RML or local laboratory will do sequencing):

- Establish field sites and train field teams (12mths)
- Sample up to 30 bats in 3 colonies monthly for 2 years (12 mths, 24mths)
- Respond to viral pulses by sampling adaptively until prevalence decreases (12 mth, 24mths)
- Analyze 700 retrospective bat samples for henipaviruses (12mths)
- PCR on samples from bats at Institut Pasteur de Madagascar (30mths)
- Sequence all positive samples available (36mths)

Historic humans and livestock samples (JH, Cambridge, UCB):

- Identify and ship historic samples to RML or local laboratory (6mths)
- PCR on samples from humans and livestock (12mths)
- Sequencing of all positive samples available (18mths)

IDENTIFY HOST IMMUNE SIGNATURES

Task 11.04 Lab: identify host immune and stress signatures in wild bats and in a captive feeding trial. MSU, with help from CSU will measure bat immune signatures. TTU will measure bat stress signatures and nutritional status. A captive feeding trial will be conducted in Ghana (Cambridge), or alternatively, if a natural nutritional stress event occurs in Australia during Phase I, this trial will be conducted in Australia (GU).

Milestones

Immunology on samples from Australia (MSU):

- Validate and optimize tests for each bat species (6mths)
- Immunological markers such as IgG and IgA, biomarkers of cell damage, gene expression of antiviral & proinflammatory proteins, and microbial killing assays for 400 samples (30mths)

Immunology on samples from Ghana (Cambridge):

- Titrate antibodies against Henipaviruses in sera from all PCR-positive bats and a sample of up to 1000 PCR-negative bats, from wild and captive colonies (24 mths).

Stress signatures on samples from Australia (TTU):

- Test up to 720 hair and fecal samples for cortisol (30mths)
- Develop methodology to use bioelectrical impedance analysis to measure body condition of bats (12mths)
- Measure body condition of 400 bats (24mths)

Captive feeding trial (Cambridge, GU)

- Conduct experimental diet manipulation to test the effect of nutritional status on immune state and viral shedding (30mths)

COLLECT ENVIRONMENTAL, ECOLOGICAL, and RESERVOIR HOST DATA

Task 11.10 Remote sensing data, longitudinal short-term weather and long-term climate data, land cover change, human population data, bat movement data. PSU will identify environmental drivers of shedding in Australia and detect large bat colonies through remote sensing. TTU will implement bat telemetry.

Milestones

Remote sensing (PSU):

- Collect data on weather, climate, and land cover change in Australia (24mths)
- Collect data on human population dynamics across space (local/region), time (seasonal/decadal) (24mths)

Bat movement data (TTU):

- Deploy GPS tracking devices on bats in resident and nomadic colonies in Australia (12mths, half deployed; 24mths all deployed)
- Collect, collate, and analyze bat movement data (36mths)

CREATE GENOTYPE-PHENOTYPE MAPS FOR HENIPAVIRUS QUASISPECIES BASED ON *IN VITRO* AND *IN VIVO* WORK

Task 11.13, Lab: in vitro experiments to assess jump potential of quasispecies to new hosts. Cornell and RML will quantify determinants of zoonotic potential for henipavirus strains and quasispecies.

Milestones

Cloning (Cornell; 24 mths):

- Prioritize sequences for 20 F and G pairs to be analyzed for receptor binding and membrane fusion (24mths)
- Synthesize and clone sequences for 20 F and G gene pairs in pCAGGS plasmids (24mths)
- Grow plasmids in bacteria for 20 pairs F and G pairs (24mths)

Receptor binding and membrane fusion assays (Cornell, with help from RML; year 2, 12mths)

- Complete receptor binding assays for 20 G sequences (year 2, 12 months)
- Complete membrane fusion assays in 3 cell lines (human, bat and pig) (year 2, 12 months)

Molecular docking with *in silico* with *in vitro* measurements (RML, with help from Cornell):

- Perform molecular docking analyses (24mths)

Task 11.08, Lab: amplification and transmission dynamics of quasispecies *in vitro* and *in vivo*. RML, with help from CSU, will undertake in vivo experiments to measure phenotypes of henipavirus strains.

Milestones

In vitro and *in vivo* work (RML):

- Use cell culture experiments to analyze growth kinetics of henipaviruses (12mths)
- Develop hamster model for infection experiments (24mths)
- Conduct infection experiments in hamster model to measure infection, shedding, & QS in model hosts (24mths)
- Compare pathogenicity and transmission characteristics in hamster studies with historic studies done by RML (30mths)
- Obtain lung samples at peak virus replication and deep sequence these samples to study QS and selective pressures in a dead-end host (30mths)
- Develop bat models for henipavirus strains with highly pathogenic characteristics in the dead-end host model (36mths)
- Conduct infection experiments and measure infection and shedding in bats (36mths)
- Upon sufficient shedding, conduct contact transmission experiments (36mths)

- Analyze inoculated vs. transmitted virus populations by deep sequencing and identify potential transmissible QS (36mths)
- Analyze QS by established long-read PCR NSG methods (ongoing 42mths)

ANALYZE DATA

Task 11.05, Data analysis: statistical analysis of field data, lab data, environmental and ecological data, and bioinformatics NGS data. Provide statistical support and manage database for project.

Milestones

Data analysis and support (MSU):

- Develop a database structure, system and procedures for providing access to data, and a data visualization platform to facilitate information sharing across tasks and institutions (12mths)
- Clean and check data as it arrives (ongoing over 24mths)
- Graphically visualize and share incoming data for full team (ongoing over 24mths)
- Manage database, analyze data as appropriate, and provide statistical support to the team (ongoing 42mths)

Specific analyses to support other Tasks:

- Use statistical modeling to investigate and quantify links among nutritional status (TTU), stress signatures (TTU), immune status (MSU) and viral shedding (GU/RML/local laboratory) in *wild Australian bats* (30 months)
- Use statistical modeling to investigate and quantify links among nutritional status (Cambridge), stress signatures (MSU), immune status (Cambridge) and viral shedding (Cambridge) *in captive bats* (42 months)

DEVELOP MODELS

Task 11.06, Stochastic models of within- and between-host virus dynamics in bats. Cambridge, with help from GU, will perform stochastic modeling of within and between host virus dynamics in bats.

Milestones

Modeling (Cambridge, GU):

- Develop models of virus transmission within bat populations using prior knowledge from each location (12mths)
- Develop generic models of within-host virus dynamics that incorporate measurable components of the bat immune system (12mths)
- Validate and refine within- and between-host models of virus dynamics in bats using data collected in each field site and laboratory (36mths)

Task 11.15, Mechanistic mathematical modeling of viral fitness within humans, bats, and other host species, iterated with lab studies. UCLA will assemble genotype-to-phenotype maps for reservoir and spillover host species.

Milestones
Viral fitness modeling (UCLA):

- Develop mechanistic model of viral life cycle within cells (12mths)
- Integrate molecular, virologic, cell culture, and animal experiment data (24mths)
- Compare fitness predictions from *in silico* vs *in vitro* data (36mths)
- Integrate models and lab data to establish empirical relations between viral traits and fitness (42mths)

Task 11.09, Phylodynamic models of quasispecies dynamics within bat populations and between host species. MSU, with help from Cambridge and UCLA, will perform phylodynamic modeling of henipaviruses in bat populations.

Milestones
Phylodynamic modeling (MSU, Cambridge, UCLA):

- Formulate model framework to link viral genetics to transmission dynamics (12mths)
- Create models of within- and between-host selection in bat populations (24mths)

Task 12.02, Multi-scale models of zoonotic transmission from bats to humans to predict quasispecies expansions and pulses of excretion. Cambridge, with help from MSU, UCLA and GU, will develop a multi-scale mechanistic modeling framework for pathogen spillover.

Milestones
Multi-scale modeling (Cambridge, MSU, UCLA, GU):

- Develop baseline tools to relate spillover modeling framework from Plowright et al. to field data (12mths)
- Adapt spillover modeling framework from Plowright et al. to henipavirus contexts; identify key challenges to operationalize (18mths)
- Integrate bat virus transmission dynamics, environmental data. and viral fitness models (30mths)
- Develop an integrative model of bat virus spillover that is operationalized to predict probability of spillover at a spatial and temporal scale relevant for intervention (42mths)
- Perform a two-step validation of models:
    - Internal validation of the fitting methods: using simulated data generated by our candidate models, we will infer the parameter values and check the accuracy and precision of the fitting method (ongoing over 42mths)
    - External validation: we will exclude parts of the data iteratively, fit the models to the remaining dataset and check that it predicts correct values for the missing data (ongoing over 42mths)

Task 11.16, Machine learning to ID virus, reservoir traits, zoonotic risk. CIES will perform machine learning analyses to prioritize surveillance by identifying combinations of bat traits and environmental factors that predict spillover.

Milestones

Machine learning analyses (CIES): (all activities below are ongoing over 36mths)

- Collate and pre-process multiple data streams from field teams (environmental data; ecological data on bat populations; data on human ecology)
- Engineer features; impute bat trait data; tune hyperparameters for selected machine learning algorithm; execute cross-validation and target shuffling procedures to diagnose and correct overfitting; produce trait profiles of bat species predicted to be henipavirus positive (first predictions at 6mths).
- Repeat procedures above for models at the ecoregion and country scales (ongoing over 36mths)
- Combine species-level predictions with environmental and human ecological features from the Australian system (i.e., corresponding with viral shedding pulses in local bat populations, satellite imagery on seasonal human population densities, fruiting phenology, climate induced stress). Identify bat species that present the greatest spillover risk to humans, and measurable features that best predict viral shedding (ongoing over 24mths)
- Incorporate data on viral shedding events and conduct machine learning on viral PCR data to identify detectable predictors of viral shedding (Phase 2)
- Assess features corresponding to parameters in a multiscale mechanistic model of viral shedding and provide machine learning support of features to be included in multi-scale models of viral dynamics (e.g., engineering features, estimating parameters impacting viral shedding) (ongoing over 18 months in Phase 2)

TA2

DEMONSTRATE PROOF OF CONCEPT FOR AN ECOLOGICAL INTERVENTION FOR SPILLOVER

Task 22.03, Proof-of-concept for preemption through strategic ecological interventions. GU, with help from TTU and PSU, will do preliminary studies to develop the proof-of-concept demonstration of an ecological intervention to stop spillover. GU, MSU, TTU, Cambridge, CIES, CSU, PSU, RML will all contribute to investigating links between nutritional stress and virus shedding (above).

Milestones.

Demonstrate that bats move from urban roosts to flowering events in native forests (GU, with help from TTU)

- Establish methodology for using movement data to validate bats moving from urban roosts to native forests (6mths)
- Acquire movement data from existing and projected sources (18mths)
- Analyse movement data (24mths).

Demonstrate that bats locate and feed in regenerated habitat

- Develop experimental design and field methods to test use of regenerated forest as feeding habitat by bats (6mths)
- Establish field sites for testing use of regenerated forest as feeding habitat and commence field sampling (12mths)
- Sample up to 30 paired regeneration sites and remnant native habitat (control) sites for feeding bats (18mths)
- Analyse feeding data (24mths)

DEMONSTRATE PROOF OF CONCEPT, FEASIBILITY, AND SCALABILITY OF CHAD/VSV VACCINATION

Task 22.02, Proof-of-concept demonstration of ChAd/VSV vaccination feasibility and scalability of ChAd/VSV vaccination in bats. RML will develop and test a scalable vectored vaccine for target henipaviruses in bats. RML, with help from Cambridge, will assess the feasibility and scalability of the vaccine in bats.

Milestones

Vaccine development (RML):

- Design novel vaccines based on TA1
- Test by comparing measures of protection with historic hamster models (12mths)
- Test the effectiveness of the vaccines against novel henipaviruses (24mths)
- Demonstrate reduced probability of virus transmission among bats and among bats and recipient host species *in vivo* (42mths)
- Quantify scalability of ChAd/VSV vaccination in captive bats in Ghana (42mths)

TRANSITION PLAN

MSU and RML will develop the research transition plan.

Milestones

- Work with the MSU technology transfer infrastructure and personnel, and with the CEPI program to develop partnerships with vaccine manufacturers (30mths)
- Developed an inter-institutional agreement to enable the transfer of our discoveries to industry for commercialization (36mths)

DEPARTMENT OF THE INTERIOR
Interior Business Center
Acquisition Services Directorate, Division III
354 South Highway 92
Sierra Vista, AZ 85635

Agent for:
Defense Advanced Research Projects Agency (DARPA)

RESEARCH COOPERATIVE AGREEMENT SCHEDULE

1. **Agreement Number**: **D18AC00031** **Amendment 0001**

2. **Recipient Name:** **Montana State University - Bozeman**
307 Montana Hall
Bozeman, MT 59717

3. **Identification Numbers**:

Tax Identification Number (TIN)**: 81-6010045**

Data Universal Numbering System (DUNS) Number**: 625447982**

Commercial and Government Entity (CAGE) Code**: 1KQE9**

Federal Interagency Code for Education (FICE)**: 002532**

Catalog of Federal Domestic Assistance (CFDA): **12.910 – Research and Technology Development**

ASAP Recipient Number: **3034514**

4. **Principal Investigator/Key Personnel**: Dr. Raina Plowright
111A Lewis Hall
P.O. Box 173520
Bozeman, MT 59717-3520

Telephone:
E-mail address:

5. The purpose of this amendment is as follows:

a. Correct the ADPM to Phillip Lamp at Points of Contact 6. e.
b. Update the Quarterly R&D Status and the Monthly Financial Management Report due dates at 14. Reporting Requirements.

6. **Item 6 - Points of Contact is hereby updated as follows:**

6. Points of Contact:

a. Agreements Officer: Department of the Interior
Interior Business Center

Acquisition Services Directorate, Division III
354 South Highway 92
Sierra Vista, AZ 85635

Attention: Doreen Vieira-Cross
Telephone:
FAX:
Email:

b. Cooperative Agreement Administrator:

Department of the Interior
Interior Business Center
Acquisition Services Directorate, Division III
354 South Highway 92
Sierra Vista, AZ 85635

Attention: Deborah Branham
Telephone:
FAX:
Email:

c. Agreements Officer's Representative:

J. Aura Gimm
Air Force Office of Scientific Research
875 N. Randolph Street
Arlington, VA 22203

Teleph
Email:

d. DARPA Program Manager (PM):

Defense Sciences Office (BTO)
675 N. Randolph Street
Arlington, VA 22203-2114

Attention: Dr. James L. Gimlett
Telephone:
Email:

e. DARPA BTO Assistant Director, Program Management (ADPM)

Attention: Phillip Lamp
Email:

7. Item 14 – Reporting Requirements is hereby updated as follows:

14. Reporting Requirements: A final DD Form 882 is required to be filed listing all subject inventions or stating that there were none. In accordance with DARPA-BAA-HR001118S0017, the frequency of the reporting requirement differs from those commonly found in financial assistance agreements due to significant Government involvement throughout the duration of the research cycle. The following reports shall be submitted and will become due on the dates as shown below:

REPORT TYPE	DUE DATE	SUBMIT TO
Quarterly R&D Status Reports	Within 45 days of the end of each quarter	See Exhibit A Attachment 1
Monthly Financial Management Report	Within 45 days of the end of each month	See Exhibit A Attachment 2
Special Technical Report	Due as required	AOR, AO, PM, & DARPA Research Services
Annual Federal Financial Report (SF 425)	29 Dec 2019 29 Dec 2020	AOR, AO, PM, ONR & DARPA Research Services
Final Technical Report	29 Dec 2020	AOR, AO, PM, ONR, DTIC*, & DARPA Research Services
Final Financial Report (SF425)	29 Dec 2020	AOR, AO, PM, ONR, DTIC*, & DARPA Research Services
Final Invention Report (DD Form 882)	28 Jan 2021	See Exhibit A Article 8 - Intellectual Property Matters

*Defense Technical Information Center
ATTN: DTIC-O
8725 John J. Kingman Road
Ft. Belvoir, VA 22060-6218

If Optional Phase II is implemented - The following reports shall be submitted and will become due on the dates as shown below:

REPORT TYPE	DUE DATE	SUBMIT TO
Quarterly R&D Status Reports	Within 45 days of the end of each quarter	See Exhibit A Attachment 1
Monthly Financial Management Report	Within 45 days of the end of each month	See Exhibit A Attachment 2
Special Technical Reports	Due as required	AOR, AO, PM, & DARPA Research Services
Annual Federal Financial Report (SF 425)	29 Dec 2021	AOR, AO, PM, ONR, & DARPA Research Services
Final Technical Report	29 JUN 2022	AOR, AO, PM, ONR, DTIC*, & DARPA Research Services
Final Financial Report (SF425)	29 JUN 2022	AOR, AO, PM, ONR, DTIC*, & DARPA Research Services
Final Invention Report (DD Form 882)	29 JUL 2022	See Exhibit A Article 8 - Intellectual Property Matters

*Defense Technical Information Center
ATTN: DTIC-O
8725 John J. Kingman Road
Ft. Belvoir, VA 22060-6218

8. Acceptance of this amendment is pursuant to Article 14 Acceptance and Amendment of Cooperative Agreement Exhibit A.

9. All other terms and conditions remain unchanged.

THIS ACTION IS MADE ON BEHALF OF A DoD CUSTOMER UTILIZING DoD FUNDS.

UNITED STATES OF AMERICA
Department of the Interior, Interior Business Center
Acquisition Services Directorate, Division III

Doreen Vieira-Cross
Agreements Officer

MONTANA STATE UNIVERSITY

Attachment 3
Subaward Agreement Contacts

MSU ID G228-19-W7329

Pass-Through Entity Contacts	Subrecipient Contacts
Institution/Organization ("Pass-through Entity") Name Montana State University Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470	**Institution/Organization ("Subrecipient")** Name Colorado State University Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Duns Number 785979618 Duns Name Colorado State University
Administrative Contact Name Leslie Schmidt Associate Vice President Research Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470 Phone (Email subawards@montana.edu	**Administrative Contact** Name Ashley Stahle Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email
Principal Investigator Name Raina Plowright Address Lewis Hall 111 Montana State University PO Box 173610 Bozeman, MT 59717-3610 Phone Email	**Principal Investigator** Name Tony Schountz Address 1692 Campus Delivery Fort Collins,CO 80523-1692 Phone Email
Financial Contact Name Jennifer Hodges Address Montana State University PO Box 173520 Bozeman, MT 59717-3520 Phone (Email	**Financial Contact** Name Kim Marrale Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email
Authorized Official Name Dale Huls Assistant Director Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470 Phone Email subawards@montana.edu	**Authorized Official** Name Julie Harvey Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email

Records: As required by Uniform Guidance, 2 CFR 200, or 45 CFR Part 75, SUBRECIPIENT will maintain appropriate and complete accounts, records, documents and other evidence showing and supporting all costs incurred under this agreement. Subrecipient must retain all records that are required by the terms of the prime award or may reasonably be considered pertinent to the prime award. PTE may verify all expenditure receipts and disburse funds in an amount equal to the approved expenditures. SUBRECIPIENT will allow access to PTE, the Montana Legislative Auditor and/or the Montana Legislative Fiscal Analyst, or other designated persons to all records as may be necessary for audit purposes and to determine compliance with this agreement.

Fly America Act: The Fly America Act requires that all travelers and others performing U.S. Government-financed air travel use U.S. flag carriers to the extent such carriers are available, even if their use would cost more. Even when the entire trip cannot be made on U.S. flag carriers to the extent possible they should be used to the farthest interchange point on a usually traveled route. 301-3.6 (b)(4)(ii). Chartered flights are also subject to the requirements. Cost of duties, visas and value added tax are unallowable. Receipts of travel expenses are required to be submitted for payment.

Liability Exposure: The parties understand and agree that the liability of the State of Montana, PTE, its officials and employees is controlled and limited by the provisions of Title 02, Chapter 09, Montana Code Annotated entitled, *Government Structure and Administration – Liability Exposure and Insurance Coverage*, and the provisions of Title 18, Chapter 01, Part 4 entitled, *Contract Actions Against the State*. Any provision of this agreement, whether or not incorporated herein by reference or otherwise, will be controlled, limited and otherwise modified to limit any liability of the State of Montana, PTE, its officials and employees to that set forth in the above cited laws.

Non-Discrimination: SUBRECIPIENT agrees that no part of this subaward will be performed in a manner which illegally discriminates against any person on the basis of race, color, religion, creed, political ideas, national origin, sex, age, marital status, physical and/or mental handicap.

Assignment Transfer and Subcontracting: There will be no assignment, transfer, or subcontracting of this agreement, or of any interest in this agreement, unless both parties agree in writing. No services required under this agreement may be performed by individuals not subject to this agreement unless both parties agree in writing.

Use of Names: Neither party will include the name of the other party or any of its employees in any advertising, sales promotion or other publicity matter without the prior written consent of the other party.

Reporting Requirements: SUBRECIPIENT will provide to PTE any requested reports necessary to the completion of the prime award, and as detailed in **Attachment 4A.**

Attachment 4A
Subaward Agreement Additional Reporting Requirements

Quarterly R& D Status Reports will be submitted within thirty (30) days after the end of each project quarter (3/31, 6/30, 9/30, and 12/31) to the Pass-through Entity's Principal Investigator identified in Attachment 3. See Exhibit A Attachment 1 for format and instructions.

Monthly Financial Management Report reports will be submitted to the Pass-through Entity's Principal Investigator identified in Attachment 3, within thirty (30) days of the end of the month. See Exhibit A Attachment 2 for format, instructions and example.

Special Technical Reports as requested by DARPA/DOI, due as required, will be submitted when requested by the Pass-through Entity's Principal Investigator identified in Attachment 3.

Final Invention Report (DD Form 882) will be submitted to the Pass-through Entity's Principal Investigator identified in Attachment 3 by 12/20/2020. See Exhibit A Attachment 3 for format and instructions.

Montana State University - Bozeman
PREEMPT Program – Cooperative Agreement D18AC00031
Quarterly R&D Status Report

Period Covered by the Report: [Date] through [Date]

Date of Report:

Project Title: Preventing emergence and spillover of bat pathogens in high-risk global hotspots
Total Dollar Value: $8,239,511.00
Program Manager: Dr. James Gimlett, DARPA

Submitted by:
[PI Name]
[Institution]
[Address]

Telephone:
Email:

Subcontractors: [Co-PI name(s) and institution(s)]

TABLE OF CONTENTS

General notes:

- **Contact the program manager and team to report any financial or technical issues** (i.e., please do not wait until a report is due to bring up major issues).
- Clearly indicate if funding from another federal agency (e.g., NIH) has been used to support any data presented.
- Clearly indicate if any content is pre-publication sensitive or proprietary.
- Delete all instructional text from this document before submitting your report.
- Support your claims with data, images, and other evidence.
- Please update the header of each report with the respective quarterly period.
- Please use the following naming convention for report filenames: QR – PI institution – period covered (e.g., QR – University of XYZ – 01OCT2018 to 31DEC2018).
- Quarterly reports are due within 30 days of the quarter end date. For example, if the period ends on March 31, the report must be submitted by April 30.
- Monthly progress updates via conference calls will be scheduled with the program manager and his team.

Definitions:

- **Functional block diagram:** describes the functions and interrelationships of a system in a flock-block diagram style so that one can easily and thoroughly understand the system and the relationship of each of the parts to the whole. If the hardware evolves throughout your project, please provide a block diagram for each evolution (example included).
- **Work Breakdown Structure (WBS):** a hierarchical and incremental decomposition of the project into phases, deliverables and work packages. It is a tree structure that shows the subdivision of effort required to achieve an objective (example included).
- **Deliverable:** a measurable and verifiable outcome or object that a project team must create and deliver according to the terms of an agreement. An intangible deliverable is a particular outcome that the team achieves. A tangible deliverable is a concrete or material object created by the team.
- **Milestone:** a milestone describes the status of the project as represented by an event or moment at which one or more project activities are complete. Milestones can represent the completion of key project tasks, conclusions reached, or questions answered that affect project schedule significantly.
- **Major finding:** data with significant impact (positive or negative).
- **Metrics update:** progress (including delays and issues) toward achieving pre-established metrics of success.
- **SETA:** Science, Engineering, and Technical Assistant (internal DARPA term for technical support staff).

1 Progress Summary

1.1 Major Findings

Briefly describe the most significant and salient accomplishment(s) achieved during the ***most recent quarter***. How has this compared to the original project plan?

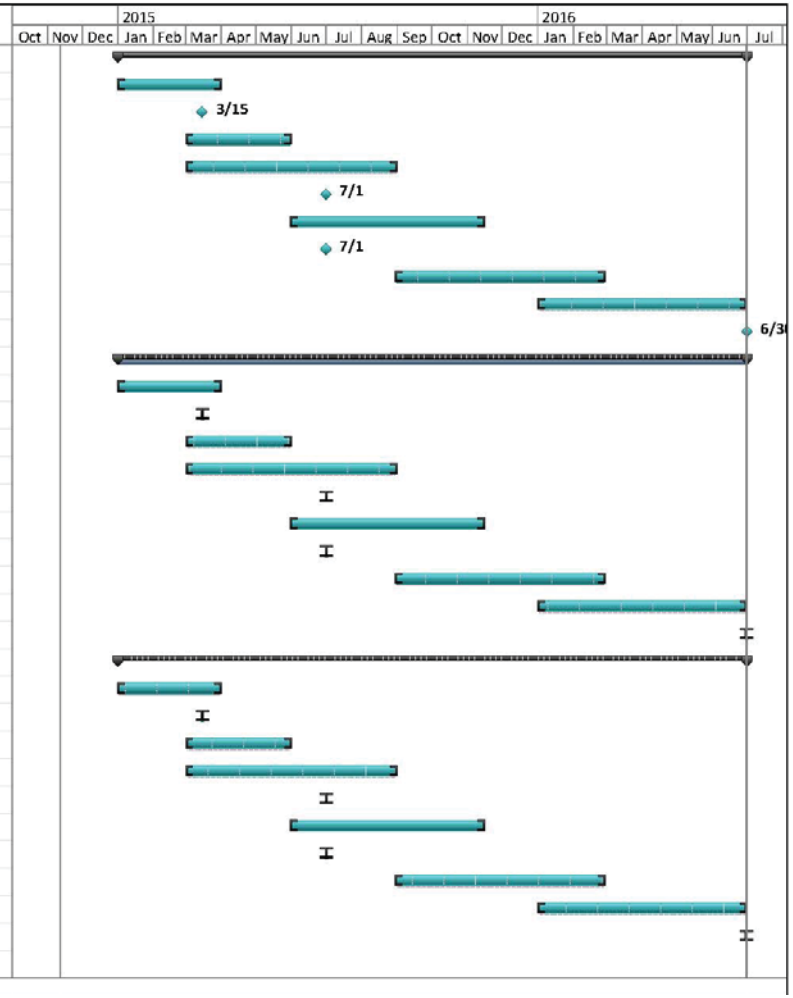
1.2 Metrics Update

Accomplishment *Include associated task #*	**Month** *Planned vs. achieved*	**Update** *Provide current status, explain any schedule discrepancies, list next steps*

2 Schedule – Milestones and Deliverables

Provide a high-level Gantt chart for Phase I that includes all milestones and deliverables for each task. An example of an acceptable chart is shown below.

ID	Task Mode	Task Name	Duration	Start	Finish	Predecessors
1		**Task**	**391 days**	**Thu 1/1/15**	**Thu 6/30/16**	
2		Subtask	64 days	Thu 1/1/15	Tue 3/31/15	
3		MS	0 days	Sun 3/15/15	Sun 3/15/15	
4		Subtask	67 days	Sun 3/1/15	Sun 5/31/15	
5		Subtask	132 days	Sun 3/1/15	Mon 8/31/15	
6		MS	0 days	Wed 7/1/15	Wed 7/1/15	
7		Subtask	122 days	Sun 5/31/15	Sun 11/15/15	
8		MS	0 days	Wed 7/1/15	Wed 7/1/15	
9		Subtask	132 days	Sun 8/30/15	Sun 2/28/16	
10		Subtask	130 days	Fri 1/1/16	Thu 6/30/16	
11		MS	0 days	Thu 6/30/16	Thu 6/30/16	
12		**Task**	**391 days**	**Thu 1/1/15**	**Thu 6/30/16**	
13		Subtask	64 days	Thu 1/1/15	Tue 3/31/15	
14		MS	1 day	Sun 3/15/15	Sun 3/15/15	
15		Subtask	67 days	Sun 3/1/15	Sun 5/31/15	
16		Subtask	132 days	Sun 3/1/15	Mon 8/31/15	
17		MS	1 day	Wed 7/1/15	Wed 7/1/15	
18		Subtask	122 days	Sun 5/31/15	Sun 11/15/15	
19		MS	1 day	Wed 7/1/15	Wed 7/1/15	
20		Subtask	132 days	Sun 8/30/15	Sun 2/28/16	
21		Subtask	130 days	Fri 1/1/16	Thu 6/30/16	
22		MS	1 day	Thu 6/30/16	Thu 6/30/16	
23		**Task**	**391 days?**	**Thu 1/1/15**	**Thu 6/30/16**	
24		Subtask	64 days	Thu 1/1/15	Tue 3/31/15	
25		MS	1 day	Sun 3/15/15	Sun 3/15/15	
26		Subtask	67 days	Sun 3/1/15	Sun 5/31/15	
27		Subtask	132 days	Sun 3/1/15	Mon 8/31/15	
28		MS	1 day	Wed 7/1/15	Wed 7/1/15	
29		Subtask	122 days	Sun 5/31/15	Sun 11/15/15	
30		MS	1 day	Wed 7/1/15	Wed 7/1/15	
31		Subtask	132 days	Sun 8/30/15	Sun 2/28/16	
32		Subtask	130 days	Fri 1/1/16	Thu 6/30/16	
33		MS	1 day	Thu 6/30/16	Thu 6/30/16	
34						



Include a corresponding table that provides:

- Short text-identifier for each milestone/deliverable
- Team members associated with each
- Schedule status (provide explanation if behind schedule or significantly ahead of schedule)
- Description of how the milestone/deliverable is contingent or dependent on other parts of the effort (if applicable)

Milestone/ Deliverable	**Team member(s)**	**Due date**	**Date initiated**	**Date completed**	**Status**	**Dependencies** *Across tasks & team members*

3 Task Progress, Accomplishments, and Plans

*Please provide updates from the **most recent quarter**, not a cumulative discussion of the project to date. Support all claims with data. Highlight major accomplishments. Provide explanations and/or justifications for any deviation from the negotiated schedule and spending plan.*

Identify the following for each major task in your SOW; this section will form the bulk of your report:

- Task number (from SOW)
- High-level task description
- Completion status (e.g., ongoing, delayed, etc.)
- Funding associated with the task (spent to date vs. remaining to spend); explain any deviations from your original spend plan

Task #/Title	Brief Description	% Complete	Total $ for task	Spent	Remaining	Explain deviations from planned expenditures

- **Describe planned vs. actual progress towards the goals, milestones, and deliverables of the task; discuss why planned expectations were met, not met, or exceeded; highlight significant accomplishments**
- List next steps
- Support claims with data, images, or other evidence
- Identify and describe all significant challenges and risks encountered during work towards the goals of this task, including:
    - Critical dependencies across tasks and teams
    - Mitigation plan
    - Level of risk (high, medium, or low)
    - Changes in risk status since proposal or last report
    - Anticipated date risk will be resolved

4 Project Coordination, Dissemination, and Translation

4.1 Project Coordination

- Summarize key project planning and coordination over the quarter, including:
  - Meeting date(s), location, purpose
  - Attendees
  - Meeting outcomes, action items

4.2 Dissemination and Translation (if applicable)

- List any new partnerships, collaborators, users, etc.
- Describe potential commercialization pathways/partners

5 Publications and Presentations

Please provide a cumulative update on current and upcoming publications.

Title, Authors	Description/Type	Status
	Presentation to Conference Name	Published
	Paper, Name of Journal	Submitted
	Letter to the Editor, Scientific Organization	In preparation

6 Patents, Invention Disclosures, IDEs, etc…

Please provide a cumulative update of current or upcoming patents, inventions, Investigational Device Exemption (IDE), etc. Examples are listed in the table below.

Title, Authors	Description/Type	Status
	Patent; Name of Patent	Accepted
	FDA IDE	Filed/submitted
	Invention Disclosure	In preparation

Appendix I – Project Context

For future reports, only update this section if any information changes. Please indicate changes using red font.

Teaming and Personnel

Organizational Chart

Insert an organizational chart for your entire team

Contact Information

Please populate the following table with contact information for each team member. Please provide general area of expertise each will provide (e.g., microfluidics). In the last column, list tasks or otherwise briefly describe each individual's involvement in the effort.

Prime Team Members and Contact Information: [Institution]

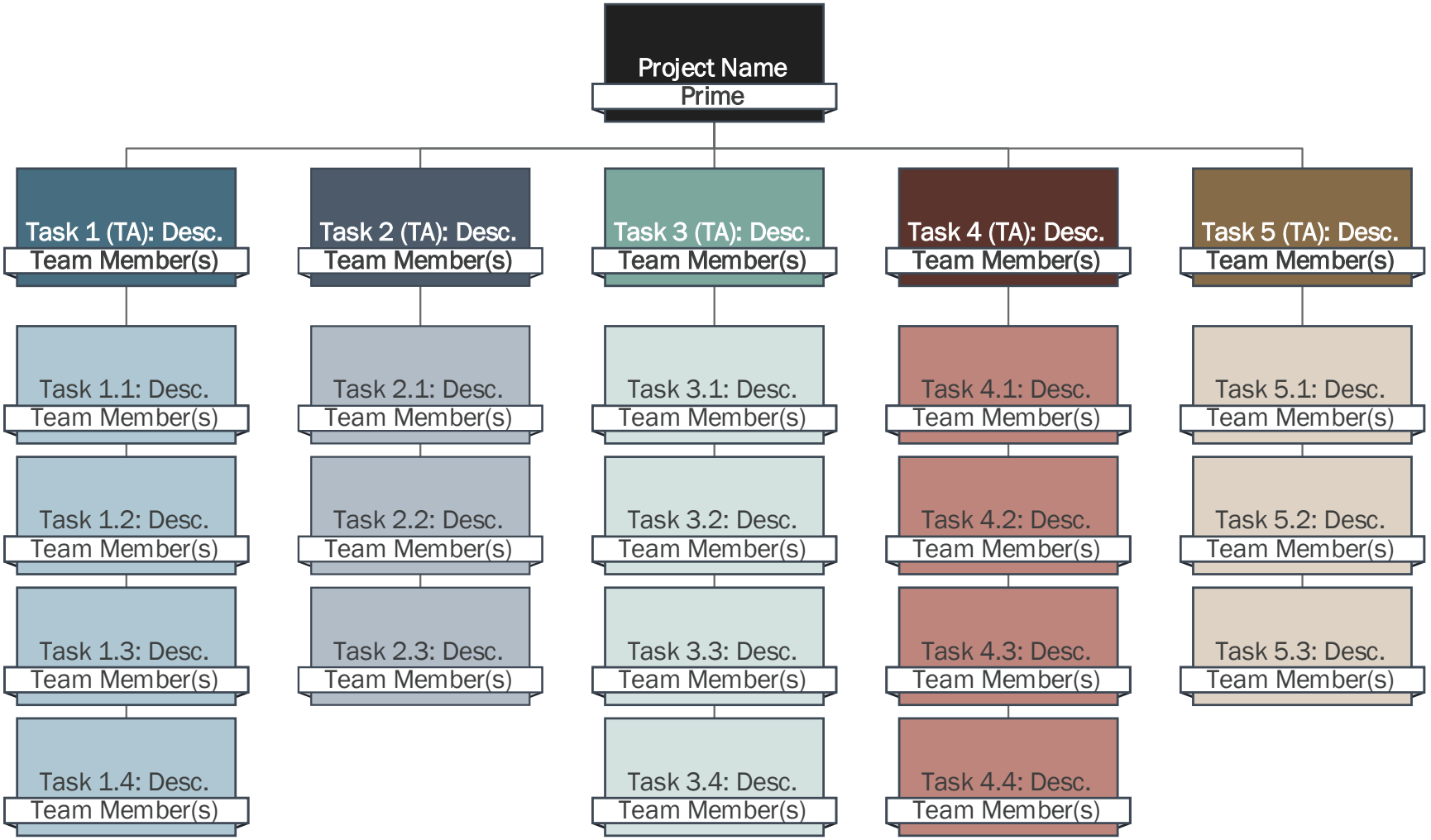
Role	Full name	Phone and email	Areas of Involvement
PI		(888) 888-8888 XXX@univ.edu	
Co-PI (expertise)		(888) 888-8888 XXX@univ.edu	
Postdoc (expertise)		(888) 888-8888 XXX@univ.edu	

Subcontract Team Members and Contact Information: [Institution]

Role	Full name	Phone and email	Areas of Involvement
PI (expertise)		(888) 888-8888 XXX@univ.edu	
Co-PI (expertise)		(888) 888-8888 XXX@univ.edu	
Postdoc (expertise)		(888) 888-8888 XXX@univ.edu	

Work Breakdown Structure

Provide breakdown of tasking and assigned team members as per the template shown below



Monthly Financial Report Template

LINK TO TEMPLATE (click here)

Please use this template to provide monthly financial updates to the PREEMPT team. As you input your data, the graph will automatically update. ***Please keep past reports in this file and create a new tab each month. We want to see all reports in the same file. Title tabs "Phase-Month-Year, " e.g., "Base - January - 2015"***

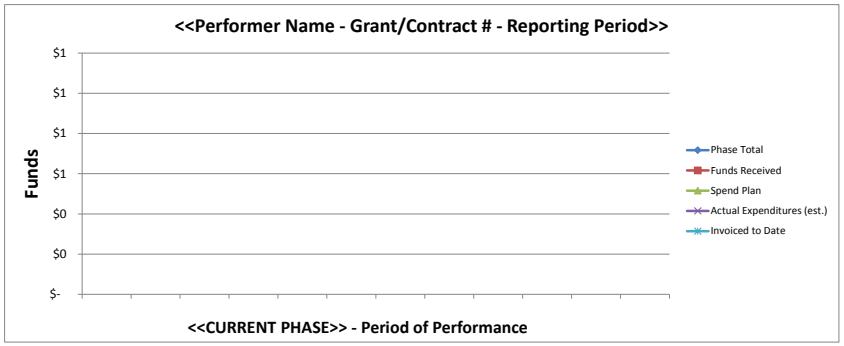
LINK TO EXAMPLE (click here)

An example of a completed template is also provided. The example graph illustrates a scenario where the performer is under spending. It is designed to show how this template will make it easy for INTERCEPT performers to clearly communicate the status of their effort to DARPA so that both can plan for and initiate contractual actions quickly and effectively.

Spend Plan Data	
Period of Performance	The financial report will only cover the current phase (e.g., Base, Option 1, etc.). Use a format similar to "Sep-2013," not "Month 6." In order to plan for continuing resolution requests, DARPA may reach out to you separately to request your projected spend rate for future phases.
Phase Total	Total for current phase *(Example Graph - total is $1,000,000)* .
Funds Received	Funds awarded to date; most efforts are funded incrementally *(Example Graph - this effort received an increment for $500,000 in Oct-2012 to exercise the base, and received the remainder of their base period funding in Mar-2013 (remaining $500,000))* .
Spend Plan	Projected Expenditures must cover the entire phase.
Actual Expenditures (est.)	Actual Expenditures should not be solely based off of invoices you have submitted or received to date. Instead, it should be an accurate (to the extent that is possible) account of the expenses you have actually incurred to date. For example, if a subcontractor has incurred but hasn't invoiced $100,000 worth of work, include the $100,000 in your actual expenditures. Or a large amount of equipment valued at $50,000 that hasn't yet been invoiced should also be factored in to the actual expenditures.
Invoiced to Date	Report the invoices you have submitted to date *(Example Graph - the scenario used in the example graph submits invoices quarterly)* .
Issues/Updates Summary (if applicable)	
Use this section as an opportunity to bring issues, concerns, or updates to the attention of DARPA. For example, you can summarize reasons for over/under-spending, potential no-cost extension requests, invoicing problems, etc.	

***Amounts for Spend Plan, Actual expenditures, Invoiced to Date are cumulative.

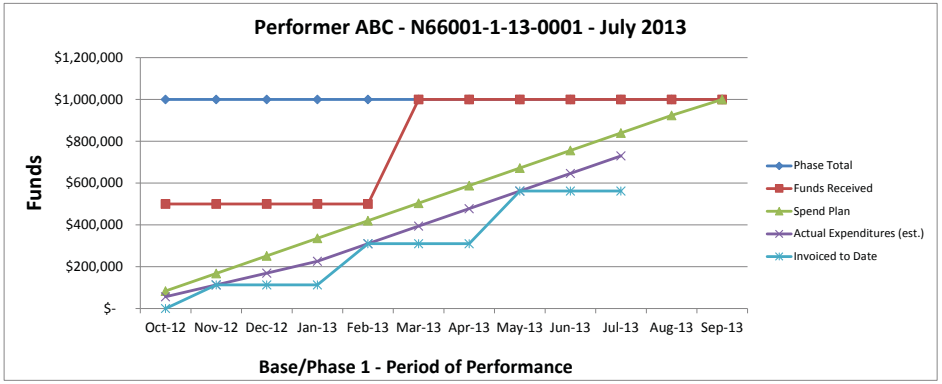
Exhibit A



Spend Plan Data												
Period of Performance (Current Phase Only)												
Phase Total												
Funds Received												
Spend Plan												
Actual Expenditures (est.)												
Invoiced to Date												

Issues/Updates Summary (if applicable)

Exhibit A



Spend Plan Data												
Period of Performance (Current Phase Only)	**Oct-12**	**Nov-12**	**Dec-12**	**Jan-13**	**Feb-13**	**Mar-13**	**Apr-13**	**May-13**	**Jun-13**	**Jul-13**	**Aug-13**	**Sep-13**
Phase Total	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000
Funds Received	$ 500,000	$ 500,000	$ 500,000	$ 500,000	$ 500,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000
Spend Plan	$ 84,000	$ 168,000	$ 252,000	$ 336,000	$ 420,000	$ 504,000	$ 588,000	$ 672,000	$ 756,000	$ 840,000	$ 924,000	$ 1,000,000
Actual Expenditures (est.)	$ 56,500	$ 113,000	$ 169,550	$ 226,100	$ 310,100	$ 394,100	$ 478,100	$ 562,100	$ 646,100	$ 730,100		
Invoiced to Date	$ -	$ 113,000	$ 113,000	$ 113,000	$ 310,100	$ 310,100	$ 310,100	$ 562,100	$ 562,100	$ 562,100		

Issues/Updates Summary (if applicable)

We anticipate that we will need to request a four-month no cost extension (NCE). The NCE is necessary due to delays we experienced while getting Subcontractor #1 under contract. Although our effort's period of performance began in October 2012, the subcontract was finalized and fully-executed in February 2013, which resulted in a four-month delay from the intended start date. Subcontractor #1 is conducting a 12-month study, and cannot speed up their experiments. We would, however, like to begin work on Option 1. We intend to perform these tasks in parallel to the extended Base Period tasks (which are primarily performed by Subcontractor #1).

REPORT OF INVENTIONS AND SUBCONTRACTS

(Pursuant to "Patent Rights" Contract Clause) (See Instructions on back)

Form Approved
OMB No. 9000-0095
Expires Oct 31, 2004

PLEASE DO NOT RETURN YOUR COMPLETED FORM TO THIS ADDRESS. RETURN COMPLETED FORM TO THE CONTRACTING OFFICER.

1.a. NAME OF CONTRACTOR/SUBCONTRACTOR	c. CONTRACT NUMBER	2.a. NAME OF GOVERNMENT PRIME CONTRACTOR	c. CONTRACT NUMBER	3. TYPE OF REPORT *(X one)*
				a. INTERIM ☐ b. FINAL ☐
b. ADDRESS *(Include ZIP Code)*	d. AWARD DATE *(YYYYMMDD)*	b. ADDRESS *(Include ZIP Code)*	d. AWARD DATE *(YYYYMMDD)*	4. REPORTING PERIOD *(YYYYMMDD)*
				a. FROM
				b. TO

SECTION I - SUBJECT INVENTIONS

5. "SUBJECT INVENTIONS" REQUIRED TO BE REPORTED BY CONTRACTOR/SUBCONTRACTOR *(If "None," so state)*

NAME(S) OF INVENTOR(S) *(Last, First, Middle Initial)* a.	TITLE OF INVENTION(S) b.	DISCLOSURE NUMBER, PATENT APPLICATION SERIAL NUMBER OR PATENT NUMBER c.	ELECTION TO FILE PATENT APPLICATIONS *(X)* d.				CONFIRMATORY INSTRUMENT OR ASSIGNMENT FORWARDED TO CONTRACTING OFFICER *(X)* e.	
			(1) UNITED STATES		(2) FOREIGN			
			(a) YES	(b) NO	(a) YES	(b) NO	(a) YES	(b) NO

f. EMPLOYER OF INVENTOR(S) NOT EMPLOYED BY CONTRACTOR/SUBCONTRACTOR		g. ELECTED FOREIGN COUNTRIES IN WHICH A PATENT APPLICATION WILL BE FILED	
(1) (a) NAME OF INVENTOR *(Last, First, Middle Initial)*	(2) (a) NAME OF INVENTOR *(Last, First, Middle Initial)*	(1) TITLE OF INVENTION	(2) FOREIGN COUNTRIES OF PATENT APPLICATION
(b) NAME OF EMPLOYER	(b) NAME OF EMPLOYER		
(c) ADDRESS OF EMPLOYER *(Include ZIP Code)*	(c) ADDRESS OF EMPLOYER *(Include ZIP Code)*		

SECTION II - SUBCONTRACTS *(Containing a "Patent Rights" clause)*

6. SUBCONTRACTS AWARDED BY CONTRACTOR/SUBCONTRACTOR *(If "None," so state)*

NAME OF SUBCONTRACTOR(S) a.	ADDRESS *(Include ZIP Code)* b.	SUBCONTRACT NUMBER(S) c.	FAR "PATENT RIGHTS" d.		DESCRIPTION OF WORK TO BE PERFORMED UNDER SUBCONTRACT(S) e.	SUBCONTRACT DATES *(YYYYMMDD)* f.	
			(1) CLAUSE NUMBER	(2) DATE *(YYYYMM)*		(1) AWARD	(2) ESTIMATED COMPLETION

SECTION III - CERTIFICATION

7. CERTIFICATION OF REPORT BY CONTRACTOR/SUBCONTRACTOR *(Not required if: (X as appropriate))* ☐ **SMALL BUSINESS or** ☐ **NONPROFIT ORGANIZATION**

I certify that the reporting party has procedures for prompt identification and timely disclosure of "Subject Inventions," that such procedures have been followed and that all "Subject Inventions" have been reported.

a. NAME OF AUTHORIZED CONTRACTOR/SUBCONTRACTOR OFFICIAL *(Last, First, Middle Initial)*	b. TITLE	c. SIGNATURE	d. DATE SIGNED

DD FORM 882 INSTRUCTIONS

GENERAL

This form is for use in submitting INTERIM and FINAL invention reports to the Contracting Officer and for use in reporting the award of subcontracts containing a "Patent Rights" clause. If the form does not afford sufficient space, multiple forms may be used or plain sheets of paper with proper identification of information by item number may be attached.

An INTERIM report is due at least every 12 months from the date of contract award and shall include (a) a listing of "Subject Inventions" during the reporting period, (b) a certification of compliance with required invention identification and disclosure procedures together with a certification of reporting of all "Subject Inventions," and (c) any required information not previously reported on subcontracts containing a "Patent Rights" clause.

A FINAL report is due within 6 months if contractor is a small business firm or domestic nonprofit organization and within 3 months for all others after completion of the contract work and shall include (a) a listing of all "Subject Inventions" required by the contract to be reported, and (b) any required information not previously reported on subcontracts awarded during the course of or under the contract and containing a "Patent Rights" clause.

While the form may be used for simultaneously reporting inventions and subcontracts, it may also be used for reporting, promptly after award, subcontracts containing a "Patent Rights" clause.

Dates shall be entered where indicated in certain items on this form and shall be entered in six or eight digit numbers in the order of year and month (YYYYMM) or year, month and day (YYYYMMDD). Example: April 1999 should be entered as 199904 and April 15, 1999 should be entered as 19990415.

1.a. Self-explanatory.

1.b. Self-explanatory.

1.c. If "same" as Item 2.c., so state.

1.d. Self-explanatory.

2.a. If "same" as Item 1.a., so state.

2.b. Self-explanatory.

2.c. Procurement Instrument Identification (PII) number of contract (DFARS 204.7003).

2.d. through 5.e. Self-explanatory.

5.f. The name and address of the employer of each inventor not employed by the contractor or subcontractor is needed because the Government's rights in a reported invention may not be determined solely by the terms of the "Patent Rights" clause in the contract.

Example 1: If an invention is made by a Government employee assigned to work with a contractor, the Government rights in such an invention will be determined under Executive Order 10096.

Example 2: If an invention is made under a contract by joint inventors and one of the inventors is a Government employee, the Government's rights in such an inventor's interest in the invention will also be determined under Executive Order 10096, except where the contractor is a small business or nonprofit organization, in which case the provisions of 35 U.S.C. 202(e) will apply.

5.g.(1) Self-explanatory.

5.g.(2) Self-explanatory with the exception that the contractor or subcontractor shall indicate, if known at the time of this report, whether applications will be filed under either the Patent Cooperation Treaty (PCT) or the European Patent Convention (EPC). If such is known, the letters PCT or EPC shall be entered after each listed country.

6.a. Self-explanatory.

6.b. Self-explanatory.

6.c. Self-explanatory.

6.d. Patent Rights Clauses are located in FAR 52.227.

6.e. Self-explanatory.

6.f. Self-explanatory.

7. Certification not required by small business firms and domestic nonprofit organizations.

7.a. through 7.d. Self-explanatory.

SUBAWARD EXPENSE BUDGET

COST REIMBURSABLE EXPENSES - NO PAYMENTS IN ADVANCE

	Amount
Salaries	10,058.00
Benefits	2,877.00
Sub Awards	0.00
Contracted Services	0.00
Supplies	0.00
Communication	0.00
Foreign Travel	0.00
Domestic Travel	1,496.00
Rent	0.00
Repair and Maint	0.00
Awards	0.00
Participant Support	0.00
Capital Equipment	0.00
Major Renovations	0.00
Facilities and Admin	7,504.00
TOTAL	**21,935.00**

Facilities and Admin (IDC) Basis: MTDC less equip, sub, part supp,awa Rate: 52% Base Amount: 14,431.00

This subaward is being issued to allow work to commence, however, no work with animals shall be authorized until IACUC/ACURO approvals are obtained. Any work with animals that occurs prior to such approval will not be reimbursed by the Pass-Through entity. Subrecipient agrees to provide documentation to Pass-Through entity of all necessary reviews and approvals prior to conducting any animal-related work.

IDENTIFY HOST IMMUNE SIGNATURES

Task 11.04 Lab: identify host immune and stress signatures in wild bats and in a captive feeding trial. CSU will provide advice on how to measure bat immune signatures.

Milestones
Immunology on samples from Australia (MSU):
• Provide advice on tests on bats from Australia (6mths)

Immunology on samples from Ghana (Cambridge):
• Provide advice on tests on bats from Australia (24 mths).

Task 11.08, Lab: amplification and transmission dynamics of quasispecies *in vitro* and *in vivo*. RML, with help from CSU, will undertake in vivo experiments to measure phenotypes of henipavirus strains.

Milestones
• Provide advice on infection experiments (24mths)
• Design experiments and develop IACUC protocols and submit paperwork for ACURO approval (24mths)

DEMONSTRATE PROOF OF CONCEPT, FEASIBILITY, AND SCALABILITY OF CHAD/VSV VACCINATION

Task 22.02, Proof-of-concept demonstration of ChAd/VSV vaccination feasibility and scalability of ChAd/VSV vaccination in bats. RML will develop and test a scalable vectored vaccine for target henipaviruses in bats. RML, with help from Cambridge, will assess the feasibility and scalability of the vaccine in bats.

Milestones
- Provide advice on vaccine development (24mths)

Email or mail invoices to:

Pass-Through Entity Financial Contact

Name	Jennifer Hodges
Address	Montana State University PO Box 173520 Bozeman, MT 59717-3520
Phone	
Email	

Invoices must meet the requirements of the Agreement Terms and Conditions.

1) Reference the MSU Subaward ID **G228-19-W7329** on all invoices.
2) Include current and cumulative costs by budget category (including cost sharing if required) on all invoices.
3) Include period covered by the invoice.
4) Invoices must be signed, dated and certified as to truth and accuracy. Invoices or vouchers requesting payment will include a certification, signed by an authorized official, which reads as follows: "By signing this report, I certify to the best of my knowledge and belief that the report is true, complete, and accurate, and the expenditures, disbursements and cash receipts are for the purposes and objectives set forth in the terms and conditions of the Federal award. I am aware that any false, fictitious, or fraudulent information, or the omission of any material fact, may subject me to criminal, civil or administrative penalties for fraud, false statements, false claims or otherwise. (U.S. Code Title 18, Section 1001 and Title 31, Sections 3729–3730 and 3801–3812)."

From: Rogers,Susan
Sent: Monday, May 6, 2019 4:09 PM
To: Harvey,Julie
Cc: Schountz,Tony
Subject: From 140925 CSU subaward with MSU PREEMPT
Attachments: CSU_MSU PreEmpt SubrecipientCommitment Yr 1 less animal work costs.pdf; Schountz UM DARPA Justification Apr 2019.docx

Hi Julie,

This is round umpteenth…. Last week MSU requested budget less the animal costs work. So I sent them the attached word doc highlighting the items that didn't include animal work. They then requested the attached form completed. I did as much as I could. They said once the Animal Work is approved by RML (BSL4 in Montana), MSU will revise award for that the original amount. In the meantime they need this document. Project started 10/1/18. I guess no subs have the subcontract yet.

This is from KR 140925 if you want to check it out. I don't think we what to do a revised budget because they should award the entire amount once the animal work is approved by whomever.

Sure hope it is what they need to get it going.

If you find a phone, it might be easier to discuss.

Susan

IDA / AIDL: M, F
Pathology: Tu, W, Th

From: Hodges, Jennifer [mailto
Sent: Thursday, May 02, 2019 3:05 PM
To: Rogers,Susan < >
Cc: LaTrielle, Sara ; Schountz,Tony
Subject: RE: CSU subaward with MSU PREEMPT

http://www.montana.edu/research/osp/documents/subcontracts/SubrecipientCommitment.pdf
Hello Susan and Tony,
We need the link above completed by the two of you. Please let me know if you have any questions.
Thank you,
Jen

From: Rogers,Susan [mailto:
Sent: Tuesday, April 30, 2019 12:32 PM
To: Hodges, Jennifer >
Cc: LaTrielle, Sara ; Schountz,Tony
Subject: RE: CSU subaward with MSU PREEMPT

Hi Jen,

Budget for non-IACUC/non-ACURO related work includes:
Schountz effort: **$12,935 =** $10,058 (salary) + $2,877 (fringe)
Bozeman, MT project meeting travel: **$1,496**
Direct Total: $14,431
F&A (54%): $7,504
Total: $21,935

I've highlighted the items in the budget justification from October 2018.

Is this sufficient or do you need something else?

Thanks,
Susan

IDA / AIDL: M, F
Pathology: Tu, W, Th

From: Schountz,Tony
Sent: Tuesday, April 30, 2019 12:16 PM
To: Hodges, Jennifer <
Cc: Schountz,Tony >; LaTrielle, Sara >; Rogers,Susan

Subject: Re: CSU subaward with MSU PREEMPT

Hi Jennifer,

Thanks very much. I would appreciate get a sub award in place sans animal work. I've cc'd Susan Rogers on this email - she is one of my departmental grant people who has been working on this.

Prior to the change in my scope of work after last October's meeting in Bozeman, I was to provide technical input (effort) and to have travel to the meetings. I paid for the travel to the October meeting with university funds and as far as I'm aware those costs have not been reimbursed. Hopefully, those can be included with this subaward. Susan can provide you with the other details on the non-animal scope of work.

Thanks,

Tony

> On Apr 30, 2019, at 11:52 AM, Hodges, Jennifer wrote:
>
> Hello Tony,
> We would like to get your subaward paperwork together while CSU is in process for ACURO.
> Could you send me the budget that is non-IACUC/non-ACURO related?
> Let me know if this is helpful to you or more of a headache.
> Thank you,
> Jen

Jennifer Hodges
Fiscal Manager
PREEMPT

—

Tony Schountz, PhD
Associate Professor
Arthropod-borne and Infectious Disease Laboratory
Department of Microbiology, Immunology and Pathology
College of Veterinary Medicine
Colorado State University
3185 Rampart Road
Fort Collins, CO 80523-1692

Montana State University (MSU)- Office of Sponsored Programs
SUBRECIPIENT COMMITMENT FORM 2019.04

Clear All Pages

To be completed by Subrecipient. Questions: contact MSU Office of Sponsored Programs, 406-994-2381 or subawards@montana.edu

Subrecipient Information

Legal Name and Address (incl zip+4)

Colorado State University
200 W. Lake St
Fort Collins, CO 80521-4593

Congressional District: CO-002

DUNS Number (9 digit) 785979618

Type of Organization: Non-US for Profit

Project Information

Address where research will take place ☑ **Same as legal address** **OR:**

Congressional District:

MSU PI: Paina Plowright **Sub PI:** Tony Schountz

Subaward Period of Performance Start: 10/01/18 **End:** 09/30/19

Amount Requested: **Cost Share Amount:**

Prime Sponsor: DARPA

Project Title: Preventing emergence and spillover of bat pathogens in high-risk global hotspots

SECTION A- CERTIFICATIONS

1. Facilities and Administrative Rates- select one:

○ **We have applied our federally negotiated F&A rates. Our negotiated rate agreement is:**

☑ **Available at the URL link**

☐ **Attached**

○ **We do not have a federally negotiated rate and have elected the 10% of Modified Direct Costs de minimis rate.**

○ **We have applied other rates as required by the prime sponsor policies/guidelines.**

2. Compliance- Our Scope of Work includes:

Human Subjects ○ **No** ○ **Yes** **Approval Date:** **OR** ☐ **Pending**

Animal Subjects ○ **No** ○ **Yes** **Approval Date:** **OR** ☐ **Pending**

Subrecipient's IRB and/or IACUC approval must be provided to Montana State University before any subaward work involving Human and/or Animal Subjects may begin. Please forward this document to MSU PI as soon as it is available.

If Human Subjects are involved, have all key personnel completed Human Subjects Training? **Yes** ○ **No** ○ **N/A** ○

3. Conflict of Interest (CoI)- select one:

○ **Not applicable because this project is not being funded by PHS (NIH, HRSA, etc.), or any other sponsor that has adopted the federal financial disclosure requirements (NSF, etc.)**

○ **Subrecipient Organization/Institution certifies that it has an active and enforced conflict of interest policy that is in compliance with the provision of 42 CFR Part 50, Subpart F "Responsibility of Applicants for Promoting Objectivity in Research". Subrecipient also certifies that, to the best of the Institution's knowledge, copies of all disclosures made by Investigators performing research hereunder, which Subrecipient has determined are Financial Conflicts of Interest, are hereby provided to MSU, including disclosure of the management, reduction or elimination of such disclosures, sufficient for MSU to make the required disclosure to the Prime Public Health Service funding agency.**

○ **Subrecipient Organization/Institution certifies that it will comply with MSU's Conflict of Interest Policy located online at: http://www2.montana.edu/policy/conflict_of_interest/ Subrecipient hereby provides to MSU copies of all Investigator disclosures of Significant Financial Interests (as defined in the policy) that are directly related to Subrecipient's work for MSU, including all information necessary for MSU to determine whether such interests are Financial Conflicts of Interest. MSU, in consultation with Subrecipient, shall determine whether the disclosed interest are Financial Conflicts of Interest and, if so, determine how such conflicts shall be managed, reduced, or eliminated and shall report such interests to the funding agency in accordance with the requirements of the Public Health Service regulations, 42 CRF Part 50, Subpart F.**

Montana State University (MSU)- Office of Sponsored Programs
SUBRECIPIENT COMMITMENT FORM

4. Ethics in Research Training (applicable to projects funded by NSF, NIFA or an NIH Training Grant)- select one:

○ **Not applicable because this project is not being funded by NSF, NIFA or an NIH Training Grant.**

◉ **Subrecipient organization/institution hereby certifies that it will ensure that all undergraduates, graduate students, and postdoctoral researchers who will be supported by this proposal will be trained on the oversight in the responsible and ethical conduct of research.**

5. Debarment and Suspension * If checked, attach explanation.

Subrecipient, the PI or any other employee or student participating in this project **are*** ☐ **are not** ☑ debarred, suspended, proposed for debarment, declared ineligible, or otherwise excluded from or ineligible for participation in federal assistance programs, federal contracts or activities.

Subrecipient, the PI or any other employee or student participating in this project **are*** ☐ **are not** ☑ presently indicted for, or otherwise criminally or civilly charged by a government entity.

Subrecipient **has*** ☐ **has not** ☑ within three (3) years preceding this offer, been convicted of or had a civil judgement rendered against them for commission of fraud or criminal offense in connection with obtaining, attempting to obtain, or performing a public (federal, state or local) contract or subcontract; violation of Federal or State antitrust statutes relating to the submission of offers; or commission of embezzlement, theft, forgery, bribery, falsification or destruction of records, making false statements or receiving stolen property.

Subrecipient **has*** ☐ **has not** ☑ within three (3) years preceding this offer, had any contract terminated for default by any Federal Agency.

SECTION B FFATA Information- complete all fields

1. Is Subrecipient owned or controlled by a parent entity? Yes ○ No ○

Note: If yes, please provide DUNS Number and location (City, State, Congressional District, and Country) of parent entity:

2. Is Subrecipient currently registered in System for Award Management, SAM.gov (https://www.sam.gov/portal/public/SAM/)

Yes ◉ No ○ **Note**: SAM.gov Registration is **required** for recipients receiving $25,000 or more from any federally funded project.

3. Executive Compensation- During the previous fiscal year my organization received eighty percent (80%) or more of its annual gross revenues in federal awards AND twenty-five million dollars ($25M) or more in annual gross revenues in federal awards. Yes ○ No ◉

My organization regularly reports information on the compensation of its senior executives in response to section 13(a) or 15(d) of the Securities Exchange Act of 1934 (15 U.S.C. 78m(a), 78 (d) or section 6104 of the Internal Revenue Code of 1986 [26 USC 6104]. Yes ◉ No ○

SECTION C Audit Status- complete all fields

1. Audit Status/ Fiscal Responsibility

○ **Subrecipient organization receives an annual audit in accordance with OMB Uniform Guidance (previously Circular A-133). Were there any findings or exceptions noted?**

No ☑ Yes ☐ If "Yes" attach an explanation.

If your most recent audit is not available on the **Federal Audit Clearinghouse**, you must provide a copy to MSU.

○ **Subrecipient organization is NOT subject to the OMB Uniform Guidance (previously A-133) audit requirements and will complete a mini-audit questionnaire prior to the establishment of a subaward agreement. Subrecipient is not subject to the UG audit requirments because organization:**

☐ Is For-Profit ☐ Is a Foreign Entity ☐ Is a US Government Entity ☐ Expended less than $750,000 (or $500,000 per OMB A-133) in US Federal funds during previous fiscal year

Please note: When applying for funds from agencies under the U.S. Department of Health and Human Services foreign organizations and for-profits that have expended a total of $500,000 or more under one or more awards from the U.S. Department of Health and Human Services (as a direct grantee and/or under a consortium participant) will be required to have a financial-related audit of all HHS awards as defined in, and in accordance with, the Government Auditing Standards or an audit that meets the requirements of OMB Uniform Guidance or Circular A-133 as applicable.

Montana State University (MSU)- Office of Sponsored Programs
SUBRECIPIENT COMMITMENT FORM

Provide the budget for the Performance Period indicated on p.1. of this form. If funding is incremental, subsequent increments will be funded through amendments once requested by MSU PI.

Proposed Subaward Budget	
Salaries	10,058
Benefits	2,877
Sub Awards	
Contracted Services	
Supplies	
Communication	
Foreign Travel	
Domestic Travel	1,496
Rent	
Repair and Maint	
Awards	
Participant Support	
Capital Equipment	
Major Renovations	
Total Direct Costs	14,431.00
Total Indirect Costs	7,504
Rate = 0.52000 enter as decimal (. ####) Base= 14,431 enter $ amount	
Total Costs	21,935

Proposed Cost Share Budget (if applicable)	
Salaries	
Benefits	
Sub Awards	
Contracted Services	
Supplies	
Communication	
Foreign Travel	
Domestic Travel	
Rent	
Repair and Maint	
Awards	
Paticipant Support	
Capital Equipment	
Major Renovations	
Total Direct Costs	0
Total Indirect Costs	0
Rate = enter as decimal (. ####) Base= enter $ amount	
Total Cost Share	0

Additional Information:

Year one budget less costs for animal work.

Montana State University (MSU) - Office of Sponsored Programs (OSP)
SUBRECIPIENT COMMITMENT FORM

Subrecipient Contacts

Please complete **all** fields on this form in order to provide the necessary information for us to proceed. Award documents and related correspondence will be delivered by email to individuals listed below. For multiple email adresses please seperate with a semi-colon.

Institution/Organization (Subrecipient)					
Name:	Colorado State University		Email:		
Address:	2002 Campus Delivery				
City:	Fort Collins	State:	CO	Zip Code (9 digits):	80523-2002

Administrative Contact					
Name:	Ashley Stahle				
Address:	Office of Sponsored Programs 2002 Campus Delivery				
City:	Fort Collins	State:		ZipCode:	80523-2002
Telephone:					

Principal Investigator (Subrecipient)					
Name:	Tony Schountz				
Address:	1692 Campus Delivery				
City:	Fort Collins	State:	CO	ZipCode:	80523-1692
Telephone:		Email:			

Financial Contact:					
Name:					
Address:	Office of Sponsored Programs 2002 Campus Delivery				
City:		State:		ZipCode:	
Telephone:		Email:			

Authorized Official: authorized to sign for the recipient institution					
Name:	Julie Harvey				
Address:	Office of Sponsored Programs 2002 Campus Delivery				
City:	Fort Collins	State:	CO	ZipCode:	80523-2002
Telephone:		Email:			

 Montana State University (MSU) - Office of Sponsored Programs (OSP)
SUBRECIPIENT COMMITMENT FORM

APPROVED FOR SUBRECIPIENT:
The information, certifications and representations above have been read, signed and made by an **authorized official** of the subrecipient named herein. The appropriate programmatic and administrative personnel involved in this application are aware of agency policy in regard to subawards and are prepared to establish the necessary inter-institutional agreements consistent with those policies. **Any work begun and/or expenses incurred prior to execution of a subaward agreement are at the Subrecipient's own risk.**

Signature of Subrecipient's Authorized Official | Date

Name and Title of Authorized Official			
Email		Phone	

MSU USE ONLY

REVIEWED AND APPROVED BY MSU PI:
MSU PI has reviewed this Subrecipiet Commitment form and certifies that (1) the information submitted with this Subrecipient Commitment Form is true, complete, and accurate to the best of their knowledge; (2) agrees to accept responsibility for monitoring the programmatic and financial performance and progress of subrecipient, including tracking Subrecipient Cost Sharing and ensuring that Subrecipient IRB/IACUC approvals are kept current during the performance of this Subaward..

Signature of MSU PI | Date

MSU PI Department		Email	

Additional comments or information:

CSU BUDGET JUSTIFICATION

Personnel:

Tony Schountz, PhD, (CSU PI, Years 1-3: 0.69 academic and 0.23 summer months / yr; Year 4: 0.19 academic and 0.06 summer months). Dr. Schountz is an experienced viral immunologist at CSU and maintains the colony of Jamaican fruit bats. He has had the colony for 12 years and has expertise handling bats for inoculations and sample collection, and development of assays to assess host responses during infection. He also has Visiting Scientist status at Rocky Mountain Laboratories where he performs BSL-4 work in collaboration with Dr. Munster. He will also perform PCR array experiments on bat host responses, which generates thousands of data points per experiment for data reduction and analysis. Fringe Rate: 28.6% Salary is calculated each year with ~2.5% inflation. **$10,058 +$2,877 = $12,935**

Miles Eckley, GRA (Yr 1: 0.98 calendar months) – Mr. Eckley will assist with the on stress responses mediated by nutrition and immune modulation and its impact on virus shedding experiments. Fringe Rate: 10.6%.

Travel:

- Travel expenses for PI to travel to RML (Hamilton, MT) for ~2 weeks to perform BSL-4 infection work and sample processing (3 trips at $2,794 per trip); travel to Bozeman, MT for Project Meetings (3 trips at $1,496 per trip). Travel costs: Phase I: $4,290 / year; Phase II: $4,290 (year 3 only).
  - Hamilton, MT (driving with project related items) - $2,794 / trip
    - Lodging:
      - Jackson, WY (half way point): 1 night each way @ $196 / night (w/ tax) = $392
      - Hamilton, MT: 10 nights @ $91/ night (w/ tax) = $910
    - Mileage = 1,600 miles (~800 miles from Fort Collins, CO to Hamilton, MT plus driving in Hamilton during trip) @ $0.49 / mi = $784
    - Per diem Meals = 12 days @ $59 / day = $708
  - Bozeman, MT $1,496 / trip
    - Airfare: $790 (non-stop)
    - Lodging: 2 nights @ $149 / night (w/ tax) = $298
    - Per diem Meals: 3 days @ $59/ day = $177
    - Car Rental: 3 days @ $77/day = $231

Other Direct:

- Bat colony maintenance: Daily bat room colony care and maintenance for project is calculated $26.85 / day. Phase I: $9,800 / yr; Phase II: year 3: $9,800, year 4: $4,900. Stress response experiment per diem charges are calculated at $4.72 / day / cage * 4 cages of 5 bats for 21 days ($396)
- Bat transportation costs: Transporting of non-infected bats to RML estimated at $1,000 / shipment. One shipment is expected each year.
- Tuition: Yr 1: $1,716 - corresponds to effort on project.

F&A: Modifiied Total Direct: 52%.

From: Stahle,Ashley
Sent: Tuesday, June 4, 2019 2:42 PM
To: Grinstead,Liz
Subject: FW: Memo to: Colorado State University G228-19-W7329 Agreement signed
Attachments: Colorado State University G228-19-W7329 Agreement.pdf

Follow Up Flag: Follow up
Flag Status: Completed

Categories: Award

I think you are waiting on this 😊

From: Nesbitt, Jennifer
Sent: Thursday, May 30, 2019 5:59 PM
To: Harvey,Julie >; Stahle,Ashley >; Schountz,Tony ; Marrale,Kim ; Plowright, Raina ; Hodges, Jennifer ; LaTrielle, Sara

Subject: Memo to: Colorado State University G228-19-W7329 Agreement signed

Attached please find the fully executed MSU Subaward referenced above**.** We look forward to working with you on this project.

Please remember: This subaward is being issued to allow work to commence, however, no work with animals shall be authorized until IACUC/ACURO approvals are obtained. Any work with animals that occurs prior to such approval will not be reimbursed by the Pass-Through entity. Subrecipient agrees to provide documentation to Pass-Through entity of all necessary reviews and approvals prior to conducting any animal-related work.

All invoices for this project should be submitted according to the procedures specified in Attachment 6, Subaward Agreement Invoicing Procedures.

If you need any further assistance, please feel free to email subawards@montana.edu or call

Sincerely,
Jennifer

Jennifer F. Nesbitt
Office of Sponsored Programs
Montana State University
Bozeman, MT 59717

Office Hours: Monday-Friday, 9:15am-4:15pm

MONTANA STATE UNIVERSITY

MONTANA STATE UNIVERSITY

Federal Subaward Agreement MSU ID G228-19-W7329

Pass-Through Entity (PTE)	Subrecipient
Name Montana State University Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470	Name Colorado State University Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins, CO 80523-2002 Duns 785979618 Colorado State University
PTE Principal Investigator: **Raina Plowright**	Principal Investigator: **Tony Schountz**
PTE Awarding Agency: **Defense Advanced Research Projects Agency**	PTE Awarding Agency ID: D18AC00031
PTE CFDA 12.910 Research and Technology Development	This subaward is subject to OMB Uniform Guidance PTE FAIN: D18AC00031

Subaward Title: Preventing emergence and spillover of bat pathogens in high-risk global hotspots

Subaward Period of Performance	Authorized Amount	**Subaward ID: G228-19-W7329**
Start **10/01/2018** End **09/30/2019**	**21,935.00**	1. Cost Sharing is Not Required 2. This award is a Cost Reimbursable agreement 3. Project Reporting is Required (Attachments 4 and 4A)

Terms and Conditions

1) PTE hereby awards a cost reimbursable subaward, as described above, to SUBRECIPIENT. The Budget and Scope of Work for this subaward are shown in Attachments 5 and 5A. In its performance of subaward work, SUBRECIPIENT shall be an independent entity and not an employee or agent of PTE.
2) PTE shall reimburse SUBRECIPIENT not more often than monthly for allowable costs.
3) All invoices shall be submitted using SUBRECIPIENT's standard invoice, but at a minimum shall include current and cumulative costs (including cost sharing), subaward number, and certification as to truth and accuracy of the invoice as required in 2 CFR 200.415 . Invoices that do not reference PTE's subaward number shall be returned to SUBRECIPIENT. Invoices and questions concerning invoice receipt or payment should be directed to the appropriate party's Financial Contact, as shown in Attachment 3 and detailed in Attachment 6.
4) A final statement of cumulative costs incurred, including cost sharing, marked "FINAL", must be submitted to PTE's Financial Contact NOT LATER THAN forty-five (45) days after subaward end date. The final statement of costs shall constitute SUBRECIPIENT's final financial report.
5) All payments shall be considered provisional and subject to adjustment within the total estimated cost in the event such adjustment is necessary as a result of an adverse audit finding against the SUBRECIPIENT.
6) PTE reserves the right to reject an invoice, in accordance with 2 CFR 200.305.
7) Matters concerning the technical performance of this subaward should be directed to the appropriate party's Principal Investigator, as shown in Attachment 3.
8) Matters concerning the request or negotiation of any changes in the terms, conditions, or amounts cited in this subaward agreement, and any changes requiring prior approval, should be directed to the appropriate party's Administrative Contact, as shown in Attachment 3. Any such changes made to this subaward agreement require the written approval of each party's Authorized Official, as shown in Attachment 3.
9) Substantive changes (for example, change in Scope of Work, Attachment 5A) made to this subaward agreement require the written approval of each party's Authorized Official as shown in Attachment 3. The PTE may issue non-substantive changes to the Period of Performance Bilaterally.
10) Each party shall be responsible for its negligent acts or omissions and the negligent acts or omissions of its employees, officers, or directors, to the extent allowed by law.
11) Either party may terminate this agreement with thirty (30) days written notice to the appropriate party's Administrative Contact, as shown in Attachment 3. PTE shall pay SUBRECIPIENT for termination costs as allowable under Uniform Guidance, 2 CFR 200, or 45 CFR Part 75 Appendix IX, "Principles for Determining Costs Applicable to Research & Development under Grants and Contracts with Hospitals," if applicable. If the PTE Awarding Agency suspends or terminates the prime award in whole or in part, PTE may suspend or terminate this subaward accordingly.
12) No-cost extensions require the approval of the PTE. Any requests for a no-cost extension should be addressed to and received by the Administrative Contact, as shown in Attachment 3, not less than thirty (30) days prior to the desired effective date of the requested change.
13) The subaward is subject to the terms and conditions of the PTE Award and other special terms and conditions, as identified in Attachment 2.
14) By signing below SUBRECIPIENT makes the certifications and assurances shown in Attachments 1 and 2.

By an Authorized Official of Montana State University	By an Authorized Official of SUBRECIPIENT
Dale Huls — 5/30/2019 Signature — Date	Signature — Date Ashley Stahle cn=Ashley Stahle, o=Colorado State University, ou=Sponsored Programs, email=ashley.stahle@colostate.edu, c=US 2019.05.30 15:03:14 -06'00'
Dale Huls, Assistant Director Office of Sponsored Programs Montana State University	Ashley Stahle, Senior Research Administrator Printed Name and Title
OSP Ref W7329-G19-228	

By signing the Subaward Agreement, the authorized official of SUBRECIPIENT certifies, to the best of his/her knowledge and belief, that:

Certification Regarding Lobbying

1) No Federal appropriated funds have been paid or will be paid, by or on behalf of the SUBRECIPIENT, to any person for influencing or attempting to influence an officer or employee of any agency, a Member of Congress, an officer or employee of Congress, or an employee of a Member of Congress in connection with the awarding of any Federal contract, the making of any Federal grant, the making of any Federal loan, the entering into of any cooperative agreement, and the extension, continuation, renewal, amendment, or modification of any Federal contract, grant, loan, or cooperative agreement.

2) If any funds other than Federal appropriated funds have been paid or will be paid to any person for influencing or intending to influence an officer or employee of any agency, a Member of Congress, an officer or employee of Congress, or an employee of a Member of Congress in connection with this Federal contract, grant, loan, or cooperative agreement, the SUBRECIPIENT shall complete and submit Standard Form -LLL, "Disclosure Form to Report Lobbying," to the PASS-THROUGH ENTITY.

3) The SUBRECIPIENT shall require that the language of this certification be included in the award documents for all subawards at all tiers (including subcontracts, subgrants, and contracts under grants, loans, and cooperative agreements) and that all subrecipients shall certify and disclose accordingly.

This certification is a material representation of fact upon which reliance was placed when this transaction was made or entered into. Submission of this certification is a prerequisite for making or entering into this transaction imposed by section 1352, title 31, U. S. Code. Any person who fails to file the required certification shall be subject to a civil penalty of not less than $10,000 and not more than $100,000 for each such failure.

Debarment, Suspension, and Other Responsibility Matters

SUBRECIPIENT certifies by signing this Subaward Agreement that neither it nor its principals are presently debarred, suspended, proposed for debarment, declared ineligible, or voluntarily excluded from participation in this transaction by any federal department or agency.

Audit and Access to Records

Subrecipient certifies by signing this Subaward Agreement that it complies with the Uniform Guidance, will provide notice of the completion of required audits and any adverse findings which impact this subaward as required by parts 200.501- 200.521, and will provide access to records as required by parts 200.336, 200.337, and 200.201 as applicable.

See Copy of Award Notice Attachment 2A.

Special Terms and Conditions:

1. Copyrights
   SUBRECIPIENT grants to PASS-THROUGH ENTITY (PTE) an irrevocable, royalty-free, nontransferable, non-exclusive right and license to use, reproduce, make derivative works, display, and perform publicly any copyrights or copyrighted material (including any computer software and its documentation and/or databases) first developed and delivered under this Agreement solely for the purpose of and only to the extent required to meet PTE's obligations to the Federal Government under its Prime Award.
2. Data Rights
   SUBRECIPIENT grants to PTE the right to use data created in the performance of this Agreement solely for the purpose of and only to the extent required to meet PTE's obligations to the Federal Government under its Prime Award.
3. Carry Forward
   Carry Forward requests must be sent to PTE's Authorized Official contact, as shown in Attachment 3.

Additional Special Terms: See Copy of Award Notice Attachment 2A.

DEPARTMENT OF THE INTERIOR
Interior Business Center
Acquisition Services Directorate, Division III
354 South Highway 92
Sierra Vista, AZ 85635

Agent for:
Defense Advanced Research Projects Agency (DARPA)

RESEARCH COOPERATIVE AGREEMENT SCHEDULE

1. **Agreement Number**: **D18AC00031**

2. **Recipient Name:** **Montana State University - Bozeman**
   307 Montana Hall
   Bozeman, MT 59717

3. **Identification Numbers**:

   Tax Identification Number (TIN)**: 81-6010045**

   Data Universal Numbering System (DUNS) Number**: 625447982**

   Commercial and Government Entity (CAGE) Code**: 1KQE9**

   Federal Interagency Code for Education (FICE)**: 002532**

   Catalog of Federal Domestic Assistance (CFDA): **12.910 – Research and Technology Development**

   ASAP Recipient Number: **3034514**

   Defense Advanced Research Projects Agency (DARPA) MIPR Number(s)**: HR0011836358**

4. **Principal Investigator/Key Personnel**: Dr. Raina Plowright
   111A Lewis Hall
   P.O. Box 173520
   Bozeman, MT 59717-3520

   Telephone:
   E-mail address

5. **Statement of Work:** The research to be accomplished is identified in the Recipient's Statement of Work and is incorporated in full text as part of this agreement. The revised budget proposal entitled "Preventing emergence and spillover of bat pathogens in high-risk global hotspots" dated 07/18/2018 and revised technical proposal dated 07/17/2018, submitted in response to Broad Agency Announcement DARPA-BAA- HR001118S0017 are incorporated by reference herein.

6. Points of Contact:

a. Agreements Officer:

Department of the Interior
Interior Business Center
Acquisition Services Directorate, Division III
354 South Highway 92
Sierra Vista, AZ 85635

Attention: Doreen Vieira-Cross
Telephone:
FAX:
Email:

b. Cooperative Agreement Administrator:

Department of the Interior
Interior Business Center
Acquisition Services Directorate, Division III
354 South Highway 92
Sierra Vista, AZ 85635

Attention: Deborah Branham
Telephone:
FAX:
Email:

c. Agreements Officer's Representative:

J. Aura Gimm
Air Force Office of Scientific Research
875 N. Randolph Street
Arlington, VA 22203

Telephone:
Email:

d. DARPA Program Manager (PM):

Defense Sciences Office (BTO)
675 N. Randolph Street
Arlington, VA 22203-2114

Attention: Dr. James L. Gimlett
Telephone:
Email:

e. DARPA DSO Assistant Director, Program Management (ADPM)

Attention: Kristen Fuller
Email:

7. Delegation of Administrative Duties: Department of the Interior/Interior Business Center (DOI/IBC) and the Office of Naval Research (ONR). See Article 17 of Exhibit A for the administration duties delegated to ONR. The cognizant ONR office that will perform the delegated duties is identified below:

Office of Naval Research
300 Fifth Ave, Suite 710
Seattle, WA 98104-2398

Phone:
Email:

8. **Period of Performance Profile:**

a.	**Base Phase I (24 Months):**	**(10/01/2018 through 09/30/2020)**	**$6,296,068.00**
b.	**Optional Phase II (18 Months):**	**(10/01/2020 through 03/31/2022)**	**$1,943,433.00 (If funded)**
c.	**Total Award Amount:**		**$8,239,511.00**

9. **Funding:** The following funds are allotted to this cooperative agreement.

FY2018/2019:	$2,719,770.00 (MIPR# HR0011836358)
Total:	$2,719,770.00

10. **Appropriation Data:** Pursuant to this action:

MIPR# HR0011836358 $2,719,770.00
Account Assignment: K G/L Account: 6100.411C0
Business Area: D000 Commitment Item: 411C00
Cost Center: DS68694000 Functional Area:
DNPAQ0000.000000 Fund: XXXD4529NP Fund Center:
DS68694000 Project/WBS: DR.F3BN8.DPBX6358 PR Acct
Assign: 01

11. **Terms and Conditions:** This cooperative agreement is subject to General Terms and Conditions for Cooperative Agreements set forth in the attached Exhibit A and to any Special Terms and Conditions contained in Item 17 of this Research Cooperative Agreement Schedule.

12. **Acceptance of Cooperative Agreement:** Acceptance of this cooperative agreement is pursuant to Article 14 of Exhibit A. The Recipient is not required to countersign the Cooperative Agreement document; however, the Recipient agrees to the conditions specified in the Research Cooperative Agreement Schedule and the Articles herein unless notice of disagreement is furnished to the Agreements Officer within 15 calendar days after the date of the Agreements Officer's signature. In case of disagreement, the Recipient shall not assess the Cooperative Agreement of any costs of the research unless and until such disagreement(s) is/are resolved.

13. **Payments:** Payments will be made in accordance with Article 3 of Exhibit A.

14. **Reporting Requirements:** A final DD Form 882 is required to be filed listing all subject inventions or stating that there were none. In accordance with DARPA-BAA-HR001118S0017, the frequency of the reporting requirement differs from those commonly found in financial assistance agreements due to significant Government involvement throughout the duration of the research cycle. The following reports shall be submitted and will become due on the dates as shown below:

REPORT TYPE	DUE DATE	SUBMIT TO
Quarterly R&D Status Reports	Within 30 days of the end of each quarter	See Exhibit A Attachment 1
Monthly Financial Management Report	Within 30 days of the end of each month	See Exhibit A Attachment 2
Special Technical Report	Due as required	AOR, AO, PM, & DARPA Research Services
Annual Federal Financial Report (SF 425)	29 Dec 2019 29 Dec 2020	AOR, AO, PM, ONR & DARPA Research Services
Final Technical Report	29 Dec 2020	AOR, AO, PM, ONR, DTIC*, & DARPA Research Services
Final Financial Report (SF425)	29 Dec 2020	AOR, AO, PM, ONR, DTIC*, & DARPA Research Services
Final Invention Report (DD Form 882)	28 Jan 2021	See Exhibit A Article 8 - Intellectual Property Matters

*Defense Technical Information Center
ATTN: DTIC-O
8725 John J. Kingman Road
Ft. Belvoir, VA 22060-6218

If Optional Phase II is implemented - The following reports shall be submitted and will become due on the dates as shown below:

REPORT TYPE	DUE DATE	SUBMIT TO
Quarterly R&D Status Reports	Within 30 days of the end of each quarter	See Exhibit A Attachment 1
Monthly Financial Management Report	Within 30 days of the end of each month	See Exhibit A Attachment 2
Special Technical Reports	Due as required	AOR, AO, PM, & DARPA Research Services
Annual Federal Financial Report (SF 425)	29 Dec 2021	AOR, AO, PM, ONR, & DARPA Research Services
Final Technical Report	29 JUN 2022	AOR, AO, PM, ONR, DTIC*, & DARPA Research Services
Final Financial Report (SF425)	29 JUN 2022	AOR, AO, PM, ONR, DTIC*, & DARPA Research Services
Final Invention Report (DD Form 882)	29 JUL 2022	See Exhibit A Article 8 - Intellectual Property Matters

*Defense Technical Information Center
ATTN: DTIC-O
8725 John J. Kingman Road
Ft. Belvoir, VA 22060-6218

15. **Substantial Involvement:** Substantial involvement is expected between the U. S. Government and the Recipient when carrying out the activity contemplated in this Agreement.

    Substantial Government involvement will include:

    a. DARPA review and approval required after completion of one phase of the project to move on to the next phase

b. DARPA monitoring of the work with the potential of redirecting work because of interrelationships with other projects
c. DARPA review and collaboration in the development of research and analyses protocols necessary to complete the work

16. Funding Increments and Options: The Government's obligation to provide funding for increments and/or options is pursuant to Article 16 of Exhibit A.

17. Special Terms and Conditions:

a. Assurance by University to adhere to the Defense Advanced Research Agency's (DARPA) policy and communication on Dual Use of Research Concerns (DURC).

i. Definitions:

1. "Dual use research" is research conducted for legitimate purposes that generates knowledge, information, technologies, and/or products that can be utilized for benevolent or harmful purposes.
2. "Dual use research of concern," or "DURC," is life sciences research that, based on current understanding, can be reasonably anticipated to provide knowledge, information, products, or technologies that could be directly misapplied to pose a significant threat with broad potential consequences to public health and safety, agricultural crops and other plants, animals, the environment, materiel, or national security.

ii. DURC Policy: Any data with potential dual use of research concerns emerging from DARPA funded research shall be evaluated by the team, communicated to DARPA, and submitted for evaluation by team's Institutional Review Entity (IRE). If the IRE and DARPA determine that results or information obtained during the course of funded effort could be considered DURC, the IRE and DARPA will jointly determine an acceptable risk mitigation plan including a responsible publication strategy to determine appropriate venues and content that can and should be released to the public.

iii. Reporting Process: The principal investigator (PI) shall collect information about team's activities (including experiments, data collection, and data processing) on any emergent issues of relevance to DURC and GOF, and send a brief monthly report to DARPA (including negative responses). Within 15 days of a notification of a potential DURC issue the PI shall submit the findings to team's Institutional Review Entity (IRE). If the IRE determines that the findings in question are not of concern, the reported findings are not subject to additional review or oversight, but future activities must continue to be assessed by the PI in monthly reports. If IRE determines the findings could be considered DURC, the PI shall notify DARPA within 10 days of IRE's assessment along with a copy of the assessment.

b. This research **DOES NOT** require the use of Human Subjects.
c. This research **DOES** require the use of Animal Subjects. See Article 15 of Exhibit A. **No animal studies may be conducted using funds from this award until Institutional Animal Care and Use Committee (IACUC) and DARPA second level review approvals are received.**

IACUC Protocol #: Pending Approval — Expiration Date: Pending Approval
Second-level Review #: Pending Approval — Renewal due date: Pending Approval

d. This research **DOES NOT** have restricted data rights.

THIS ACTION IS MADE ON BEHALF OF A DoD CUSTOMER UTILIZING DoD FUNDS.

UNITED STATES OF AMERICA
Department of the Interior, Interior Business Center
Acquisition Services Directorate, Division III

DOREEN VIEIRA-CROSS
Digitally signed by DOREEN VIEIRA-CROSS
Date: 2018.09.21 15:32:40 -07'00'

Doreen Vieira-Cross
Agreements Officer

Exhibit A: General Terms and Conditions
Attachment 1: Quarterly Status Report Template
Attachment 2: Monthly Financial Detail Spreadsheet Example
Attachment 3: Revised Statement of Work, dated 17 Jul 2018

EXHIBIT A

JULY 2018
DARPA AGENCY SPECIFIC TERMS AND CONDITIONS

This award is subject to the DoD Research and Development (R&D) general terms and conditions, which can be found at https://www.onr navy mil/Contracts-Grants/submit-proposal/grants-proposal/grants-terms-conditions.aspx under the header "DoD Research and Development General Terms and Conditions," dated July, 2018 and are incorporated herein. The DARPA Agency Specific Terms and Conditions supplement the DoD Research and Development general terms and conditions. This document addresses agency-specific concerns in addition to the above referenced regulations. Award recipients (hereafter, recipient) are accountable for all applicable statutory and regulatory requirements that govern these awards, even if not specifically listed in this document or documents referenced herein.

ORDER OF PRECEDENCE

Any inconsistencies in the requirements of this award shall be resolved in the following order:

- Federal statutes
- Federal regulations
- 2 CFR part 200, as modified and supplemented by DoD's interim implementation found in 2 CFR part 1103
- Award-specific terms and conditions (DARPA Agency Specific terms and conditions)
- DoD Research and Development general terms and conditions

In case of disagreement with any requirements of this award, the Recipient shall contact the Agreements Officer listed in the award document in order to resolve the issue. The Recipient shall not assess any costs to the award or accept any payments until the issue is resolved.

1. Research Responsibility
2. Amendment of Cooperative Agreement
3. Payments
4. Prior Approvals
5. Reports
6. Public Release or Dissemination of Information
7. Acknowledgment of Sponsorship
8. Intellectual Property Matters
9. Activities Abroad
10. Security
11. Research Involving Recombinant DNA Molecules
12. Restrictions on Printing
13. Prohibition on Awarding to Entities that Require Certain Internal Confidentiality Agreements
14. Acceptance and Amendment of Cooperative Agreement
15. Live Organisms – Human and Animal Subjects
16. Funding Increments and/or Options
17. Delegation of Administrative Duties
18. Rights in Technical Data, Computer Software, and Copyright
19. Changes in Performance Period

1) Research Responsibility:

a) The Recipient has full responsibility for the conduct of the research activity supported by this Cooperative Agreement, in accordance with the Recipient's proposal, and the terms and conditions specified in this Cooperative Agreement. Recipients are encouraged to suggest or propose to discontinue or modify unpromising lines of investigation or to explore interesting leads which may appear during the development of the research. However, they must consult the Agreement Officer's Representative (AOR) through the Agreement Officer (AO) before significantly deviating from the objectives or overall program of the research originally proposed.

b) The Recipient shall immediately notify the Agreement Officer of developments that have a significant impact on the award-supported activities. Also, notification shall be given in the case of problems, delays, or adverse conditions which materially impair the ability to meet the objectives of the award. This notification shall include a statement of the action taken or contemplated, and any assistance needed to resolve the situation.

2) **Amendment of Cooperative Agreement:** The only method by which this Cooperative Agreement can be amended is by a formal, written amendment signed by the Agreements Officer. No other communications, whether oral or in writing, shall modify this Cooperative Agreement.

3) **Payments**:

a) Requests for payment for this effort shall be submitted through the Department of the Treasury's Automated Standard Application Payments System (ASAP). Once the Government has submitted a completed ASAP Participation Request forms to ASAP, Recipient will receive an e-mail with further instructions from ASAP.

The recipient organization can use on-line process to request payments. Payment requests are approved or rejected automatically unless placed on review or based on the amount of available funds in the ASAP account. The available balance for an ASAP account is displayed when initiating the payment request. Recipient organizations will receive immediate notification of approval or rejection for all on-line payment requests with the exception of those subject to review. The timing and amount of cash advances shall be as close as is administratively feasible to the Recipient's actual disbursements for direct program costs and the proportionate share of any allowable indirect costs.

b) The Recipient may be paid in advance, provided they comply with the requirements of 2CFR 200.305(b)(1).

c) Reimbursement is the preferred method when the requirements for advance payment cannot be met.

d) Liquidation. The Recipient shall liquidate all obligations incurred under the Cooperative Agreement no later than 90 days after the date of completion. The Recipient shall promptly refund any balances of unobligated cash that the Government has advanced or paid and that is not authorized to be retained by the Recipient for use in other projects. The Agreements Officer is authorized to make a settlement for any upward or downward adjustments to the Federal share of costs after closeout reports are received.

4) **Prior Approvals:** In addition to the prior approvals required by the DoD R&D general terms and conditions, prior written approval is required for the following actions:

The subaward, transfer, or contracting out of any work under this award, unless described in the Recipient's proposal and specifically approved and funded in the Cooperative Agreement Schedule. The Recipient's request for approval shall include the following supporting data:

(i) Basis for contractor selection;
(ii) Justification for lack of competition when competitive bids or offers are not obtained;
(iii) Basis for award cost or price, to include price or cost analysis performed by the Recipient; and
(iv) Approval of the AOR.

5) **Reports**: Reports shall be furnished as specified in the Cooperative Agreement. Report types & descriptions include:

a) Report Types

1) *Quarterly R&D Status Report* - This report is due within 30 calendar days of the end of the previous quarter and shall keep the Government informed of Recipient activity and progress toward accomplishment of Cooperative Agreement objectives and advancement in state-of-the-art on the research and development involved.

2) *Phase Completion Report* - This report is due within 30 calendar days of the end of each phase describing the progress made on the specific milestones as laid out in the SOW.

3) *Monthly Financial Management Report* - This report is due as specified in the Cooperative Agreement and shall be monthly expenditure report that documents cumulative spending and provides a schedule of tasks and events for each report period, with financial expenditures broken down by task.

4) *Annual Technical Report* - This report is due as specified in the Cooperative Agreement, shall document the results of the complete effort. It shall contain brief information on each of the following:

1. A comparison of actual accomplishments with the goals and objectives established for the Cooperative Agreement, the findings of the investigator, or both.
2. Reasons why established goals were not met, if appropriate.
3. Other pertinent information

5) *Special Technical Report* - This report, due as required, shall document the results of a significant task, test, event or symposium.

6) *Final Technical Report* - This report, due 90 days after expiration or termination of the Cooperative Agreement, shall document the results of the complete effort. It shall contain brief information on each of the following:

a) A comparison of actual accomplishments with the goals and objectives established for the Cooperative Agreement, the findings of the investigator, or both.

b) Reasons why established goals were not met, if appropriate.

c) Other pertinent information.

7) *Financial Status Repor*t- shall be submitted on a Standard Form 425 "Federal Financial Report (FFR)" as follows.

a) Interim Status Report – This report is due within 90 days of the end of the interim reporting period (annually). The report shall be on a cash or accrual basis, depending on how the Recipient's accounting records are normally kept.

b) Final Financial Status Report - This report is due 90 days after completion of the Cooperative Agreement. The report shall be on a cash or accrual basis, depending on how the Recipient's accounting records are normally kept.

8) *Report of Federal Cash Transactions [applicable only to advance payment Cooperative Agreements]* – This report, due 15 days following the end of each quarter, shall be submitted on a Standard Form 425. The Recipient shall provide forecasts of Federal cash requirements in the "Remarks" section of the report.

6) Public Release or Dissemination of Information:

a) At this time, DARPA expects the work performed under this Cooperative Agreement to be fundamental research, and it is, therefore, not subject to publication restrictions. Papers resulting from unclassified contracted fundamental research are exempt from prepublication controls and requirements, pursuant to DoD Instruction 5230.27 dated October 6, 1987.

b) All papers resulting from this Cooperative Agreement will include the following

distribution statement: "Approved for public release; distribution is unlimited."

c) Should the character of the research change during Cooperative Agreement performance so that the research is no longer considered fundamental, the Cooperative Agreement will be modified to impose the restrictions on public release and dissemination of information that apply to those research efforts that are not considered fundamental research.

7) Acknowledgment of Sponsorship:

a) The Recipient agrees that in the release of information relating to this Cooperative Agreement, such release shall include a statement to the effect that (1) the project or effort depicted was or is sponsored by the Defense Advanced Research Projects Agency, (2) the content of the information does not necessarily reflect the position or the policy of the Government, and (3) no official endorsement should be inferred.

b) For the purpose of this article, information includes news releases, articles, manuscripts, brochures, advertisements, still and motion pictures, speeches, trade association proceedings, symposia, etc.

c) Nothing in the foregoing shall affect compliance with the requirements of the clause entitled "Security."

8) Intellectual Property Matters: Questions regarding intellectual property matters should be referred to the Agreements Officer (AO). All patent reports (interim and final) shall be submitted using the i-Edison.gov reporting website (http://s-edison.info.nih.gov/iEdison). In the event the Recipient is unable to submit reports through i-Edison, the Recipient may utilize DD Form 882, Report of Inventions and Subcontracts, for submission of interim and final invention reports. The DD Form 882 and all invention disclosures shall be submitted to the AO for proper disposition no later than 120 days after the end of the period of performance.

9) Activities Abroad: The Recipient shall assure that project activities carried on outside the United States are coordinated as necessary with appropriate Government authorities and that appropriate licenses, permits, or approvals are obtained prior to undertaking proposed activities. The awarding agency does not assume responsibility for Recipient compliance with the laws and regulations of the country in which the activities are to be conducted.

10) Security: The Recipient may not be granted access to classified information under this Cooperative Agreement. If security restrictions should happen to apply to certain aspects of the proposed research, the Recipient will be so informed. In the event that the scientific work under this Cooperative Agreement may need classification, or involve access to or storage of any classified data, the Government shall make its decision on the need to classify, or require such access or storage, within 30 days after receipt of written notice from the Recipient. If the decision is affirmative, the Government shall invoke the clause in reference to the "Termination"

proceedings in the DoD R&D general terms and conditions.

11) Research Involving Recombinant DNA Molecules: Any Recipient performing research involving recombinant DNA molecules and/or organisms and viruses containing recombinant DNA molecules agrees, by acceptance of this award, to comply with the National Institutes of Health "Guidelines for Research Involving Recombinant DNA Molecules," July 5, 1994 (59 FR 34496) as amended, or such later revision of those guidelines as may be published in the Federal Register.

12) Restrictions on Printing: Unless otherwise authorized in writing by the AO, reports, data, or other written material produced using funds provided by this Cooperative Agreement and submitted hereunder shall be reproduced only by duplicating processes and shall not exceed 5,000 single page reports or a total of 25,000 pages of a multiple page report. These restrictions do not preclude the writing, editing, and preparation of manuscript or reproducible copy of related illustrative materials if required as a part of this Cooperative Agreement, or incidental printing such as forms or materials necessary to be used by the Recipient to respond to the terms of the Cooperative Agreement. To satisfy the requirements of the Defense Technical Information Center, at least one copy of each technical report submitted to the Defense Technical Information Center must be black typing or reproduction of black on white paper or suitable for reproduction by photographic techniques. Reprints of published technical articles are not within the scope of this paragraph.

In accordance with Executive Order 12873, dated October 20, 1993, as amended by Executive Order 12995, dated March 25, 1996, the Recipient is encouraged to submit paper documents, such as letters or reports, that are printed/copied double-sided on recycled paper that has at least 30 percent postconsumer material.

13) Prohibition on Awarding to Entities that Require Certain Internal Confidentiality Agreements:

a) The Recipient shall not require employees, contractors, or subrecipients seeking to report fraud, waste, or abuse to sign or comply with internal confidentiality agreements or statements prohibiting or otherwise restricting such employees or contractors from lawfully reporting such waste, fraud, or abuse to a designated investigative or law enforcement representative of a Federal department or agency authorized to receive such information.

b) The Recipient must notify its employees, contractors, or subrecipients that the prohibitions and restrictions of any internal confidentiality agreements inconsistent with paragraph (a) of this award provision are no longer in effect.

c) The prohibition in paragraph (a) of this award provision does not contravene requirements applicable to any form issued by a Federal department or agency governing the nondisclosure of classified information.

d) If the Government determines that the Recipient is not in compliance with this award provision, it:

1) Will prohibit the Recipient's use of any funds under this award, in accordance with Federal appropriations law; and

2) May pursue other remedies available for the Recipient's material failure to comply with award terms and conditions.

14) Acceptance and Amendment of Cooperative Agreement:

1) The only method by which this Cooperative Agreement can be amended is by a formal, written amendment signed by the Agreements Officer. No other communications, whether oral or in writing, are valid.

2) The Recipient is not required to countersign the Cooperative Agreement document; however, the Recipient agrees to the conditions specified in the Research Cooperative Agreement Schedule and the Articles herein unless notice of disagreement is furnished to the Agreements Officer within 15 calendar days after the date of the Agreements Officer's signature.

In case of disagreement, the Recipient shall not assess the Cooperative Agreement of any costs of the research unless and until such disagreement(s) is/are resolved.

15) Live Organisms – Human and Animal Subjects:

a) Human Subjects. Cooperative Agreement funds may NOT be used for research that uses uninformed or nonvoluntary humans as experimental subjects. The Recipient is responsible for the protection of the rights and welfare of any human subjects involved in research, development, and related activities supported by this Cooperative Agreement. The Recipient agrees to comply with the Common Federal Policy for the Protection of Human Subjects, codified by the Department of Health and Human Services at 45 CFR part 46 implemented by the Department of Defense at 32 CFR part 219.

Department of the Interior/Interior Business Center (DOI/IBC) collaborates with the Institutional Review Board (IRB) and the U. S. Army Medical Research and Materiel Command (USAMRMC) for DARPA's Second-Level review. No work can be performed on human subjects without a Second-Level review and approval.

b) Animal Welfare. The Recipient shall register its research, development, test, and evaluation or training facility with the Secretary of Agriculture in accordance with 7 U.S.C. 2136 and 9 CFR subpart C, and section 2.30, unless otherwise exempt from this requirement by meeting the conditions in 7 U.S.C. 2136 and 9 CFR parts 1 through 4 for the duration of the activity. The Contractor shall have its proposed animal use approved in accordance with Department of Defense Instruction (DoDI) 3216.01, Use of Animals in DoD Programs, by a DoD Component Headquarters Oversight Office. The Contractor shall furnish evidence of such registration and approval to the Contracting Officer before beginning work under this agreement."

DOI/IBC collaborates with Institutional Animal Care and Use Committee (IACUC) for DARPA's Second-Level review. No work can be performed on animal subjects without a Second-Level review and approval.

The Recipient shall make its animals, and all premises, facilities, vehicles, equipment, and records that support animal care available during business hours and at other times mutually agreeable to the Contractor and the United States Department of Agriculture Office of Animal and Plant Health Inspection Service (USDA/APHIS) representative, personnel representing the DoD component oversight offices, as well as the Contracting Officer, to ascertain that the Contractor is compliant with 7 U.S.C. 2131-2159 and 9 CFR parts 1 through 4.

(1) The Recipient shall acquire animals in accordance with DoDI 3216.01, current at time of award (http://www.dtic.mil/whs/directives/corres/pdf/321601p.pdf).

(2) The Recipient agrees that the care and use of animals will conform with the pertinent laws of the United States, regulations of the Department of Agriculture, and policies and procedures of the Department of Defense (see 7 U.S.C. 2131 et seq., and 9 CFR subchapter A, parts 1 through 4, DoDI 3216.01, Army Regulation 40-33/ SECNAVINST 3900.38C/AFMAN 40-401(I)/DARPAINST 18/USUHSINST 3203). The Contractor shall also comply with DoDI 1322.24, Medical Readiness Training, if this contract includes acquisition of training.

(3) The Agreements Officer may immediately suspend, in whole or in part, work and further payments under this contract for failure to comply with the requirements of paragraphs (a) through (c) of this clause.

(1) The suspension will stay in effect until the Recipient complies with the requirements.

(2) Failure to complete corrective action within the time specified by the Contracting Officer may result in termination of this contract and, if applicable, removal of the Contractor's name from the approved vendor list for live animals used in medical training.

The recipient may request registration of its facility by contacting USDA/APHIS/AC, 4700 River Road, Unit 84, Riverdale, MD 20737-1234, or via the APHIS Animal Care website at: http://www.aphis.usda.gov/wps/portal/aphis/ourfocus/animalwelfare.

The Recipient shall include the substance of this clause, including this paragraph in all subcontracts involving research, development, test, and evaluation or training that use live vertebrate animals.

c) In the event a revised technical proposal with human or animal subject research is incorporated under this Cooperative Agreement, Recipient shall obtain all reviews and approvals prior to beginning any testing on humans or animals.

d) This article shall be flowed down to subcontractors, suitably modified to ensure that the recipient fully complies with this article.

16) Funding Increments and/or Options: The Recipient is advised that the Government's obligation to provide funding for funding increments and/or options included in the Cooperative Agreement is contingent upon (i) satisfactory performance and (ii) the availability of funds. Accordingly, no legal liability on the part of the Government exists unless or until (i) funds are made available to the Government and notice of such availability is confirmed in writing to the Recipient and (ii) performance of the research is deemed satisfactory in the judgment of the Agreements Officer.

17) Delegation of Administrative Duties: The administrative duties listed below have been delegated to the Office of Naval Research (ONR) identified in Item 7 of the Cooperative Agreement Schedule:

a) During performance:

1) Perform government furnished property administration.

2) Receive interim technical, cost/financial and patent reports from Recipient.

3) Review and adjudicate audit findings after receipt of the audit report and ensure that the recipient takes appropriate and timely corrective action, if required.

b) Upon expiration of agreement:

1) Receive final technical, cost/financial and patent reports from Recipient.

2) Obtain final government property report. Perform plant clearance, if required.

3) Assist the awarding Agreements Officer in resolving any questioned costs. Order audit from Department of Health and Human Services (DHHS), if applicable.

4) Perform cost sharing adjustments, if applicable.

5) Assure that all refunds due the Government are received.

6) Complete and submit to the awarding Agreements Officer a Completion Statement for this award.

18) Rights in Technical Data, Computer Software, and Copyright:

(a) Technical Data and Computer Software. Rights are as specified in 2CFR 200.315(d).

(b) Copyright. Rights are as specified in 2CFR 200.315(b).

19) Changes in Performance Period:

Recipient may initiate a one-time extension of the period of performance by up to 12 months unless one or more of the conditions outlined in subparagraphs a.-c. below apply. For one-time extensions, the Recipient must notify the Federal awarding agency in writing with the supporting reasons and revised period of performance at least 30 calendar days before the end of the period of performance specified in the award. This one-time extension may not be exercised merely for the purpose of using unobligated balances.

Extensions require explicit prior Federal awarding agency approval when:

a) The terms and conditions of the award prohibit the extension.

b) The extension requires additional Federal funds.

c) The extension involves any change in the approved objectives or scope of the project.

Montana State University - Bozeman
PREEMPT Program – Cooperative Agreement D18AC00031
Quarterly R&D Status Report

Period Covered by the Report: [Date] through [Date]

Date of Report:

Project Title: Preventing emergence and spillover of bat pathogens in high-risk global hotspots
Total Dollar Value: $8,239,511.00
Program Manager: Dr. James Gimlett, DARPA

Submitted by:
[PI Name]
[Institution]
[Address]

Telephone:
Email:

Subcontractors: [Co-PI name(s) and institution(s)]

TABLE OF CONTENTS

General notes:

- **Contact the program manager and team to report any financial or technical issues** (i.e., please do not wait until a report is due to bring up major issues).
- Clearly indicate if funding from another federal agency (e.g., NIH) has been used to support any data presented.
- Clearly indicate if any content is pre-publication sensitive or proprietary.
- Delete all instructional text from this document before submitting your report.
- Support your claims with data, images, and other evidence.
- Please update the header of each report with the respective quarterly period.
- Please use the following naming convention for report filenames: QR – PI institution – period covered (e.g., QR – University of XYZ – 01OCT2018 to 31DEC2018).
- Quarterly reports are due within 30 days of the quarter end date. For example, if the period ends on March 31, the report must be submitted by April 30.
- Monthly progress updates via conference calls will be scheduled with the program manager and his team.

Definitions:

- **Functional block diagram:** describes the functions and interrelationships of a system in a flock-block diagram style so that one can easily and thoroughly understand the system and the relationship of each of the parts to the whole. If the hardware evolves throughout your project, please provide a block diagram for each evolution (example included).
- **Work Breakdown Structure (WBS):** a hierarchical and incremental decomposition of the project into phases, deliverables and work packages. It is a tree structure that shows the subdivision of effort required to achieve an objective (example included).
- **Deliverable:** a measurable and verifiable outcome or object that a project team must create and deliver according to the terms of an agreement. An intangible deliverable is a particular outcome that the team achieves. A tangible deliverable is a concrete or material object created by the team.
- **Milestone:** a milestone describes the status of the project as represented by an event or moment at which one or more project activities are complete. Milestones can represent the completion of key project tasks, conclusions reached, or questions answered that affect project schedule significantly.
- **Major finding:** data with significant impact (positive or negative).
- **Metrics update:** progress (including delays and issues) toward achieving pre-established metrics of success.
- **SETA:** Science, Engineering, and Technical Assistant (internal DARPA term for technical support staff).

1 Progress Summary

1.1 Major Findings

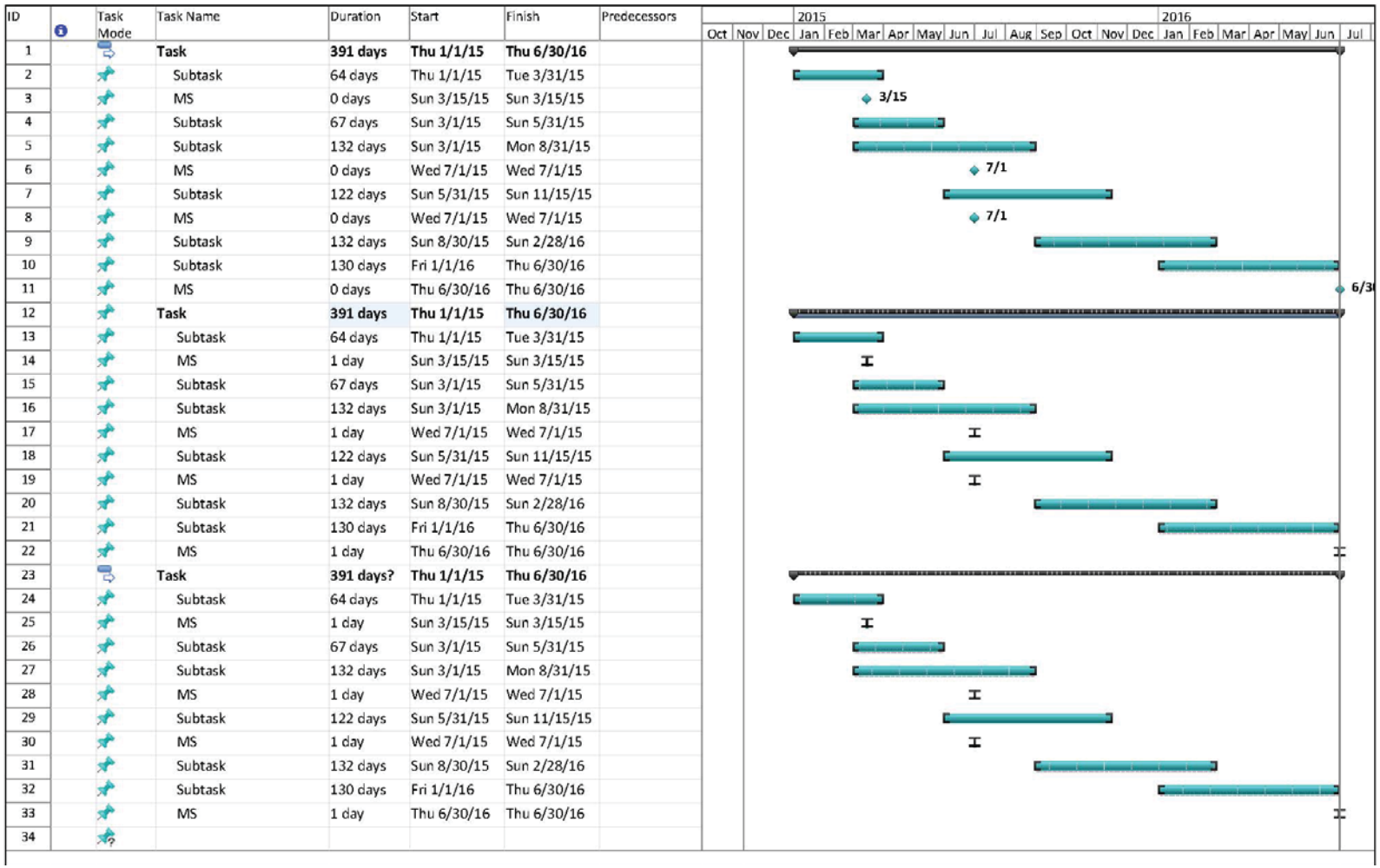
Briefly describe the most significant and salient accomplishment(s) achieved during the ***most recent quarter***. How has this compared to the original project plan?

1.2 Metrics Update

Accomplishment *Include associated task #*	**Month** *Planned vs. achieved*	**Update** *Provide current status, explain any schedule discrepancies, list next steps*

2 Schedule – Milestones and Deliverables

Provide a high-level Gantt chart for Phase I that includes all milestones and deliverables for each task. An example of an acceptable chart is shown below.



ID	Task Mode	Task Name	Duration	Start	Finish	Predecessors
1		**Task**	**391 days**	**Thu 1/1/15**	**Thu 6/30/16**	
2		Subtask	64 days	Thu 1/1/15	Tue 3/31/15	
3		MS	0 days	Sun 3/15/15	Sun 3/15/15	
4		Subtask	67 days	Sun 3/1/15	Sun 5/31/15	
5		Subtask	132 days	Sun 3/1/15	Mon 8/31/15	
6		MS	0 days	Wed 7/1/15	Wed 7/1/15	
7		Subtask	122 days	Sun 5/31/15	Sun 11/15/15	
8		MS	0 days	Wed 7/1/15	Wed 7/1/15	
9		Subtask	132 days	Sun 8/30/15	Sun 2/28/16	
10		Subtask	130 days	Fri 1/1/16	Thu 6/30/16	
11		MS	0 days	Thu 6/30/16	Thu 6/30/16	
12		**Task**	**391 days**	**Thu 1/1/15**	**Thu 6/30/16**	
13		Subtask	64 days	Thu 1/1/15	Tue 3/31/15	
14		MS	1 day	Sun 3/15/15	Sun 3/15/15	
15		Subtask	67 days	Sun 3/1/15	Sun 5/31/15	
16		Subtask	132 days	Sun 3/1/15	Mon 8/31/15	
17		MS	1 day	Wed 7/1/15	Wed 7/1/15	
18		Subtask	122 days	Sun 5/31/15	Sun 11/15/15	
19		MS	1 day	Wed 7/1/15	Wed 7/1/15	
20		Subtask	132 days	Sun 8/30/15	Sun 2/28/16	
21		Subtask	130 days	Fri 1/1/16	Thu 6/30/16	
22		MS	1 day	Thu 6/30/16	Thu 6/30/16	
23		**Task**	**391 days?**	**Thu 1/1/15**	**Thu 6/30/16**	
24		Subtask	64 days	Thu 1/1/15	Tue 3/31/15	
25		MS	1 day	Sun 3/15/15	Sun 3/15/15	
26		Subtask	67 days	Sun 3/1/15	Sun 5/31/15	
27		Subtask	132 days	Sun 3/1/15	Mon 8/31/15	
28		MS	1 day	Wed 7/1/15	Wed 7/1/15	
29		Subtask	122 days	Sun 5/31/15	Sun 11/15/15	
30		MS	1 day	Wed 7/1/15	Wed 7/1/15	
31		Subtask	132 days	Sun 8/30/15	Sun 2/28/16	
32		Subtask	130 days	Fri 1/1/16	Thu 6/30/16	
33		MS	1 day	Thu 6/30/16	Thu 6/30/16	
34						

Include a corresponding table that provides:

- Short text-identifier for each milestone/deliverable
- Team members associated with each
- Schedule status (provide explanation if behind schedule or significantly ahead of schedule)
- Description of how the milestone/deliverable is contingent or dependent on other parts of the effort (if applicable)

Milestone/ Deliverable	**Team member(s)**	**Due date**	**Date initiated**	**Date completed**	**Status**	**Dependencies** *Across tasks & team members*

3 Task Progress, Accomplishments, and Plans

*Please provide updates from the **most recent quarter**, not a cumulative discussion of the project to date. Support all claims with data. Highlight major accomplishments. Provide explanations and/or justifications for any deviation from the negotiated schedule and spending plan.*

Identify the following for each major task in your SOW; this section will form the bulk of your report:

- Task number (from SOW)
- High-level task description
- Completion status (e.g., ongoing, delayed, etc.)
- Funding associated with the task (spent to date vs. remaining to spend); explain any deviations from your original spend plan

Task #/Title	Brief Description	% Complete	Total $ for task	Spent	Remaining	Explain deviations from planned expenditures

- **Describe planned vs. actual progress towards the goals, milestones, and deliverables of the task; discuss why planned expectations were met, not met, or exceeded; highlight significant accomplishments**
- List next steps
- Support claims with data, images, or other evidence
- Identify and describe all significant challenges and risks encountered during work towards the goals of this task, including:
    - Critical dependencies across tasks and teams
    - Mitigation plan
    - Level of risk (high, medium, or low)
    - Changes in risk status since proposal or last report
    - Anticipated date risk will be resolved

4 Project Coordination, Dissemination, and Translation

4.1 Project Coordination

- Summarize key project planning and coordination over the quarter, including:
  - Meeting date(s), location, purpose
  - Attendees
  - Meeting outcomes, action items

4.2 Dissemination and Translation (if applicable)

- List any new partnerships, collaborators, users, etc.
- Describe potential commercialization pathways/partners

5 Publications and Presentations

Please provide a cumulative update on current and upcoming publications.

Title, Authors	Description/Type	Status
	Presentation to Conference Name	Published
	Paper, Name of Journal	Submitted
	Letter to the Editor, Scientific Organization	In preparation

6 Patents, Invention Disclosures, IDEs, etc…

Please provide a cumulative update of current or upcoming patents, inventions, Investigational Device Exemption (IDE), etc. Examples are listed in the table below.

Title, Authors	Description/Type	Status
	Patent; Name of Patent	Accepted
	FDA IDE	Filed/submitted
	Invention Disclosure	In preparation

Appendix I – Project Context

For future reports, only update this section if any information changes. Please indicate changes using red font.

Teaming and Personnel

Organizational Chart

Insert an organizational chart for your entire team

Contact Information

Please populate the following table with contact information for each team member. Please provide general area of expertise each will provide (e.g., microfluidics). In the last column, list tasks or otherwise briefly describe each individual's involvement in the effort.

Prime Team Members and Contact Information: [Institution]

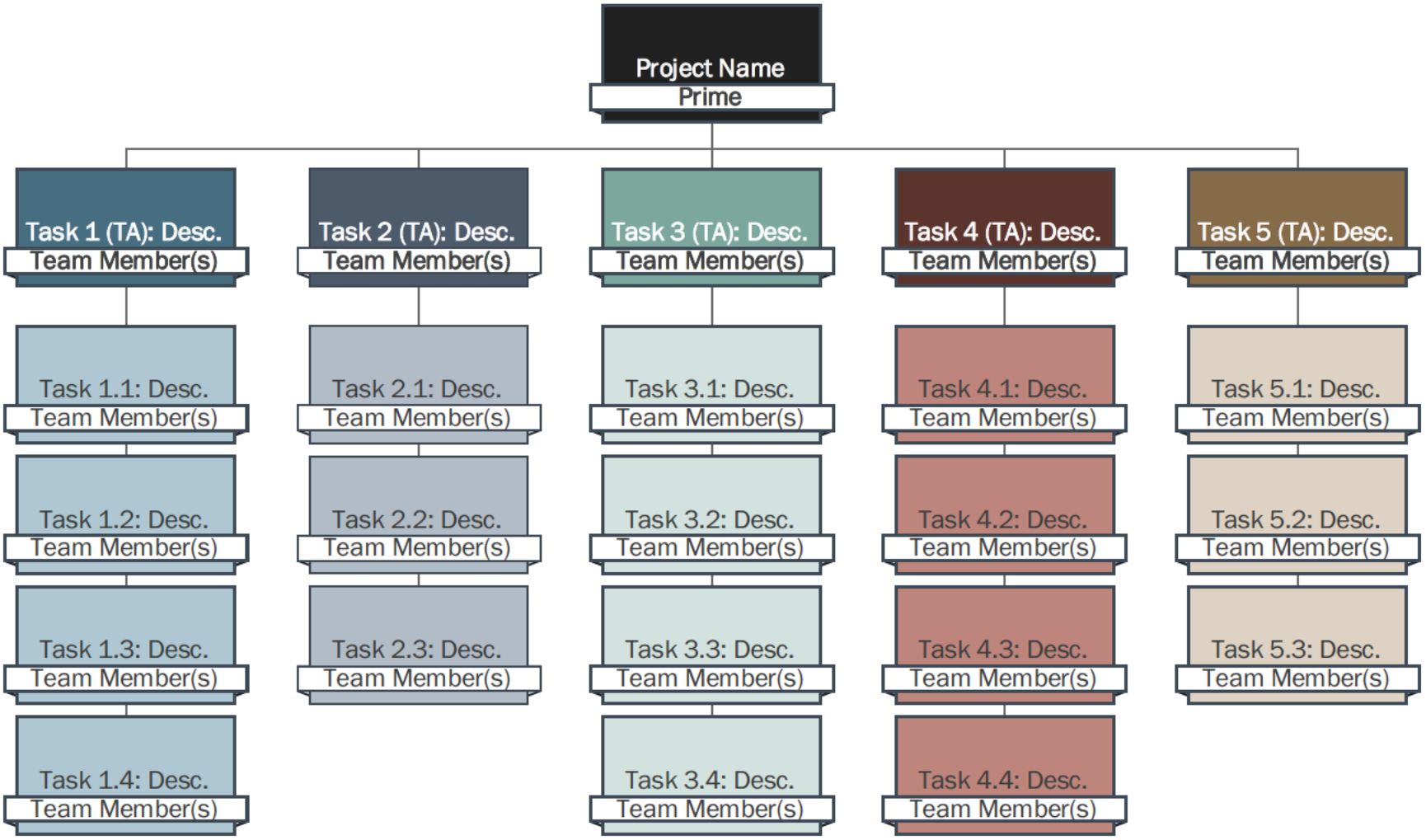
Role	Full name	Phone and email	Areas of Involvement
PI		(888) 888-8888 XXX@univ.edu	
Co-PI (expertise)		(888) 888-8888 XXX@univ.edu	
Postdoc (expertise)		(888) 888-8888 XXX@univ.edu	

Subcontract Team Members and Contact Information: [Institution]

Role	Full name	Phone and email	Areas of Involvement
PI (expertise)		(888) 888-8888 XXX@univ.edu	
Co-PI (expertise)		(888) 888-8888 XXX@univ.edu	
Postdoc (expertise)		(888) 888-8888 XXX@univ.edu	

Work Breakdown Structure

Provide breakdown of tasking and assigned team members as per the template shown below



Monthly Financial Report Template

LINK TO TEMPLATE (click here)

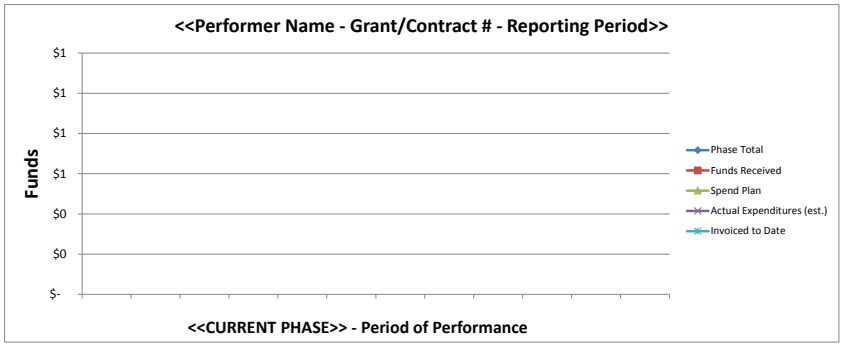
Please use this template to provide monthly financial updates to the PREEMPT team. As you input your data, the graph will automatically update. ***Please keep past reports in this file and create a new tab each month. We want to see all reports in the same file. Title tabs "Phase-Month-Year, " e.g., "Base - January - 2015"***

LINK TO EXAMPLE (click here)

An example of a completed template is also provided. The example graph illustrates a scenario where the performer is under spending. It is designed to show how this template will make it easy for INTERCEPT performers to clearly communicate the status of their effort to DARPA so that both can plan for and initiate contractual actions quickly and effectively.

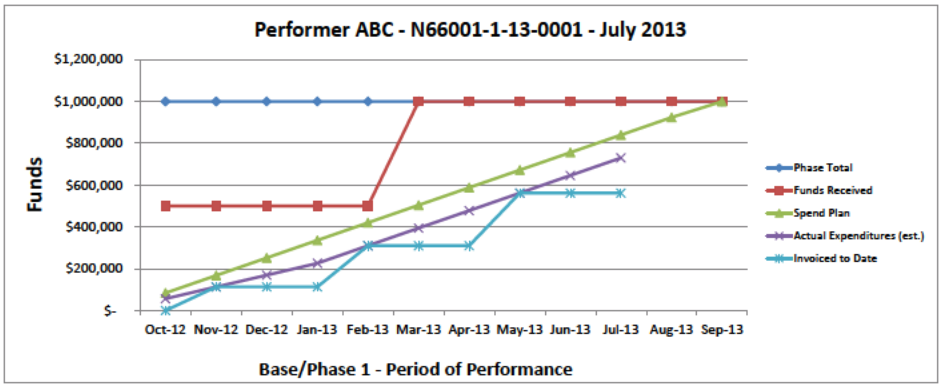
Spend Plan Data	
Period of Performance	The financial report will only cover the current phase (e.g., Base, Option 1, etc.). Use a format similar to "Sep-2013," not "Month 6." In order to plan for continuing resolution requests, DARPA may reach out to you separately to request your projected spend rate for future phases.
Phase Total	Total for current phase *(Example Graph - total is $1,000,000)* .
Funds Received	Funds awarded to date; most efforts are funded incrementally *(Example Graph - this effort received an increment for $500,000 in Oct-2012 to exercise the base, and received the remainder of their base period funding in Mar-2013 (remaining $500,000))* .
Spend Plan	Projected Expenditures must cover the entire phase.
Actual Expenditures (est.)	Actual Expenditures should not be solely based off of invoices you have submitted or received to date. Instead, it should be an accurate (to the extent that is possible) account of the expenses you have actually incurred to date. For example, if a subcontractor has incurred but hasn't invoiced $100,000 worth of work, include the $100,000 in your actual expenditures. Or a large amount of equipment valued at $50,000 that hasn't yet been invoiced should also be factored in to the actual expenditures.
Invoiced to Date	Report the invoices you have submitted to date *(Example Graph - the scenario used in the example graph submits invoices quarterly)* .
Issues/Updates Summary (if applicable)	
Use this section as an opportunity to bring issues, concerns, or updates to the attention of DARPA. For example, you can summarize reasons for over/under-spending, potential no-cost extension requests, invoicing problems, etc.	

***Amounts for Spend Plan, Actual expenditures, Invoiced to Date are cumulative.



Spend Plan Data												
Period of Performance (Current Phase Only)												
Phase Total												
Funds Received												
Spend Plan												
Actual Expenditures (est.)												
Invoiced to Date												

Issues/Updates Summary (if applicable)



Spend Plan Data												
Period of Performance (Current Phase Only)	Oct-12	Nov-12	Dec-12	Jan-13	Feb-13	Mar-13	Apr-13	May-13	Jun-13	Jul-13	Aug-13	Sep-13
Phase Total	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000
Funds Received	$ 500,000	$ 500,000	$ 500,000	$ 500,000	$ 500,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000
Spend Plan	$ 84,000	$ 168,000	$ 252,000	$ 336,000	$ 420,000	$ 504,000	$ 588,000	$ 672,000	$ 756,000	$ 840,000	$ 924,000	$ 1,000,000
Actual Expenditures (est.)	$ 56,500	$ 113,000	$ 169,550	$ 226,100	$ 310,100	$ 394,100	$ 478,100	$ 562,100	$ 646,100	$ 730,100		
Invoiced to Date	$ -	$ 113,000	$ 113,000	$ 113,000	$ 310,100	$ 310,100	$ 310,100	$ 562,100	$ 562,100	$ 562,100		

Issues/Updates Summary (if applicable)

We anticipate that we will need to request a four-month no cost extension (NCE). The NCE is necessary due to delays we experienced while getting Subcontractor #1 under contract. Although our effort's period of performance began in October 2012, the subcontract was finalized and fully-executed in February 2013, which resulted in a four-month delay from the intended start date. Subcontractor #1 is conducting a 12-month study, and cannot speed up their experiments. We would, however, like to begin work on Option 1. We intend to perform these tasks in parallel to the extended Base Period tasks (which are primarily performed by Subcontractor #1).

Preventing emergence and spillover of bat viruses in high-risk global hotspots

STATEMENT OF WORK

July 17th 2018

Milestones by Task

CIES: Cary Institute of Ecosystem Studies; **CSU**: Colorado State University; **Cornell**: Cornell University; **GU**: Griffith University; **JH**: Johns Hopkins University; **MSU: Montana State University**; **PSU**: Penn State University; **RML**: Rocky Mountain Laboratories; **TTU**: Texas Tech University; **UCB**: University of California, Berkeley; **UCLA**: University of California, Los Angeles; **Cambridge**: University of Cambridge.

Note that Rocky Mountain Laboratories (RML) is funded separately by DARPA via IAA/MIPR to NIAID.

TA1

COLLECT AND ANALYZE FIELD SAMPLES

Task 11.01, Data collection: longitudinal sampling of wild bat populations and a captive population. Cambridge, GU, JH, and UCB, with assistance from MSU and TTU, will sample multiple bat populations longitudinally in multiple locations and ship retrospective bat samples to RML or local laboratory for analyses (11.03).

Task 11.02, Data collection: retrospective analysis of bat samples. Cambridge, GU, JH, and UCB will identify, locate, and ship retrospective bat samples to RML or local laboratory for analyses (11.03).

Task 11.03, Lab: screening, metagenomics to identify virus and quasispecies. RML and Cambridge or local laboratory will screen and sequence samples from bats; create a list of sequences that have spilled over from bats to other species; and select sequences for genotype-phenotype modeling.

Task 11.12, Lab: screening retrospective samples from human/domestic livestock hosts. Cambridge, JH, and UCB will identify, locate, and ship retrospective human/livestock samples to RML or local laboratory for analysis; RML or local laboratory will screen samples and create a list of sequences that have spilled over from bats to other species.

Milestones

Australia (GU will do field collection and RML or local laboratory will do sequencing):

- Establish field sites and train field teams (6mths)
- Sample up to 40 bats in 4 bat colonies monthly for 2 years (12mths, 24mths)
- Respond to spillover events or viral pulses within the study area by sampling adaptively until prevalence decreases (12mths, 24mths)
- PCR on all samples for Hendra virus (30mths)
- Sequence all positive samples available (36mths)
- Analyze 1000 retrospective bat samples for henipaviruses (24mths).

Bangladesh (JH will do field collection and in-country PCR; RML will do sequencing):

- Sample up to 40 bats in 4 colonies monthly for 2 years (24mths)
- Respond to spillover events or viral pulses by sampling adaptively until prevalence decreases (24mths)
- PCR on samples for Nipah virus (30mths)
- Sequence all positive samples available (36mths)
- Analyze retrospective bat samples for henipaviruses (24mths).

Ghana (Cambridge will do field collection and laboratory analyses, with some help from RML):

- Locate retrospective human and animal samples suitable for testing and establish sequencing pipeline (6 months)
- Sample up to 120 bats per quarter in 3 colonies, perform PCR testing on the first batches and send positive sample for sequencing (12 months)
- Update sampling effort in bat colonies for year 2 based on 12 months result, for PCR and sequencing, with up to 500 bats to be caught in year 2 (24mths)
- Sample bats in the captive colony every 3 months (24mths)
- Sequence all positive samples available (36mths)

Madagascar (UCB will do field collection and PCR, and RML or local laboratory will do sequencing):

- Establish field sites and train field teams (12mths)
- Sample up to 30 bats in 3 colonies monthly for 2 years (12 mths, 24mths)
- Respond to viral pulses by sampling adaptively until prevalence decreases (12 mth, 24mths)
- Analyze 700 retrospective bat samples for henipaviruses (12mths)
- PCR on samples from bats at Institut Pasteur de Madagascar (30mths)
- Sequence all positive samples available (36mths)

Historic humans and livestock samples (JH, Cambridge, UCB):

- Identify and ship historic samples to RML or local laboratory (6mths)
- PCR on samples from humans and livestock (12mths)
- Sequencing of all positive samples available (18mths)

IDENTIFY HOST IMMUNE SIGNATURES

Task 11.04 Lab: identify host immune and stress signatures in wild bats and in a captive feeding trial. MSU, with help from CSU will measure bat immune signatures. TTU will measure bat stress signatures and nutritional status. A captive feeding trial will be conducted in Ghana (Cambridge), or alternatively, if a natural nutritional stress event occurs in Australia during Phase I, this trial will be conducted in Australia (GU).

Milestones

Immunology on samples from Australia (MSU):

- Validate and optimize tests for each bat species (6mths)
- Immunological markers such as IgG and IgA, biomarkers of cell damage, gene expression of antiviral & proinflammatory proteins, and microbial killing assays for 400 samples (30mths)

Immunology on samples from Ghana (Cambridge):

- Titrate antibodies against Henipaviruses in sera from all PCR-positive bats and a sample of up to 1000 PCR-negative bats, from wild and captive colonies (24 mths).

Stress signatures on samples from Australia (TTU):

- Test up to 720 hair and fecal samples for cortisol (30mths)
- Develop methodology to use bioelectrical impedance analysis to measure body condition of bats (12mths)
- Measure body condition of 400 bats (24mths)

Captive feeding trial (Cambridge, GU)

- Conduct experimental diet manipulation to test the effect of nutritional status on immune state and viral shedding (30mths)

COLLECT ENVIRONMENTAL, ECOLOGICAL, and RESERVOIR HOST DATA

Task 11.10 Remote sensing data, longitudinal short-term weather and long-term climate data, land cover change, human population data, bat movement data. PSU will identify environmental drivers of shedding in Australia and detect large bat colonies through remote sensing. TTU will implement bat telemetry.

Milestones

Remote sensing (PSU):

- Collect data on weather, climate, and land cover change in Australia (24mths)
- Collect data on human population dynamics across space (local/region), time (seasonal/decadal) (24mths)

Bat movement data (TTU):

- Deploy GPS tracking devices on bats in resident and nomadic colonies in Australia (12mths, half deployed; 24mths all deployed)
- Collect, collate, and analyze bat movement data (36mths)

CREATE GENOTYPE-PHENOTYPE MAPS FOR HENIPAVIRUS QUASISPECIES BASED ON *IN VITRO* AND *IN VIVO* WORK

Task 11.13, Lab: in vitro experiments to assess jump potential of quasispecies to new hosts. Cornell and RML will quantify determinants of zoonotic potential for henipavirus strains and quasispecies.

Milestones

Cloning (Cornell; 24 mths):

- Prioritize sequences for 20 F and G pairs to be analyzed for receptor binding and membrane fusion (24mths)
- Synthesize and clone sequences for 20 F and G gene pairs in pCAGGS plasmids (24mths)
- Grow plasmids in bacteria for 20 pairs F and G pairs (24mths)

Receptor binding and membrane fusion assays (Cornell, with help from RML; year 2, 12mths)

- Complete receptor binding assays for 20 G sequences (year 2, 12 months)
- Complete membrane fusion assays in 3 cell lines (human, bat and pig) (year 2, 12 months)

Molecular docking with *in silico* with *in vitro* measurements (RML, with help from Cornell):

- Perform molecular docking analyses (24mths)

Task 11.08, Lab: amplification and transmission dynamics of quasispecies *in vitro* and *in vivo*. RML, with help from CSU, will undertake in vivo experiments to measure phenotypes of henipavirus strains.

Milestones

In vitro and *in vivo* work (RML):

- Use cell culture experiments to analyze growth kinetics of henipaviruses (12mths)
- Develop hamster model for infection experiments (24mths)
- Conduct infection experiments in hamster model to measure infection, shedding, & QS in model hosts (24mths)
- Compare pathogenicity and transmission characteristics in hamster studies with historic studies done by RML (30mths)
- Obtain lung samples at peak virus replication and deep sequence these samples to study QS and selective pressures in a dead-end host (30mths)
- Develop bat models for henipavirus strains with highly pathogenic characteristics in the dead-end host model (36mths)
- Conduct infection experiments and measure infection and shedding in bats (36mths)
- Upon sufficient shedding, conduct contact transmission experiments (36mths)

- Analyze inoculated vs. transmitted virus populations by deep sequencing and identify potential transmissible QS (36mths)
- Analyze QS by established long-read PCR NSG methods (ongoing 42mths)

ANALYZE DATA

Task 11.05, Data analysis: statistical analysis of field data, lab data, environmental and ecological data, and bioinformatics NGS data. Provide statistical support and manage database for project.

Milestones

Data analysis and support (MSU):

- Develop a database structure, system and procedures for providing access to data, and a data visualization platform to facilitate information sharing across tasks and institutions (12mths)
- Clean and check data as it arrives (ongoing over 24mths)
- Graphically visualize and share incoming data for full team (ongoing over 24mths)
- Manage database, analyze data as appropriate, and provide statistical support to the team (ongoing 42mths)

Specific analyses to support other Tasks:

- Use statistical modeling to investigate and quantify links among nutritional status (TTU), stress signatures (TTU), immune status (MSU) and viral shedding (GU/RML/local laboratory) in *wild Australian bats* (30 months)
- Use statistical modeling to investigate and quantify links among nutritional status (Cambridge), stress signatures (MSU), immune status (Cambridge) and viral shedding (Cambridge) *in captive bats* (42 months)

DEVELOP MODELS

Task 11.06, Stochastic models of within- and between-host virus dynamics in bats. Cambridge, with help from GU, will perform stochastic modeling of within and between host virus dynamics in bats.

Milestones

Modeling (Cambridge, GU):

- Develop models of virus transmission within bat populations using prior knowledge from each location (12mths)
- Develop generic models of within-host virus dynamics that incorporate measurable components of the bat immune system (12mths)
- Validate and refine within- and between-host models of virus dynamics in bats using data collected in each field site and laboratory (36mths)

Task 11.15, Mechanistic mathematical modeling of viral fitness within humans, bats, and other host species, iterated with lab studies. UCLA will assemble genotype-to-phenotype maps for reservoir and spillover host species.

Milestones
Viral fitness modeling (UCLA):

- Develop mechanistic model of viral life cycle within cells (12mths)
- Integrate molecular, virologic, cell culture, and animal experiment data (24mths)
- Compare fitness predictions from *in silico* vs *in vitro* data (36mths)
- Integrate models and lab data to establish empirical relations between viral traits and fitness (42mths)

Task 11.09, Phylodynamic models of quasispecies dynamics within bat populations and between host species. MSU, with help from Cambridge and UCLA, will perform phylodynamic modeling of henipaviruses in bat populations.

Milestones
Phylodynamic modeling (MSU, Cambridge, UCLA):

- Formulate model framework to link viral genetics to transmission dynamics (12mths)
- Create models of within- and between-host selection in bat populations (24mths)

Task 12.02, Multi-scale models of zoonotic transmission from bats to humans to predict quasispecies expansions and pulses of excretion. Cambridge, with help from MSU, UCLA and GU, will develop a multi-scale mechanistic modeling framework for pathogen spillover.

Milestones
Multi-scale modeling (Cambridge, MSU, UCLA, GU):

- Develop baseline tools to relate spillover modeling framework from Plowright et al. to field data (12mths)
- Adapt spillover modeling framework from Plowright et al. to henipavirus contexts; identify key challenges to operationalize (18mths)
- Integrate bat virus transmission dynamics, environmental data. and viral fitness models (30mths)
- Develop an integrative model of bat virus spillover that is operationalized to predict probability of spillover at a spatial and temporal scale relevant for intervention (42mths)
- Perform a two-step validation of models:
    - Internal validation of the fitting methods: using simulated data generated by our candidate models, we will infer the parameter values and check the accuracy and precision of the fitting method (ongoing over 42mths)
    - External validation: we will exclude parts of the data iteratively, fit the models to the remaining dataset and check that it predicts correct values for the missing data (ongoing over 42mths)

Task 11.16, Machine learning to ID virus, reservoir traits, zoonotic risk. CIES will perform machine learning analyses to prioritize surveillance by identifying combinations of bat traits and environmental factors that predict spillover.

Milestones

Machine learning analyses (CIES): (all activities below are ongoing over 36mths)

- Collate and pre-process multiple data streams from field teams (environmental data; ecological data on bat populations; data on human ecology)
- Engineer features; impute bat trait data; tune hyperparameters for selected machine learning algorithm; execute cross-validation and target shuffling procedures to diagnose and correct overfitting; produce trait profiles of bat species predicted to be henipavirus positive (first predictions at 6mths).
- Repeat procedures above for models at the ecoregion and country scales (ongoing over 36mths)
- Combine species-level predictions with environmental and human ecological features from the Australian system (i.e., corresponding with viral shedding pulses in local bat populations, satellite imagery on seasonal human population densities, fruiting phenology, climate induced stress). Identify bat species that present the greatest spillover risk to humans, and measurable features that best predict viral shedding (ongoing over 24mths)
- Incorporate data on viral shedding events and conduct machine learning on viral PCR data to identify detectable predictors of viral shedding (Phase 2)
- Assess features corresponding to parameters in a multiscale mechanistic model of viral shedding and provide machine learning support of features to be included in multi-scale models of viral dynamics (e.g., engineering features, estimating parameters impacting viral shedding) (ongoing over 18 months in Phase 2)

TA2

DEMONSTRATE PROOF OF CONCEPT FOR AN ECOLOGICAL INTERVENTION FOR SPILLOVER

Task 22.03, Proof-of-concept for preemption through strategic ecological interventions. GU, with help from TTU and PSU, will do preliminary studies to develop the proof-of-concept demonstration of an ecological intervention to stop spillover. GU, MSU, TTU, Cambridge, CIES, CSU, PSU, RML will all contribute to investigating links between nutritional stress and virus shedding (above).

Milestones.

Demonstrate that bats move from urban roosts to flowering events in native forests (GU, with help from TTU)

- Establish methodology for using movement data to validate bats moving from urban roosts to native forests (6mths)
- Acquire movement data from existing and projected sources (18mths)
- Analyse movement data (24mths).

Demonstrate that bats locate and feed in regenerated habitat

- Develop experimental design and field methods to test use of regenerated forest as feeding habitat by bats (6mths)
- Establish field sites for testing use of regenerated forest as feeding habitat and commence field sampling (12mths)
- Sample up to 30 paired regeneration sites and remnant native habitat (control) sites for feeding bats (18mths)
- Analyse feeding data (24mths)

DEMONSTRATE PROOF OF CONCEPT, FEASIBILITY, AND SCALABILITY OF CHAD/VSV VACCINATION

Task 22.02, Proof-of-concept demonstration of ChAd/VSV vaccination feasibility and scalability of ChAd/VSV vaccination in bats. RML will develop and test a scalable vectored vaccine for target henipaviruses in bats. RML, with help from Cambridge, will assess the feasibility and scalability of the vaccine in bats.

Milestones

Vaccine development (RML):

- Design novel vaccines based on TA1
- Test by comparing measures of protection with historic hamster models (12mths)
- Test the effectiveness of the vaccines against novel henipaviruses (24mths)
- Demonstrate reduced probability of virus transmission among bats and among bats and recipient host species *in vivo* (42mths)
- Quantify scalability of ChAd/VSV vaccination in captive bats in Ghana (42mths)

TRANSITION PLAN

MSU and RML will develop the research transition plan.

Milestones

- Work with the MSU technology transfer infrastructure and personnel, and with the CEPI program to develop partnerships with vaccine manufacturers (30mths)
- Developed an inter-institutional agreement to enable the transfer of our discoveries to industry for commercialization (36mths)

DEPARTMENT OF THE INTERIOR
Interior Business Center
Acquisition Services Directorate, Division III
354 South Highway 92
Sierra Vista, AZ 85635

Agent for:
Defense Advanced Research Projects Agency (DARPA)

RESEARCH COOPERATIVE AGREEMENT SCHEDULE

1. **Agreement Number**: **D18AC00031** **Amendment 0001**

2. **Recipient Name:** **Montana State University - Bozeman**
307 Montana Hall
Bozeman, MT 59717

3. **Identification Numbers**:

Tax Identification Number (TIN)**: 81-6010045**

Data Universal Numbering System (DUNS) Number**: 625447982**

Commercial and Government Entity (CAGE) Code**: 1KQE9**

Federal Interagency Code for Education (FICE)**: 002532**

Catalog of Federal Domestic Assistance (CFDA): **12.910 – Research and Technology Development**

ASAP Recipient Number: **3034514**

4. **Principal Investigator/Key Personnel**: Dr. Raina Plowright
111A Lewis Hall
P.O. Box 173520
Bozeman, MT 59717-3520

Telephone:
E-mail address:

5. The purpose of this amendment is as follows:

a. Correct the ADPM to Phillip Lamp at Points of Contact 6. e.
b. Update the Quarterly R&D Status and the Monthly Financial Management Report due dates at 14. Reporting Requirements.

6. **Item 6 - Points of Contact is hereby updated as follows:**

6. Points of Contact:

a. Agreements Officer: Department of the Interior
Interior Business Center

Acquisition Services Directorate, Division III
354 South Highway 92
Sierra Vista, AZ 85635

Attention: Doreen Vieira-Cross
Telephone:
FAX:
Email:

b. Cooperative Agreement Administrator:

Department of the Interior
Interior Business Center
Acquisition Services Directorate, Division III
354 South Highway 92
Sierra Vista, AZ 85635

Attention: Deborah Branham
Telephone:
FAX:
Email:

c. Agreements Officer's Representative:

J. Aura Gimm
Air Force Office of Scientific Research
875 N. Randolph Street
Arlington, VA 22203

Teleph
Email:

d. DARPA Program Manager (PM):

Defense Sciences Office (BTO)
675 N. Randolph Street
Arlington, VA 22203-2114

Attention: Dr. James L. Gimlett
Telephone:
Email:

e. DARPA BTO Assistant Director, Program Management (ADPM)

Attention: Phillip Lamp
Email:

7. Item 14 – Reporting Requirements is hereby updated as follows:

14. Reporting Requirements: A final DD Form 882 is required to be filed listing all subject inventions or stating that there were none. In accordance with DARPA-BAA-HR001118S0017, the frequency of the reporting requirement differs from those commonly found in financial assistance agreements due to significant Government involvement throughout the duration of the research cycle. The following reports shall be submitted and will become due on the dates as shown below:

REPORT TYPE	DUE DATE	SUBMIT TO
Quarterly R&D Status Reports	Within 45 days of the end of each quarter	See Exhibit A Attachment 1
Monthly Financial Management Report	Within 45 days of the end of each month	See Exhibit A Attachment 2
Special Technical Report	Due as required	AOR, AO, PM, & DARPA Research Services
Annual Federal Financial Report (SF 425)	29 Dec 2019 29 Dec 2020	AOR, AO, PM, ONR & DARPA Research Services
Final Technical Report	29 Dec 2020	AOR, AO, PM, ONR, DTIC*, & DARPA Research Services
Final Financial Report (SF425)	29 Dec 2020	AOR, AO, PM, ONR, DTIC*, & DARPA Research Services
Final Invention Report (DD Form 882)	28 Jan 2021	See Exhibit A Article 8 - Intellectual Property Matters

*Defense Technical Information Center
ATTN: DTIC-O
8725 John J. Kingman Road
Ft. Belvoir, VA 22060-6218

If Optional Phase II is implemented - The following reports shall be submitted and will become due on the dates as shown below:

REPORT TYPE	DUE DATE	SUBMIT TO
Quarterly R&D Status Reports	Within 45 days of the end of each quarter	See Exhibit A Attachment 1
Monthly Financial Management Report	Within 45 days of the end of each month	See Exhibit A Attachment 2
Special Technical Reports	Due as required	AOR, AO, PM, & DARPA Research Services
Annual Federal Financial Report (SF 425)	29 Dec 2021	AOR, AO, PM, ONR, & DARPA Research Services
Final Technical Report	29 JUN 2022	AOR, AO, PM, ONR, DTIC*, & DARPA Research Services
Final Financial Report (SF425)	29 JUN 2022	AOR, AO, PM, ONR, DTIC*, & DARPA Research Services
Final Invention Report (DD Form 882)	29 JUL 2022	See Exhibit A Article 8 - Intellectual Property Matters

*Defense Technical Information Center
ATTN: DTIC-O
8725 John J. Kingman Road
Ft. Belvoir, VA 22060-6218

8. Acceptance of this amendment is pursuant to Article 14 Acceptance and Amendment of Cooperative Agreement Exhibit A.

9. All other terms and conditions remain unchanged.

THIS ACTION IS MADE ON BEHALF OF A DoD CUSTOMER UTILIZING DoD FUNDS.

UNITED STATES OF AMERICA
Department of the Interior, Interior Business Center
Acquisition Services Directorate, Division III

Doreen Vieira-Cross
Agreements Officer

MONTANA STATE UNIVERSITY

Attachment 3
Subaward Agreement Contacts

MSU ID G228-19-W7329

Pass-Through Entity Contacts	Subrecipient Contacts
Institution/Organization ("Pass-through Entity") Name Montana State University Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470	**Institution/Organization ("Subrecipient")** Name Colorado State University Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Duns Number 785979618 Duns Name Colorado State University
Administrative Contact Name Leslie Schmidt Associate Vice President Research Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470 Phone Email subawards@montana.edu	**Administrative Contact** Name Ashley Stahle Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email
Principal Investigator Name Raina Plowright Address Lewis Hall 111 Montana State University PO Box 173610 Bozeman, MT 59717-3610 Phone Email	**Principal Investigator** Name Tony Schountz Address 1692 Campus Delivery Fort Collins,CO 80523-1692 Phone Email
Financial Contact Name Jennifer Hodges Address Montana State University PO Box 173520 Bozeman, MT 59717-3520 Phone Email	**Financial Contact** Name Kim Marrale Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email
Authorized Official Name Dale Huls Assistant Director Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470 Phone Email subawards@montana.edu	**Authorized Official** Name Julie Harvey Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email

Records: As required by Uniform Guidance, 2 CFR 200, or 45 CFR Part 75, SUBRECIPIENT will maintain appropriate and complete accounts, records, documents and other evidence showing and supporting all costs incurred under this agreement. Subrecipient must retain all records that are required by the terms of the prime award or may reasonably be considered pertinent to the prime award. PTE may verify all expenditure receipts and disburse funds in an amount equal to the approved expenditures. SUBRECIPIENT will allow access to PTE, the Montana Legislative Auditor and/or the Montana Legislative Fiscal Analyst, or other designated persons to all records as may be necessary for audit purposes and to determine compliance with this agreement.

Fly America Act: The Fly America Act requires that all travelers and others performing U.S. Government-financed air travel use U.S. flag carriers to the extent such carriers are available, even if their use would cost more. Even when the entire trip cannot be made on U.S. flag carriers to the extent possible they should be used to the farthest interchange point on a usually traveled route. 301-3.6 (b)(4)(ii). Chartered flights are also subject to the requirements. Cost of duties, visas and value added tax are unallowable. Receipts of travel expenses are required to be submitted for payment.

Liability Exposure: The parties understand and agree that the liability of the State of Montana, PTE, its officials and employees is controlled and limited by the provisions of Title 02, Chapter 09, Montana Code Annotated entitled, *Government Structure and Administration – Liability Exposure and Insurance Coverage*, and the provisions of Title 18, Chapter 01, Part 4 entitled, *Contract Actions Against the State*. Any provision of this agreement, whether or not incorporated herein by reference or otherwise, will be controlled, limited and otherwise modified to limit any liability of the State of Montana, PTE, its officials and employees to that set forth in the above cited laws.

Non-Discrimination: SUBRECIPIENT agrees that no part of this subaward will be performed in a manner which illegally discriminates against any person on the basis of race, color, religion, creed, political ideas, national origin, sex, age, marital status, physical and/or mental handicap.

Assignment Transfer and Subcontracting: There will be no assignment, transfer, or subcontracting of this agreement, or of any interest in this agreement, unless both parties agree in writing. No services required under this agreement may be performed by individuals not subject to this agreement unless both parties agree in writing.

Use of Names: Neither party will include the name of the other party or any of its employees in any advertising, sales promotion or other publicity matter without the prior written consent of the other party.

Reporting Requirements: SUBRECIPIENT will provide to PTE any requested reports necessary to the completion of the prime award, and as detailed in **Attachment 4A.**

Attachment 4A
Subaward Agreement Additional Reporting Requirements

Quarterly R& D Status Reports will be submitted within thirty (30) days after the end of each project quarter (3/31, 6/30, 9/30, and 12/31) to the Pass-through Entity's Principal Investigator identified in Attachment 3. See Exhibit A Attachment 1 for format and instructions.

Monthly Financial Management Report reports will be submitted to the Pass-through Entity's Principal Investigator identified in Attachment 3, within thirty (30) days of the end of the month. See Exhibit A Attachment 2 for format, instructions and example.

Special Technical Reports as requested by DARPA/DOI, due as required, will be submitted when requested by the Pass-through Entity's Principal Investigator identified in Attachment 3.

Final Invention Report (DD Form 882) will be submitted to the Pass-through Entity's Principal Investigator identified in Attachment 3 by 12/20/2020. See Exhibit A Attachment 3 for format and instructions.

Montana State University - Bozeman
PREEMPT Program – Cooperative Agreement D18AC00031
Quarterly R&D Status Report

Period Covered by the Report: [Date] through [Date]

Date of Report:

Project Title: Preventing emergence and spillover of bat pathogens in high-risk global hotspots
Total Dollar Value: $8,239,511.00
Program Manager: Dr. James Gimlett, DARPA

Submitted by:
[PI Name]
[Institution]
[Address]

Telephone:
Email:

Subcontractors: [Co-PI name(s) and institution(s)]

TABLE OF CONTENTS

General notes:

- **Contact the program manager and team to report any financial or technical issues** (i.e., please do not wait until a report is due to bring up major issues).
- Clearly indicate if funding from another federal agency (e.g., NIH) has been used to support any data presented.
- Clearly indicate if any content is pre-publication sensitive or proprietary.
- Delete all instructional text from this document before submitting your report.
- Support your claims with data, images, and other evidence.
- Please update the header of each report with the respective quarterly period.
- Please use the following naming convention for report filenames: QR – PI institution – period covered (e.g., QR – University of XYZ – 01OCT2018 to 31DEC2018).
- Quarterly reports are due within 30 days of the quarter end date. For example, if the period ends on March 31, the report must be submitted by April 30.
- Monthly progress updates via conference calls will be scheduled with the program manager and his team.

Definitions:

- **Functional block diagram:** describes the functions and interrelationships of a system in a flock-block diagram style so that one can easily and thoroughly understand the system and the relationship of each of the parts to the whole. If the hardware evolves throughout your project, please provide a block diagram for each evolution (example included).
- **Work Breakdown Structure (WBS):** a hierarchical and incremental decomposition of the project into phases, deliverables and work packages. It is a tree structure that shows the subdivision of effort required to achieve an objective (example included).
- **Deliverable:** a measurable and verifiable outcome or object that a project team must create and deliver according to the terms of an agreement. An intangible deliverable is a particular outcome that the team achieves. A tangible deliverable is a concrete or material object created by the team.
- **Milestone:** a milestone describes the status of the project as represented by an event or moment at which one or more project activities are complete. Milestones can represent the completion of key project tasks, conclusions reached, or questions answered that affect project schedule significantly.
- **Major finding:** data with significant impact (positive or negative).
- **Metrics update:** progress (including delays and issues) toward achieving pre-established metrics of success.
- **SETA:** Science, Engineering, and Technical Assistant (internal DARPA term for technical support staff).

1 Progress Summary

1.1 Major Findings

Briefly describe the most significant and salient accomplishment(s) achieved during the ***most recent quarter***. How has this compared to the original project plan?

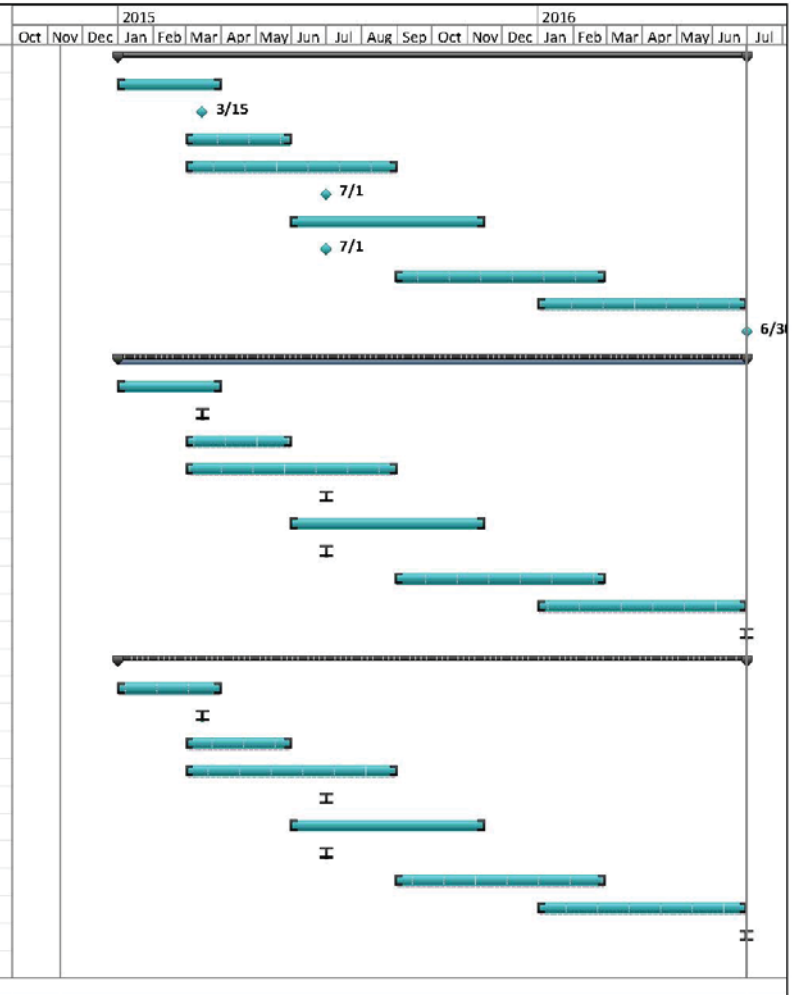
1.2 Metrics Update

Accomplishment *Include associated task #*	**Month** *Planned vs. achieved*	**Update** *Provide current status, explain any schedule discrepancies, list next steps*

2 Schedule – Milestones and Deliverables

Provide a high-level Gantt chart for Phase I that includes all milestones and deliverables for each task. An example of an acceptable chart is shown below.

ID	Task Mode	Task Name	Duration	Start	Finish	Predecessors
1		**Task**	**391 days**	**Thu 1/1/15**	**Thu 6/30/16**	
2		Subtask	64 days	Thu 1/1/15	Tue 3/31/15	
3		MS	0 days	Sun 3/15/15	Sun 3/15/15	
4		Subtask	67 days	Sun 3/1/15	Sun 5/31/15	
5		Subtask	132 days	Sun 3/1/15	Mon 8/31/15	
6		MS	0 days	Wed 7/1/15	Wed 7/1/15	
7		Subtask	122 days	Sun 5/31/15	Sun 11/15/15	
8		MS	0 days	Wed 7/1/15	Wed 7/1/15	
9		Subtask	132 days	Sun 8/30/15	Sun 2/28/16	
10		Subtask	130 days	Fri 1/1/16	Thu 6/30/16	
11		MS	0 days	Thu 6/30/16	Thu 6/30/16	
12		**Task**	**391 days**	**Thu 1/1/15**	**Thu 6/30/16**	
13		Subtask	64 days	Thu 1/1/15	Tue 3/31/15	
14		MS	1 day	Sun 3/15/15	Sun 3/15/15	
15		Subtask	67 days	Sun 3/1/15	Sun 5/31/15	
16		Subtask	132 days	Sun 3/1/15	Mon 8/31/15	
17		MS	1 day	Wed 7/1/15	Wed 7/1/15	
18		Subtask	122 days	Sun 5/31/15	Sun 11/15/15	
19		MS	1 day	Wed 7/1/15	Wed 7/1/15	
20		Subtask	132 days	Sun 8/30/15	Sun 2/28/16	
21		Subtask	130 days	Fri 1/1/16	Thu 6/30/16	
22		MS	1 day	Thu 6/30/16	Thu 6/30/16	
23		**Task**	**391 days?**	**Thu 1/1/15**	**Thu 6/30/16**	
24		Subtask	64 days	Thu 1/1/15	Tue 3/31/15	
25		MS	1 day	Sun 3/15/15	Sun 3/15/15	
26		Subtask	67 days	Sun 3/1/15	Sun 5/31/15	
27		Subtask	132 days	Sun 3/1/15	Mon 8/31/15	
28		MS	1 day	Wed 7/1/15	Wed 7/1/15	
29		Subtask	122 days	Sun 5/31/15	Sun 11/15/15	
30		MS	1 day	Wed 7/1/15	Wed 7/1/15	
31		Subtask	132 days	Sun 8/30/15	Sun 2/28/16	
32		Subtask	130 days	Fri 1/1/16	Thu 6/30/16	
33		MS	1 day	Thu 6/30/16	Thu 6/30/16	
34						



Include a corresponding table that provides:

- Short text-identifier for each milestone/deliverable
- Team members associated with each
- Schedule status (provide explanation if behind schedule or significantly ahead of schedule)
- Description of how the milestone/deliverable is contingent or dependent on other parts of the effort (if applicable)

Milestone/ Deliverable	**Team member(s)**	**Due date**	**Date initiated**	**Date completed**	**Status**	**Dependencies** *Across tasks & team members*

3 Task Progress, Accomplishments, and Plans

*Please provide updates from the **most recent quarter**, not a cumulative discussion of the project to date. Support all claims with data. Highlight major accomplishments. Provide explanations and/or justifications for any deviation from the negotiated schedule and spending plan.*

Identify the following for each major task in your SOW; this section will form the bulk of your report:

- Task number (from SOW)
- High-level task description
- Completion status (e.g., ongoing, delayed, etc.)
- Funding associated with the task (spent to date vs. remaining to spend); explain any deviations from your original spend plan

Task #/Title	Brief Description	% Complete	Total $ for task	Spent	Remaining	Explain deviations from planned expenditures

- **Describe planned vs. actual progress towards the goals, milestones, and deliverables of the task; discuss why planned expectations were met, not met, or exceeded; highlight significant accomplishments**
- List next steps
- Support claims with data, images, or other evidence
- Identify and describe all significant challenges and risks encountered during work towards the goals of this task, including:
    - Critical dependencies across tasks and teams
    - Mitigation plan
    - Level of risk (high, medium, or low)
    - Changes in risk status since proposal or last report
    - Anticipated date risk will be resolved

4 Project Coordination, Dissemination, and Translation

4.1 Project Coordination

- Summarize key project planning and coordination over the quarter, including:
  - Meeting date(s), location, purpose
  - Attendees
  - Meeting outcomes, action items

4.2 Dissemination and Translation (if applicable)

- List any new partnerships, collaborators, users, etc.
- Describe potential commercialization pathways/partners

5 Publications and Presentations

Please provide a cumulative update on current and upcoming publications.

Title, Authors	Description/Type	Status
	Presentation to Conference Name	Published
	Paper, Name of Journal	Submitted
	Letter to the Editor, Scientific Organization	In preparation

6 Patents, Invention Disclosures, IDEs, etc…

Please provide a cumulative update of current or upcoming patents, inventions, Investigational Device Exemption (IDE), etc. Examples are listed in the table below.

Title, Authors	Description/Type	Status
	Patent; Name of Patent	Accepted
	FDA IDE	Filed/submitted
	Invention Disclosure	In preparation

Appendix I – Project Context

For future reports, only update this section if any information changes. Please indicate changes using red font.

Teaming and Personnel

Organizational Chart

Insert an organizational chart for your entire team

Contact Information

Please populate the following table with contact information for each team member. Please provide general area of expertise each will provide (e.g., microfluidics). In the last column, list tasks or otherwise briefly describe each individual's involvement in the effort.

Prime Team Members and Contact Information: [Institution]

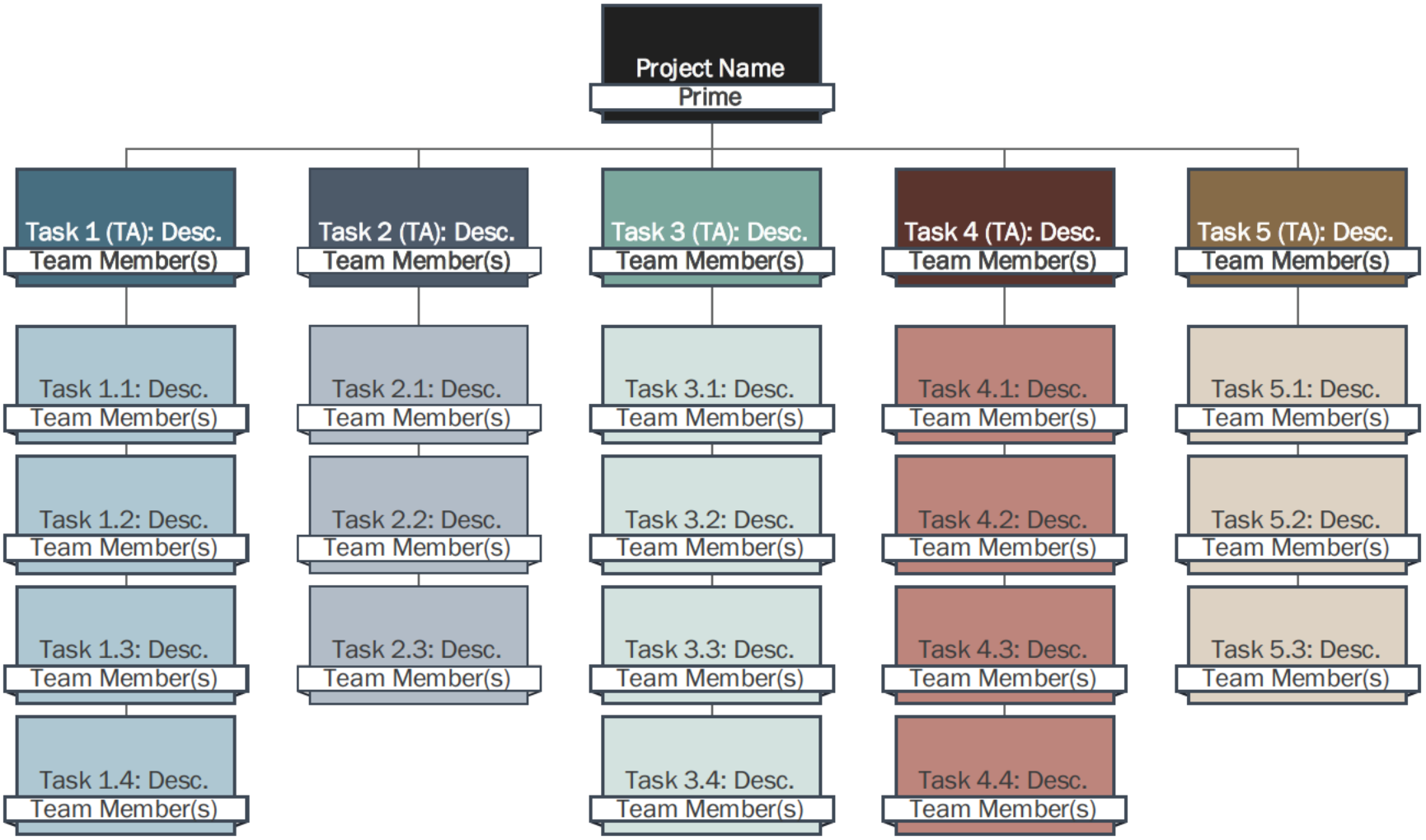
Role	Full name	Phone and email	Areas of Involvement
PI		(888) 888-8888 XXX@univ.edu	
Co-PI (expertise)		(888) 888-8888 XXX@univ.edu	
Postdoc (expertise)		(888) 888-8888 XXX@univ.edu	

Subcontract Team Members and Contact Information: [Institution]

Role	Full name	Phone and email	Areas of Involvement
PI (expertise)		(888) 888-8888 XXX@univ.edu	
Co-PI (expertise)		(888) 888-8888 XXX@univ.edu	
Postdoc (expertise)		(888) 888-8888 XXX@univ.edu	

Work Breakdown Structure

Provide breakdown of tasking and assigned team members as per the template shown below



Monthly Financial Report Template

LINK TO TEMPLATE (click here)

Please use this template to provide monthly financial updates to the PREEMPT team. As you input your data, the graph will automatically update. ***Please keep past reports in this file and create a new tab each month. We want to see all reports in the same file. Title tabs "Phase-Month-Year, " e.g., "Base - January - 2015"***

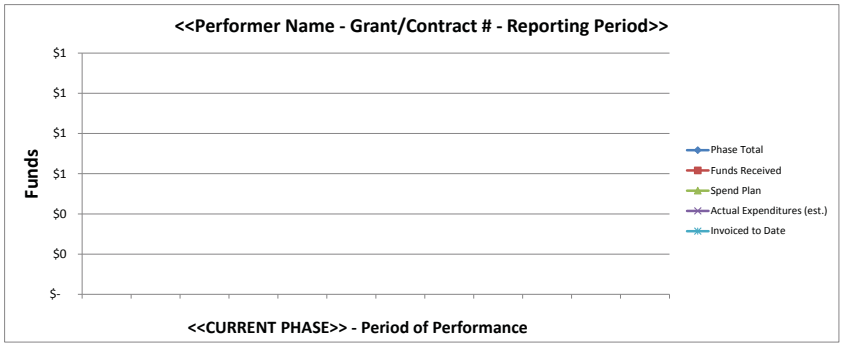
LINK TO EXAMPLE (click here)

An example of a completed template is also provided. The example graph illustrates a scenario where the performer is under spending. It is designed to show how this template will make it easy for INTERCEPT performers to clearly communicate the status of their effort to DARPA so that both can plan for and initiate contractual actions quickly and effectively.

Spend Plan Data	
Period of Performance	The financial report will only cover the current phase (e.g., Base, Option 1, etc.). Use a format similar to "Sep-2013," not "Month 6." In order to plan for continuing resolution requests, DARPA may reach out to you separately to request your projected spend rate for future phases.
Phase Total	Total for current phase *(Example Graph - total is $1,000,000)* .
Funds Received	Funds awarded to date; most efforts are funded incrementally *(Example Graph - this effort received an increment for $500,000 in Oct-2012 to exercise the base, and received the remainder of their base period funding in Mar-2013 (remaining $500,000))* .
Spend Plan	Projected Expenditures must cover the entire phase.
Actual Expenditures (est.)	Actual Expenditures should not be solely based off of invoices you have submitted or received to date. Instead, it should be an accurate (to the extent that is possible) account of the expenses you have actually incurred to date. For example, if a subcontractor has incurred but hasn't invoiced $100,000 worth of work, include the $100,000 in your actual expenditures. Or a large amount of equipment valued at $50,000 that hasn't yet been invoiced should also be factored in to the actual expenditures.
Invoiced to Date	Report the invoices you have submitted to date *(Example Graph - the scenario used in the example graph submits invoices quarterly)* .
Issues/Updates Summary (if applicable)	
Use this section as an opportunity to bring issues, concerns, or updates to the attention of DARPA. For example, you can summarize reasons for over/under-spending, potential no-cost extension requests, invoicing problems, etc.	

***Amounts for Spend Plan, Actual expenditures, Invoiced to Date are cumulative.

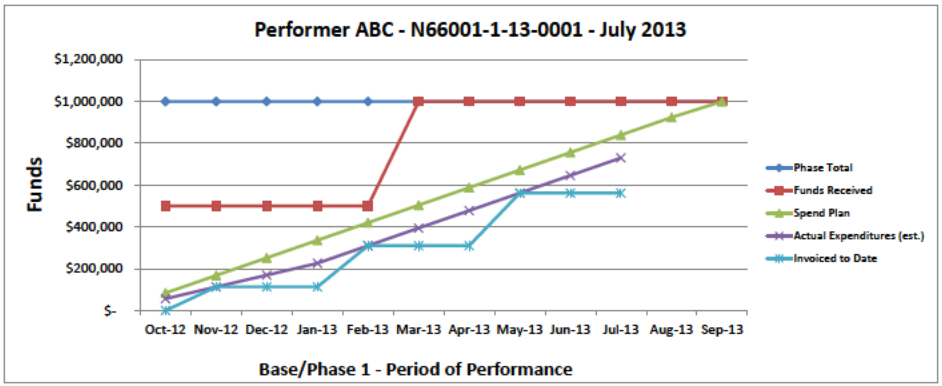
Exhibit A



Spend Plan Data												
Period of Performance (Current Phase Only)												
Phase Total												
Funds Received												
Spend Plan												
Actual Expenditures (est.)												
Invoiced to Date												

Issues/Updates Summary (if applicable)

Exhibit A



Spend Plan Data												
Period of Performance (Current Phase Only)	Oct-12	Nov-12	Dec-12	Jan-13	Feb-13	Mar-13	Apr-13	May-13	Jun-13	Jul-13	Aug-13	Sep-13
Phase Total	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000
Funds Received	$ 500,000	$ 500,000	$ 500,000	$ 500,000	$ 500,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000	$ 1,000,000
Spend Plan	$ 84,000	$ 168,000	$ 252,000	$ 336,000	$ 420,000	$ 504,000	$ 588,000	$ 672,000	$ 756,000	$ 840,000	$ 924,000	$ 1,000,000
Actual Expenditures (est.)	$ 56,500	$ 113,000	$ 169,550	$ 226,100	$ 310,100	$ 394,100	$ 478,100	$ 562,100	$ 646,100	$ 730,100		
Invoiced to Date	$ -	$ 113,000	$ 113,000	$ 113,000	$ 310,100	$ 310,100	$ 310,100	$ 562,100	$ 562,100	$ 562,100		

Issues/Updates Summary (if applicable)
We anticipate that we will need to request a four-month no cost extension (NCE). The NCE is necessary due to delays we experienced while getting Subcontractor #1 under contract. Although our effort's period of performance began in October 2012, the subcontract was finalized and fully-executed in February 2013, which resulted in a four-month delay from the intended start date. Subcontractor #1 is conducting a 12-month study, and cannot speed up their experiments. We would, however, like to begin work on Option 1. We intend to perform these tasks in parallel to the extended Base Period tasks (which are primarily performed by Subcontractor #1).

REPORT OF INVENTIONS AND SUBCONTRACTS

(Pursuant to "Patent Rights" Contract Clause) (See Instructions on back)

Form Approved
OMB No. 9000-0095
Expires Oct 31, 2004

PLEASE DO NOT RETURN YOUR COMPLETED FORM TO THIS ADDRESS. RETURN COMPLETED FORM TO THE CONTRACTING OFFICER.

1.a. NAME OF CONTRACTOR/SUBCONTRACTOR	c. CONTRACT NUMBER	2.a. NAME OF GOVERNMENT PRIME CONTRACTOR	c. CONTRACT NUMBER	3. TYPE OF REPORT *(X one)*
				a. INTERIM ☐ b. FINAL ☐
b. ADDRESS *(Include ZIP Code)*	d. AWARD DATE *(YYYYMMDD)*	b. ADDRESS *(Include ZIP Code)*	d. AWARD DATE *(YYYYMMDD)*	4. REPORTING PERIOD *(YYYYMMDD)*
				a. FROM
				b. TO

SECTION I - SUBJECT INVENTIONS

5. "SUBJECT INVENTIONS" REQUIRED TO BE REPORTED BY CONTRACTOR/SUBCONTRACTOR *(If "None," so state)*

NAME(S) OF INVENTOR(S) *(Last, First, Middle Initial)* a.	TITLE OF INVENTION(S) b.	DISCLOSURE NUMBER, PATENT APPLICATION SERIAL NUMBER OR PATENT NUMBER c.	ELECTION TO FILE PATENT APPLICATIONS *(X)* d.				CONFIRMATORY INSTRUMENT OR ASSIGNMENT FORWARDED TO CONTRACTING OFFICER *(X)* e.	
			(1) UNITED STATES		(2) FOREIGN			
			(a) YES	(b) NO	(a) YES	(b) NO	(a) YES	(b) NO

f. EMPLOYER OF INVENTOR(S) NOT EMPLOYED BY CONTRACTOR/SUBCONTRACTOR		g. ELECTED FOREIGN COUNTRIES IN WHICH A PATENT APPLICATION WILL BE FILED	
(1) (a) NAME OF INVENTOR *(Last, First, Middle Initial)*	(2) (a) NAME OF INVENTOR *(Last, First, Middle Initial)*	(1) TITLE OF INVENTION	(2) FOREIGN COUNTRIES OF PATENT APPLICATION
(b) NAME OF EMPLOYER	(b) NAME OF EMPLOYER		
(c) ADDRESS OF EMPLOYER *(Include ZIP Code)*	(c) ADDRESS OF EMPLOYER *(Include ZIP Code)*		

SECTION II - SUBCONTRACTS *(Containing a "Patent Rights" clause)*

6. SUBCONTRACTS AWARDED BY CONTRACTOR/SUBCONTRACTOR *(If "None," so state)*

NAME OF SUBCONTRACTOR(S) a.	ADDRESS *(Include ZIP Code)* b.	SUBCONTRACT NUMBER(S) c.	FAR "PATENT RIGHTS" d.		DESCRIPTION OF WORK TO BE PERFORMED UNDER SUBCONTRACT(S) e.	SUBCONTRACT DATES *(YYYYMMDD)* f.	
			(1) CLAUSE NUMBER	(2) DATE *(YYYYMM)*		(1) AWARD	(2) ESTIMATED COMPLETION

SECTION III - CERTIFICATION

7. CERTIFICATION OF REPORT BY CONTRACTOR/SUBCONTRACTOR *(Not required if: (X as appropriate))* ☐ **SMALL BUSINESS or** ☐ **NONPROFIT ORGANIZATION**

I certify that the reporting party has procedures for prompt identification and timely disclosure of "Subject Inventions," that such procedures have been followed and that all "Subject Inventions" have been reported.

a. NAME OF AUTHORIZED CONTRACTOR/SUBCONTRACTOR OFFICIAL *(Last, First, Middle Initial)*	b. TITLE	c. SIGNATURE	d. DATE SIGNED

DD FORM 882 INSTRUCTIONS

GENERAL

This form is for use in submitting INTERIM and FINAL invention reports to the Contracting Officer and for use in reporting the award of subcontracts containing a "Patent Rights" clause. If the form does not afford sufficient space, multiple forms may be used or plain sheets of paper with proper identification of information by item number may be attached.

An INTERIM report is due at least every 12 months from the date of contract award and shall include (a) a listing of "Subject Inventions" during the reporting period, (b) a certification of compliance with required invention identification and disclosure procedures together with a certification of reporting of all "Subject Inventions," and (c) any required information not previously reported on subcontracts containing a "Patent Rights" clause.

A FINAL report is due within 6 months if contractor is a small business firm or domestic nonprofit organization and within 3 months for all others after completion of the contract work and shall include (a) a listing of all "Subject Inventions" required by the contract to be reported, and (b) any required information not previously reported on subcontracts awarded during the course of or under the contract and containing a "Patent Rights" clause.

While the form may be used for simultaneously reporting inventions and subcontracts, it may also be used for reporting, promptly after award, subcontracts containing a "Patent Rights" clause.

Dates shall be entered where indicated in certain items on this form and shall be entered in six or eight digit numbers in the order of year and month (YYYYMM) or year, month and day (YYYYMMDD). Example: April 1999 should be entered as 199904 and April 15, 1999 should be entered as 19990415.

1.a. Self-explanatory.

1.b. Self-explanatory.

1.c. If "same" as Item 2.c., so state.

1.d. Self-explanatory.

2.a. If "same" as Item 1.a., so state.

2.b. Self-explanatory.

2.c. Procurement Instrument Identification (PII) number of contract (DFARS 204.7003).

2.d. through 5.e. Self-explanatory.

5.f. The name and address of the employer of each inventor not employed by the contractor or subcontractor is needed because the Government's rights in a reported invention may not be determined solely by the terms of the "Patent Rights" clause in the contract.

Example 1: If an invention is made by a Government employee assigned to work with a contractor, the Government rights in such an invention will be determined under Executive Order 10096.

Example 2: If an invention is made under a contract by joint inventors and one of the inventors is a Government employee, the Government's rights in such an inventor's interest in the invention will also be determined under Executive Order 10096, except where the contractor is a small business or nonprofit organization, in which case the provisions of 35 U.S.C. 202(e) will apply.

5.g.(1) Self-explanatory.

5.g.(2) Self-explanatory with the exception that the contractor or subcontractor shall indicate, if known at the time of this report, whether applications will be filed under either the Patent Cooperation Treaty (PCT) or the European Patent Convention (EPC). If such is known, the letters PCT or EPC shall be entered after each listed country.

6.a. Self-explanatory.

6.b. Self-explanatory.

6.c. Self-explanatory.

6.d. Patent Rights Clauses are located in FAR 52.227.

6.e. Self-explanatory.

6.f. Self-explanatory.

7. Certification not required by small business firms and domestic nonprofit organizations.

7.a. through 7.d. Self-explanatory.

SUBAWARD EXPENSE BUDGET

COST REIMBURSABLE EXPENSES - NO PAYMENTS IN ADVANCE

	Amount
Salaries	10,058.00
Benefits	2,877.00
Sub Awards	0.00
Contracted Services	0.00
Supplies	0.00
Communication	0.00
Foreign Travel	0.00
Domestic Travel	1,496.00
Rent	0.00
Repair and Maint	0.00
Awards	0.00
Participant Support	0.00
Capital Equipment	0.00
Major Renovations	0.00
Facilities and Admin	7,504.00
TOTAL	**21,935.00**

Facilities and Admin (IDC) Basis: MTDC less equip, sub, part supp,awa Rate: 52% Base Amount: 14,431.00

This subaward is being issued to allow work to commence, however, no work with animals shall be authorized until IACUC/ACURO approvals are obtained. Any work with animals that occurs prior to such approval will not be reimbursed by the Pass-Through entity. Subrecipient agrees to provide documentation to Pass-Through entity of all necessary reviews and approvals prior to conducting any animal-related work.

IDENTIFY HOST IMMUNE SIGNATURES

Task 11.04 Lab: identify host immune and stress signatures in wild bats and in a captive feeding trial. CSU will provide advice on how to measure bat immune signatures.

Milestones
Immunology on samples from Australia (MSU):
• Provide advice on tests on bats from Australia (6mths)

Immunology on samples from Ghana (Cambridge):
• Provide advice on tests on bats from Australia (24 mths).

Task 11.08, Lab: amplification and transmission dynamics of quasispecies *in vitro* and *in vivo*. RML, with help from CSU, will undertake in vivo experiments to measure phenotypes of henipavirus strains.

Milestones
• Provide advice on infection experiments (24mths)
• Design experiments and develop IACUC protocols and submit paperwork for ACURO approval (24mths)

DEMONSTRATE PROOF OF CONCEPT, FEASIBILITY, AND SCALABILITY OF CHAD/VSV VACCINATION

Task 22.02, Proof-of-concept demonstration of ChAd/VSV vaccination feasibility and scalability of ChAd/VSV vaccination in bats. RML will develop and test a scalable vectored vaccine for target henipaviruses in bats. RML, with help from Cambridge, will assess the feasibility and scalability of the vaccine in bats.

Milestones
- Provide advice on vaccine development (24mths)

Email or mail invoices to:

Pass-Through Entity Financial Contact

Name Jennifer Hodges

Address
Montana State University
PO Box 173520
Bozeman, MT 59717-3520

Phone (

Email

Invoices must meet the requirements of the Agreement Terms and Conditions.

1) Reference the MSU Subaward ID **G228-19-W7329** on all invoices.
2) Include current and cumulative costs by budget category (including cost sharing if required) on all invoices.
3) Include period covered by the invoice.
4) Invoices must be signed, dated and certified as to truth and accuracy. Invoices or vouchers requesting payment will include a certification, signed by an authorized official, which reads as follows: "By signing this report, I certify to the best of my knowledge and belief that the report is true, complete, and accurate, and the expenditures, disbursements and cash receipts are for the purposes and objectives set forth in the terms and conditions of the Federal award. I am aware that any false, fictitious, or fraudulent information, or the omission of any material fact, may subject me to criminal, civil or administrative penalties for fraud, false statements, false claims or otherwise. (U.S. Code Title 18, Section 1001 and Title 31, Sections 3729–3730 and 3801–3812)."

From: Grinstead,Liz
Sent: Thursday, August 20, 2020 7:39 AM
To: OSP PostAward Group
Cc: Harvey,Julie
Subject: FW: Memo to: Colorado State University G228-19-W7329 Amendment 2 draft
Attachments: Colorado State University G228-19-W7329 Amend 2.pdf

Hi All,

Could you please process?

Thank you!

Liz Grinstead
Senior Research Administrator

During the COVID-19 outbreak, CSU's Office of Sponsored Programs will continue with normal operations, though employees will be working remotely.

From: Nesbitt, Jennifer
Sent: Wednesday, August 19, 2020 4:45 PM
To: Harvey,Julie ; Grinstead,Liz >; Schountz,Tony ; kim.marrale Plowright, Raina >; von Sehlen, Jennifer >
Subject: Memo to: Colorado State University G228-19-W7329 Amendment 2 draft

Attached is a PDF of **MSU Subaward Number G228-19-W7329 Amendment 2** (Project Director Tony Schountz) for your review. If the agreement terms and conditions meet your approval, please have it signed (manual or electronic accepted) by your institution's authorized representative and return at your earliest convenience. Upon final execution, a scanned fully executed copy will be returned for your file.

Return signed documents **by email to**: subawards@montana.edu

I trust that the sub-award is in agreement with your understanding; however, if there is need for a change, please contact subawards@montana.edu or call as soon as possible. Do not make changes in the document as prepared until a mutual agreement has been reached.

Sincerely,
Jennifer

Jennifer F. Nesbitt
Office of Sponsored Programs
Montana State University
Bozeman, MT 59717

During the COVID-19 outbreak, MSU's Office of Sponsored Programs will continue with normal operations, though employees are working remotely. I am available Monday- Friday via email, and if needed, by phone or WebEx. Please email me as a first point of contact.

MONTANA STATE UNIVERSITY

Federal Subaward Amendment 2 MSU ID G228-19-W7329

Pass-Through Entity (PTE)	Subrecipient
Name Montana State University Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470	Name Colorado State University Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins, CO 80523-2002 Duns 785979618 Colorado State University
PTE Principal Investigator: Raina Plowright	Principal Investigator: Tony Schountz
PTE Awarding Agency: Defense Advanced Research Projects Agency	PTE Awarding Agency ID: D18AC00031
PTE CFDA 12.910 Research and Technology Development	This subaward is subject to OMB Uniform Guidance PTE FAIN: D18AC00031

Subaward Title: Preventing emergence and spillover of bat pathogens in high-risk global hotspots

Subaward Period of Performance	Authorized Amount	**Subaward ID: G228-19-W7329**
Start **10/01/2018** End **09/30/2020**	**85,686.09**	1. Cost Sharing is Not Required 2. This award is a Cost Reimbursable agreement 3. Project Reporting is Required (Attachments 4 and 4A)

Amendments to Original Agreement

The parties agree to amend the above referenced agreement as follows.

The total consideration for this project is increased SEVEN THOUSAND TWO HUNDRED THIRTY-SIX dollars AND 09/100 ($7,236.09) in accordance with the Revised Budget to a total of EIGHTY-FIVE THOUSAND SIX HUNDRED EIGHTY-SIX dollars AND 09/100 ($85,686.09). See Attachment 5.

All other terms and conditions of the subaward remain the full force and effect. This amendment will become effective on the date of the last signature, although costs may be accrued prior to that date.

By an Authorized Official of Montana State University	By an Authorized Official of SUBRECIPIENT
Signature _____ Date _____ Dale Huls, Assistant Director Office of Sponsored Programs Montana State University OSP Ref W7329-G19-228	Signature _____ Date _____ Printed Name and Title _____

MONTANA STATE UNIVERSITY

Attachment 3
Subaward Amendment 2 Contacts

MSU ID G228-19-W7329

Pass-Through Entity Contacts	Subrecipient Contacts
Institution/Organization ("Pass-through Entity") Name Montana State University Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470	**Institution/Organization ("Subrecipient")** Name Colorado State University Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Duns Number 785979618 Duns Name Colorado State University
Administrative Contact Name Leslie Schmidt Associate Vice President Research Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470 Phone Email subawards@montana.edu	**Administrative Contact** Name Liz Grinstead Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email
Principal Investigator Name Raina Plowright Address Lewis Hall 111 Montana State University PO Box 173610 Bozeman, MT 59717-3610 Phone Email	**Principal Investigator** Name Tony Schountz Address 1692 Campus Delivery Fort Collins,CO 80523-1692 Phone Email
Financial Contact Name Jennifer Hodges Address Montana State University PO Box 173520 Bozeman, MT 59717-3520 Phone Email	**Financial Contact** Name Kim Marrale Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email
Authorized Official Name Dale Huls Assistant Director Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470 Phone Email	**Authorized Official** Name Julie Harvey Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email

SUBAWARD EXPENSE BUDGET

COST REIMBURSABLE EXPENSES - NO PAYMENTS IN ADVANCE

	Previous Amount	Amendment Amount	Total
Salaries	23,000.00	-2,632.64	20,367.36
Benefits	6,583.00	-757.93	5,825.07
Sub Awards	0.00	0.00	0.00
Contracted Services	15,582.00	0.00	15,582.00
Supplies	660.00	6,018.00	6,678.00
Communication	0.00	0.00	0.00
Foreign Travel	0.00	0.00	0.00
Domestic Travel	5,787.00	2,133.16	7,920.16
Rent	0.00	0.00	0.00
Repair and Maint	0.00	0.00	0.00
Awards	0.00	0.00	0.00
Participant Support	0.00	0.00	0.00
Capital Equipment	0.00	0.00	0.00
Major Renovations	0.00	0.00	0.00
Facilities and Admin	26,838.00	2,475.50	29,313.50
TOTAL	**78,450.00**	**7,236.09**	**85,686.09**

Facilities and Admin (IDC) Basis: MTDC less equip, sub, part supp,awa Rate: 52% Base Amount: 51,372.00

From: Nesbitt, Jennifer
Sent: Wednesday, November 13, 2019 5:42 PM
To: Harvey,Julie; Stahle,Ashley; Schountz,Tony; kim.marrale Plowright, Raina; Hodges, Jennifer
Subject: Memo to: Colorado State University G228-19-W7329 Amendment 1 draft
Attachments: Colorado State University G228-19-W7329 Amend 1.pdf

Attached is a PDF of **MSU Subaward Number G228-19-W7329 Amendment 1** (Project Director Tony Schountz) for your review. If the agreement terms and conditions meet your approval, please have it signed (manual or electronic accepted) by your institution's authorized representative and return at your earliest convenience. Upon final execution, a scanned fully executed copy will be returned for your file.

Return signed documents **by email to**: subawards@montana.edu

I trust that the sub-award is in agreement with your understanding; however, if there is need for a change, please contact subawards@montana.edu or call as soon as possible. Do not make changes in the document as prepared until a mutual agreement has been reached.

Sincerely,
Jennifer

Jennifer F. Nesbitt
Office of Sponsored Programs
Montana State University
Bozeman, MT 59717

Office Hours: Monday-Friday, 9:15am-4:15pm

MONTANA STATE UNIVERSITY

Federal Subaward Amendment 1 MSU ID G228-19-W7329

Pass-Through Entity (PTE)	Subrecipient
Name Montana State University Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470	Name Colorado State University Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins, CO 80523-2002 Duns 785979618 Colorado State University
PTE Principal Investigator: **Raina Plowright**	Principal Investigator: **Tony Schountz**
PTE Awarding Agency: **Defense Advanced Research Projects Agency**	PTE Awarding Agency ID: D18AC00031
PTE CFDA 12.910 Research and Technology Development	This subaward is subject to OMB Uniform Guidance PTE FAIN: D18AC00031
Subaward Title: Preventing emergence and spillover of bat pathogens in high-risk global hotspots	

Subaward Period of Performance	Authorized Amount	**Subaward ID: G228-19-W7329**
Start **10/01/2018** End **09/30/2020** Incremental Funded Estimate End **09/30/2020**	**34,423.45** Incremental Estimated Total **85,686.09**	1. Cost Sharing is Not Required 2. This award is a Cost Reimbursable agreement 3. Project Reporting is Required (Attachments 4 and 4A)

Amendments to Original Agreement

The parties agree to amend the above referenced agreement as follows.

The Subaward Period of Performance is hereby extended to 09/30/2020.

The total consideration for this project is increased TWELVE THOUSAND FOUR HUNDRED EIGHTY-EIGHT dollars AND 45/100 ($12,488.45) in accordance with the Revised Budget to a total of THIRTY-FOUR THOUSAND FOUR HUNDRED TWENTY-THREE dollars AND 45/100 ($34,423.45). See Attachment 5.

All other terms and conditions of the subaward remain the full force and effect. This amendment will become effective on the date of the last signature, although costs may be accrued prior to that date.

By an Authorized Official of Montana State University	By an Authorized Official of SUBRECIPIENT
Signature _____ Date _____ Dale Huls, Assistant Director Office of Sponsored Programs Montana State University OSP Ref W7329-G19-228	Signature _____ Date _____ Printed Name and Title _____

MONTANA STATE UNIVERSITY

Attachment 3
Subaward Amendment 1 Contacts

MSU ID G228-19-W7329

Pass-Through Entity Contacts	Subrecipient Contacts
Institution/Organization ("Pass-through Entity") Name Montana State University Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470	**Institution/Organization ("Subrecipient")** Name Colorado State University Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Duns Number 785979618 Duns Name Colorado State University
Administrative Contact Name Leslie Schmidt Associate Vice President Research Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470 Phone 81 Email subawards@montana.edu	**Administrative Contact** Name Ashley Stahle Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email
Principal Investigator Name Raina Plowright Address Lewis Hall 111 Montana State University PO Box 173610 Bozeman, MT 59717-3610 Phone Email	**Principal Investigator** Name Tony Schountz Address 1692 Campus Delivery Fort Collins,CO 80523-1692 Phone Email
Financial Contact Name Jennifer Hodges Address Montana State University PO Box 173520 Bozeman, MT 59717-3520 Phone Email	**Financial Contact** Name Kim Marrale Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email
Authorized Official Name Dale Huls Assistant Director Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470 Phone Email	**Authorized Official** Name Julie Harvey Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email

MONTANA STATE UNIVERSITY

Attachment 5
Subaward Amendment 1 Budget

MSU ID G228-19-W7329

SUBAWARD EXPENSE BUDGET

COST REIMBURSABLE EXPENSES - NO PAYMENTS IN ADVANCE

	Previous Amount	Amendment Amount	Total
Salaries	10,058.00	6,720.00	16,778.00
Benefits	2,877.00	0.00	2,877.00
Sub Awards	0.00	0.00	0.00
Contracted Services	0.00	0.00	0.00
Supplies	0.00	0.00	0.00
Communication	0.00	0.00	0.00
Foreign Travel	0.00	0.00	0.00
Domestic Travel	1,496.00	1,496.00	2,992.00
Rent	0.00	0.00	0.00
Repair and Maint	0.00	0.00	0.00
Awards	0.00	0.00	0.00
Participant Support	0.00	0.00	0.00
Capital Equipment	0.00	0.00	0.00
Major Renovations	0.00	0.00	0.00
Facilities and Admin	7,504.00	4,272.45	11,776.45
TOTAL	**21,935.00**	**12,488.45**	**34,423.45**

Facilities and Admin (IDC) Basis: MTDC less equip, sub, part supp,awa Rate: 52% Base Amount: 22,647.00

From: Harvey,Julie
Sent: Tuesday, December 10, 2019 9:22 AM
To: Nesbitt, Jennifer; Hodges, Jennifer; Schountz,Tony; Plowright, Raina
Cc: Rogers,Susan
Subject: RE: Memo to: Colorado State University G228-19-W7329 Amendment 1 draft REVISED
Attachments: PE 5363098 Schountz AMD 01 Revised Montana State.pdf

Hello,

Sorry for the delay. The partially executed amendment is attached. We look forward to receiving the fully executed copy.

Thank you,
Julie

Julie Harvey
Research Administrator

Please note: the Office of Sponsored Programs will be closed during the CSU holiday shutdown (December 23, 2019 through December 29, 2019). If forms or correspondence are received during that time, there will be a delay in our reviews or responses until our return to the office on December 30, 2019 at the earliest.

From: Nesbitt, Jennifer
Sent: Wednesday, November 27, 2019 12:49 PM
To: Grinstead,Liz >; Stahle,Ashley >; Harvey,Julie >; Hodges, Jennifer ; Schountz,Tony >; Plowright, Raina >; kim.marrale
Harvey,Julie
Cc: Rogers,Susan
Subject: RE: Memo to: Colorado State University G228-19-W7329 Amendment 1 draft REVISED

Here is the revised agreement. Let me know if I missed anything!
Sincerely,
Jennifer

Jennifer F. Nesbitt
Office of Sponsored Programs
Montana State University
Bozeman, MT 59717

Office Hours: Monday-Friday, 9:15am-4:15pm

From: Grinstead,Liz >
Sent: Wednesday, November 27, 2019 11:29 AM
To: Nesbitt, Jennifer ; Stahle,Ashley >; Harvey,Julie ; Hodges, Jennifer < Schountz,Tony ; Plowright, Raina < >; kim.marrale Harvey,Julie >
Cc: Rogers,Susan
Subject: RE: Memo to: Colorado State University G228-19-W7329 Amendment 1 draft REVISED

Hi Jennifer,

My contact info is as follows:
p
Address- 2002 Campus Delivery
Fort Collins, CO 80523-2002
Email as below.

Thank you!

Liz Grinstead
Interim Senior Research Administrator

From: Nesbitt, Jennifer <
Sent: Wednesday, November 27, 2019 11:27 AM
To: Stahle,Ashley >; Harvey,Julie >; Hodges, Jennifer >; Schountz,Tony Plowright, Raina >; kim.marrale ; Harvey,Julie ; Grinstead,Liz <
Cc: Rogers,Susan
Subject: RE: Memo to: Colorado State University G228-19-W7329 Amendment 1 draft REVISED

Thanks for the information.

I will leave Julie in as Auth Official and replace you as Admin Contact with Ashley. Is her info the same as yours, or does she have a different phone and/or address? Once I have that info I will update and resend the amendment.

Jennifer

Jennifer F. Nesbitt
Office of Sponsored Programs
Montana State University
Bozeman, MT 59717

Office Hours: Monday-Friday, 9:15am-4:15pm

From: Stahle,Ashley
Sent: Wednesday, November 27, 2019 11:21 AM
To: Nesbitt, Jennifer ; Harvey,Julie >; Hodges, Jennifer >; Schountz,Tony ; Plowright, Raina >; kim.marrale ; Harvey,Julie Grinstead,Liz >
Cc: Rogers,Susan <
Subject: RE: Memo to: Colorado State University G228-19-W7329 Amendment 1 draft REVISED

Dear Jennifer,

I have switched roles in OSP. Julie Harvey and Liz Grinstead are your POC for this project. I have included them both to this email.

Thanks,
Ashley

Ashley Stahle
Assistant Director of Sponsored Programs, Director of Post-Award
Mailing Address: 2002 Campus Delivery | Fort Collins, CO 80523-2002

From: Nesbitt, Jennifer >
Sent: Tuesday, November 26, 2019 12:20 PM
To: Harvey,Julie ; Hodges, Jennifer ; Schountz,Tony >; Plowright, Raina >; Stahle,Ashley kim.marrale
Cc: Rogers,Susan <
Subject: RE: Memo to: Colorado State University G228-19-W7329 Amendment 1 draft REVISED

Per the clarifications noted below, please find a revised Amendment 1 for MSU Subaward G228-19-W7329.

If the agreement terms and conditions meet your approval, please have it signed (manual or electronic accepted) by your institution's authorized representative and return at your earliest convenience. Upon final execution, a scanned fully executed copy will be returned for your file.

Return signed documents **by email to**: subawards@montana.edu

I trust that the sub-award is in agreement with your understanding; however, if there is need for a change, please contact subawards@montana.edu or call as soon as possible. Do not make changes in the document as prepared until a mutual agreement has been reached.

Sincerely,
Jennifer

Jennifer F. Nesbitt
Office of Sponsored Programs
Montana State University
Bozeman, MT 59717

Office Hours: Monday-Friday, 9:15am-4:15pm

MONTANA STATE UNIVERSITY

From: Harvey,Julie >
Sent: Monday, November 25, 2019 11:40 AM
To: Hodges, Jennifer >; Nesbitt, Jennifer ; Schountz,Tony >; Plowright, Raina
Cc: Rogers,Susan >
Subject: RE: Memo to: Colorado State University G228-19-W7329 Amendment 1 draft

Hi, Jennifer,

Upon further review of our documents and after talking with Susan Rogers, it looks like we still need the remaining Year 1 budget for the animal work as well as the animal work for the first part of Year 2 now that we have received our ACURO approval.

Also, Susan had received the attached Subaward Modification Request, is this an amendment that is still in process? If so, the $12,488.45 from the attached Amendment 1 would need to be removed from the total of $56,515.

	Remainder Yr 1	Yr 2 (60%)	Total
Schountz, Tony		$ 7,491	$ 7,491
Eckley, Miles	$ 5,451		$ 5,451
Schountz fringe		$ 2,142	$ 2,142
Eckley fringe	$ 1,564		$ 1,564
Materials	$ 660		$ 660
Bat Per Diem	$ 8,702	$ 5,880	$ 14,582
Bat Overnight Shipping	$ 1,000		$ 1,000
Hamilton Trip	$ 2,794		$ 2,794
Bozeman		$ 1,496	$ 1,496
Direct Total	**$ 20,172**	**$ 17,009**	**$ 37,181**
F&A	$ 10,489	$ 8,845	$ 19,334
Total	**$ 30,661**	**$ 25,854**	**$ 56,515**

Thanks,

Julie Harvey
Research Administrator

From: Harvey,Julie
Sent: Monday, November 25, 2019 10:55 AM
To: Hodges, Jennifer ; Nesbitt, Jennifer ; Schountz,Tony Plowright, Raina

Cc: Rogers,Susan >
Subject: RE: Memo to: Colorado State University G228-19-W7329 Amendment 1 draft

Hi, Jennifer,

Please find attached a copy of the partially executed amendment. We look forward to receiving the fully executed copy.

Thanks,

Julie Harvey
Research Administrator

From: Harvey,Julie
Sent: Thursday, November 21, 2019 11:26 AM
To: Hodges, Jennifer >; Nesbitt, Jennifer ; Schountz,Tony ; Plowright, Raina >
Subject: RE: Memo to: Colorado State University G228-19-W7329 Amendment 1 draft

Thank you! I have forwarded the amendment on for signature here and will return it as soon as it has been signed.

Julie

Julie Harvey
Research Administrator

From: Hodges, Jennifer
Sent: Thursday, November 21, 2019 10:04 AM
To: Harvey,Julie >; Nesbitt, Jennifer ; Schountz,Tony ; Plowright, Raina
Subject: RE: Memo to: Colorado State University G228-19-W7329 Amendment 1 draft

Hello Julie,
We have received 60% of Year 2 funds. Once we receive the remaining, the subaward will be modified to the full Year 2 amount.
Thank you,
Jen

From: Harvey,Julie [mailto
Sent: Thursday, November 21, 2019 9:35 AM
To: Nesbitt, Jennifer < >; Schountz,Tony ; Plowright, Raina ; Hodges, Jennifer
Subject: RE: Memo to: Colorado State University G228-19-W7329 Amendment 1 draft

Hi, Jennifer,

We are just curious, now that we have provided our ACURO approval information, if the rest of the budget will be released?

Thanks,

Julie Harvey
Research Administrator

From: Nesbitt, Jennifer >
Sent: Wednesday, November 13, 2019 5:42 PM
To: Harvey,Julie >; Stahle,Ashley ; Schountz,Tony < >; kim.marrale Plowright, Raina < Hodges, Jennifer
Subject: Memo to: Colorado State University G228-19-W7329 Amendment 1 draft

Attached is a PDF of **MSU Subaward Number G228-19-W7329 Amendment 1** (Project Director Tony Schountz) for your review. If the agreement terms and conditions meet your approval, please have it signed (manual or electronic accepted) by your institution's authorized representative and return at your earliest convenience. Upon final execution, a scanned fully executed copy will be returned for your file.

Return signed documents **by email to**: subawards@montana.edu

I trust that the sub-award is in agreement with your understanding; however, if there is need for a change, please contact subawards@montana.edu or call as soon as possible. Do not make changes in the document as prepared until a mutual agreement has been reached.

Sincerely,
Jennifer

Jennifer F. Nesbitt
Office of Sponsored Programs
Montana State University
Bozeman, MT 59717

Office Hours: Monday-Friday, 9:15am-4:15pm

MONTANA STATE UNIVERSITY

Federal Subaward Amendment 1 MSU ID G228-19-W7329

Pass-Through Entity (PTE)	Subrecipient
Name Montana State University Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470	Name Colorado State University Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins, CO 80523-2002 Duns 785979618 Colorado State University
PTE Principal Investigator: **Raina Plowright**	Principal Investigator: **Tony Schountz**
PTE Awarding Agency: **Defense Advanced Research Projects Agency**	PTE Awarding Agency ID: D18AC00031
PTE CFDA 12.910 Research and Technology Development	This subaward is subject to OMB Uniform Guidance PTE FAIN: D18AC00031
Subaward Title: Preventing emergence and spillover of bat pathogens in high-risk global hotspots	

Subaward Period of Performance	Authorized Amount	**Subaward ID: G228-19-W7329**
Start **10/01/2018** End **09/30/2020** Incremental Funded Estimate End **09/30/2020**	**78,450.00** Incremental Estimated Total **85,686.09**	1. Cost Sharing is Not Required 2. This award is a Cost Reimbursable agreement 3. Project Reporting is Required (Attachments 4 and 4A)

Amendments to Original Agreement

The parties agree to amend the above referenced agreement as follows.

The Subaward Period of Performance is hereby extended to 09/30/2020.

The total consideration for this project is increased FIFTY-SIX THOUSAND FIVE HUNDRED FIFTEEN dollars AND 00/100 ($56,515.00) in accordance with the Revised Budget to a total of SEVENTY-EIGHT THOUSAND FOUR HUNDRED FIFTY dollars AND 00/100 ($78,450.00). See Attachment 5.

All other terms and conditions of the subaward remain the full force and effect. This amendment will become effective on the date of the last signature, although costs may be accrued prior to that date.

By an Authorized Official of Montana State University	By an Authorized Official of SUBRECIPIENT
Signature _____ Date _____ Dale Huls, Assistant Director Office of Sponsored Programs Montana State University OSP Ref W7329-G19-228	Signature _____ Date 12/10/19 Ashley Stahle, Assistant Director, OSP Printed Name and Title

MONTANA STATE UNIVERSITY

Attachment 3
Subaward Amendment 1 Contacts

MSU ID G228-19-W7329

Pass-Through Entity Contacts	Subrecipient Contacts
Institution/Organization ("Pass-through Entity") Name Montana State University Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470	**Institution/Organization ("Subrecipient")** Name Colorado State University Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Duns Number 785979618 Duns Name Colorado State University
Administrative Contact Name Leslie Schmidt Associate Vice President Research Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470 Phone Email subawards@montana.edu	**Administrative Contact** Name Ashley Stahle Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email
Principal Investigator Name Raina Plowright Address Lewis Hall 111 Montana State University PO Box 173610 Bozeman, MT 59717-3610 Phone 9 Email	**Principal Investigator** Name Tony Schountz Address 1692 Campus Delivery Fort Collins,CO 80523-1692 Phone Email
Financial Contact Name Jennifer Hodges Address Montana State University PO Box 173520 Bozeman, MT 59717-3520 Phone Email	**Financial Contact** Name Kim Marrale Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email
Authorized Official Name Dale Huls Assistant Director Address Office of Sponsored Programs PO Box 172470 Bozeman, MT 59717-2470 Phone Email subawards@montana.edu	**Authorized Official** Name Julie Harvey Address Office of Sponsored Programs 2002 Campus Delivery Fort Collins,CO 80523-2002 Phone Email

MONTANA STATE UNIVERSITY

Attachment 5
Subaward Amendment 1 Budget

MSU ID G228-19-W7329

SUBAWARD EXPENSE BUDGET

COST REIMBURSABLE EXPENSES - NO PAYMENTS IN ADVANCE

	Previous Amount	Amendment Amount	Total
Salaries	10,058.00	12,942.00	23,000.00
Benefits	2,877.00	3,706.00	6,583.00
Sub Awards	0.00	0.00	0.00
Contracted Services	0.00	15,582.00	15,582.00
Supplies	0.00	660.00	660.00
Communication	0.00	0.00	0.00
Foreign Travel	0.00	0.00	0.00
Domestic Travel	1,496.00	4,291.00	5,787.00
Rent	0.00	0.00	0.00
Repair and Maint	0.00	0.00	0.00
Awards	0.00	0.00	0.00
Participant Support	0.00	0.00	0.00
Capital Equipment	0.00	0.00	0.00
Major Renovations	0.00	0.00	0.00
Facilities and Admin	7,504.00	19,334.00	26,838.00
TOTAL	**21,935.00**	**56,515.00**	**78,450.00**

Facilities and Admin (IDC) Basis: MTDC less equip, sub, part supp,awa Rate: 52% Base Amount: 51,612.00