

From: EcoHealth Alliance
Sent: Thu, 18 Feb 2021 14:59:25 +0000
To: Morens, David (NIH/NIAID) [E]
Subject: Check out our latest report on defense, military, and security sector engagement in global public health



EcoHealth Alliance

It's been a while.

We've so dearly missed seeing you all at the Cosmos Club. As the vaccine rolls out, we hope to get back to D.C. soon, but until then we hope that you are well and safe.

Today, we released our latest report on defense, military, and security sector engagement in global health security and we wanted you to be some of the first to see it. The 88-page report is a thorough analysis of specific ways these separate but related sectors can assist in efforts to prevent, detect, and respond to outbreaks of emerging infectious disease. You can download the full report—or a short summary—[on our website](#).



Download the full report [here](#)



Download the report summary [here](#)

Until we may see each other again!

-- the EcoHealth Alliance team



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You are receiving this email because you opted in at our website or attended one of our events.

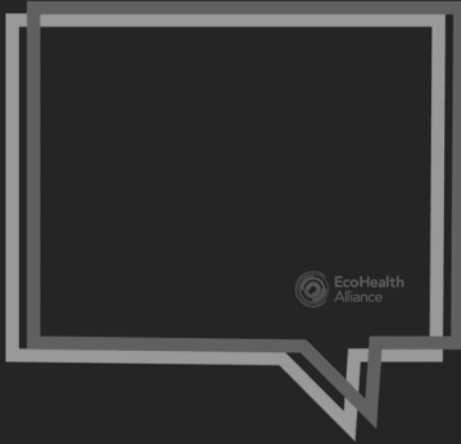
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520 Eighth Avenue
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New York, New York 10018

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From: EcoHealth Alliance
Sent: Thu, 4 Mar 2021 14:59:29 +0000
To: Morens, David (NIH/NIAID) [E]
Subject: An ounce of prevention is worth a pound of cure #12



YOU'RE INVITED

to a virtual event in support of EcoHealth Alliance
and our vital work preventing future pandemics

Thursday, April 29 / 8 PM (ET)

HONORING

The MTV Staying Alive Foundation
&
the law firm of Tarter Krinsky & Drogin

BROADCAST HOST

Soledad O'Brien

Award-Winning Documentarian,
Journalist, and CEO of
Soledad O'Brien Productions



Your support matters now more than ever

EcoHealth Alliance is at the forefront of the current COVID-19 pandemic
and working toward alleviating the risk of future emerging diseases.

Please consider supporting our vital work today.

[more details](#)

Event is open to the public. Sponsorship and VIP ticket
packages are available for purchase.

FOR MORE INFORMATION

Please contact the EcoHealth Alliance benefit office at
benefit@ecohealthalliance.org / 914.231.6180

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Lisa Silvershein

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Madelyn & Steven Wils

VICE-CHAIRS


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Dr. Lillian Wu & Dr. Ralph Gomory

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Virginia C. Mars
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NIH-57707-000859

Event is open to the public. Sponsorship and VIP ticket packages are available for [purchase](#).

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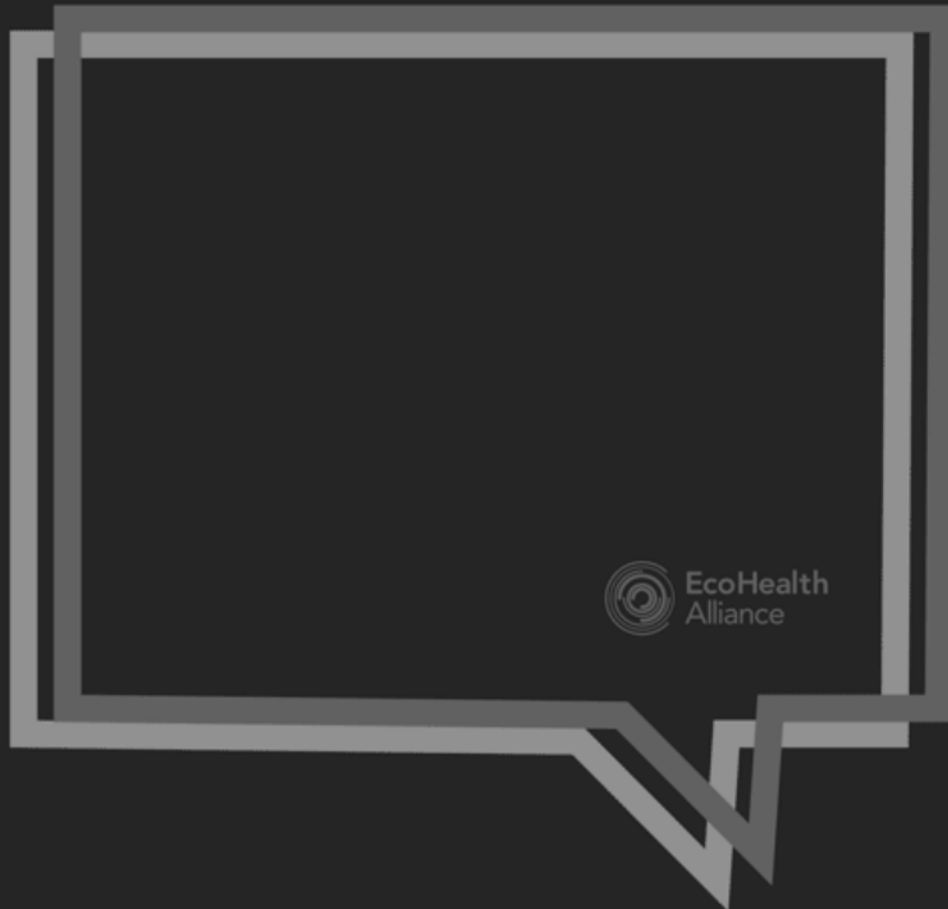
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From: EcoHealth Alliance
Sent: Thu, 25 Mar 2021 15:59:47 +0000
To: Morens, David (NIH/NIADD) [E]
Subject: We want our MTV




This year has shown us all the importance of scientific communication. Research and discovery can only truly lead to positive change when those findings are communicated in accurate and equitable ways to the communities impacted.

That's why EcoHealth Alliance is excited to honor the MTV Staying Alive Foundation during our virtual benefit on April 29.



We hope you will join us on April 29 as we come together to discuss how we can prevent pandemics and how EcoHealth Alliance plans to seize this moment to implement practical solutions for the problems of a Pandemic Era. Hear from global leaders in the science, medical, technology, and public health communities about the work that needs to be done to put an end to it.

The event is open to the public. Sponsorship and VIP ticket packages are available for [purchase](#).

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New York, New York 10018

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From: (b)(6)
Sent: Wed, 17 Mar 2021 18:31:23 +0000
To: (b)(6) Peter Daszak; Morens, David (NIH/NIAID) [E];
Keusch, Gerald T; Aleksei Chmura
Subject: Peter, Jerry, David Call

Peter Daszak is inviting you to a scheduled Zoom meeting.

Topic: Peter, Jerry, David Call
Time: Mar 17, 2021 03:10 PM Eastern Time (US and Canada)

Join Zoom Meeting

(b)(6)

Meeting ID: (b)(6)
Passcode: (b)(6)

(b)(6) US (New York)

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From: Jon Epstein
Sent: Wed, 22 Sep 2021 13:39:40 -0400
To: Morens, David (NIH/NIAID) [E]
Subject: Re: Request for support (b)(6) letter

Thanks, David. I really appreciate that - it's an especially tough stance for him to take given the current political climate - but absolutely correct nonetheless.

I'm certainly as focused as ever on the work. And there's plenty to do. (b)(6) and please pass on my gratitude to Tony, as well.

Talk soon,
Jon

On Wed, Sep 22, 2021 at 1:16 PM Morens, David (NIH/NIAID) [E] (b)(6) wrote:

Jon, (b)(6)

(b)(6)

Yesterday I had a zoom call with Tony and repeated to him the importance of working with international colleagues to characterize bats and the sarbecoviruses they carry not only in China but all over SEA and elsewhere. He agreed to make statements like that in published papers, and that is usually a first step in his taking an active interest.

Slowly, an important area of science is catching up to you. (b)(6)


(b)(6)


David


David M. Morens, M.D.

CAPT, United States Public Health Service

Senior Advisor to the Director
Office of the Director
National Institute of Allergy and Infectious Diseases
National Institutes of Health
Building 31, Room 7A-03
31 Center Drive, MSC 2520
Bethesda, MD 20892-2520

 (b)(6) (assistant: Whitney Robinson)

 301 496 4409

 (b)(6)

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From: Jon Epstein (b)(6)
Sent: Wednesday, September 22, 2021 12:48 PM
To: Morens, David (NIH/NIAID) [E] (b)(6)
Subject: Re: Request for support (b)(6) letter

Hey David,

I hope you're doing well. I wanted to get back to you to let you know that (b)(6)
(b)(6)
(b)(6) I wanted to sincerely thank you for writing a letter of support. (b)(6)

It would be nice to engage with the (b)(6) a bit more in the upcoming years.

Looking forward to the next opportunity to get together.

Cheers,

Jon

On Wed, Jan 20, 2021 at 3:23 PM Morens, David (NIH/NIAID) [E] (b)(6) wrote:

Buy me a beer sometime!, maybe in Vienna..... An honor to support this, as I think very highly of you, and have said so to Peter many times. (He always agrees, of course).


So, I just uploaded it and I hope it went through. I got a confirmation email. However when I lined up and then hit the "upload" button, I did not get a chance to preview what I uploaded, just a very quick, like 1 second, thank you for uploading. Maybe that's the way they do it

David


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On Wed, Jan 20, 2021 at 2:48 PM Morens, David (NIH/NIAID) [E] (b)(6) wrote:

Jon, will do. I just finished it but need to proof read and go over it one more time. Writing this thing reminded me all over again what a great and promising scientist you are. If the (b)(6) don't take you, it will be a travesty.



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(b)(6) (assistant: Whitney Robinson)



301 496 4409



(b)(6)

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Would you mind ping me when you submit the (b)(6) letter of reference? The system won't let me submit the application until your letter is received.

Thanks,

Jon

On Mon, Jan 18, 2021 at 5:21 PM Morens, David (NIH/NIAID) [E] (b)(6) wrote:

TY. I will be on it tomorrow. Today am (b)(6). D

Sent from my iPhone

David M Morens

OD, NIAID, NIH

On Jan 18, 2021, at 17:15, Jon Epstein (b)(6) wrote:

Attaching a current NIH biosketch - this may be more useful than my full CV.

-Jon

On Mon, Jan 18, 2021 at 5:04 PM Jon Epstein (b)(6) wrote:

(b)(6) have been able to get vaccinated.

(b)(6)

Stay safe :)

On Mon, Jan 18, 2021 at 5:00 PM Morens, David (NIH/NIAID) [E] (b)(6) wrote:

That should be all i need, if not i will get back to you. It is due by Wednesday night

(b)(6) No one i know at nih has been vaccinated, only the ill patients, plus the folks taking care of covid patients plus the nih police and fire fighters

D

Sent from my iPhone

David M Morens

OD, NIAID, NIH

On Jan 18, 2021, at 16:54, Jon Epstein (b)(6) wrote:

perfect - and sincerely appreciated.

I've sent you both my CV and the short essay they requested, which highlights a few things. If you want anything else, let me know.

Cheers,

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p.S. (b)(6)

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Meanwhile, here's the short paragraph they asked me for (below), and my CV, if you want to use those.

Cheers,

Jon

| | |
|----------|--------|
| Describe | (b)(6) |
| (b)(6) | |

250 words

(b)(6)

On Sun, Jan 17, 2021 at 1:52 PM Morens, David (NIH/NIAID) [E] (b)(6)
wrote:

Jon, yes, absolutely, I will be happy to fo so. Please get me all materials/info asap. D

Sent from my iPhone

David M Morens

OD, NIAID, NIH

On Jan 17, 2021, at 13:18, Jon Epstein (b)(6) wrote:

Hi David,

I hope you're doing well. I'm applying to (b)(6)

(b)(6)

(b)(6)

Would you be willing to be a professional reference? I'd need a letter of support from you. I can send you some language, if you're willing.

The application deadline is Jan 20th, but I'm trying to find out when the reference letters are due.

Sorry for the last minute request, and I'll absolutely understand if you're unable to do it.

Thanks, in advance, for considering.

Cheers,

Jon

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

(b)(6) (direct)
(b)(6) (mobile)

web: ecohealthalliance.org

Twitter: [@epsteinjon](https://twitter.com/epsteinjon)

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

--

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From: Morens, David (NIH/NIAID) [E]
Sent: Wed, 20 Jan 2021 21:36:17 +0000
To: Jon Epstein
Bcc: Morens, David (NIH/NIAID) [E]
Subject: Re: Request for support (b)(6) letter

I think it will get reversed eventually, even though we were able to get EH more money than was stolen. Lots of folks outside nih are working on it. It's the injustice that rankles, but as MLK believed "the arc of history bends toward justice". It just might take some time to get there. D

Sent from my iPhone
David M Morens
OD, NIAID, NIH

On Jan 20, 2021, at 16:33, Jon Epstein (b)(6) wrote:

I know he watched (and drank to) the inauguration as per his twitter account!

It would be good to get that grant decision reversed.

On Wed, Jan 20, 2021 at 3:32 PM Morens, David (NIH/NIAID) [E] (b)(6) wrote:

And then there is the unfinished issue of undoing whT Trump did to the EcoHealth grant. I hope Peter is able to see some of this in China. D

Sent from my iPhone
David M Morens
OD, NIAID, NIH

On Jan 20, 2021, at 15:29, Jon Epstein (b)(6) wrote:

Me too, I thought Biden was pitch perfect. A seriously good speech (says the choir). There was this tangible sense of relief when it became official. He's got his work cut out for him, but I'm hopeful.

See you soon.
-Jon

On Wed, Jan 20, 2021 at 3:24 PM Morens, David (NIH/NIAID) [E] (b)(6) wrote:


PS, yes I did enjoy today's events, I forgot to say. I had the inauguration on while I typed up the letter, and stopped typing for the best parts of the show (Biden's speech, not J Lo).....

David


David M. Morens, M.D.

CAPT, United States Public Health Service

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 (b)(6) (assistant: Whitney Robinson)

 301 496 4409

 (b)(6)

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Stay safe :)

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(b)(6) No one i know at nih has
been vaccinated, only the ill patients, plus the folks taking care of covid patients plus the nih
police and fire fighters

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Sent from my iPhone

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Describe (b)(6)
(b)(6)

250 words

(b)(6)

(b)(6)

On Sun, Jan 17, 2021 at 1:52 PM Morens, David (NIH/NIAID) [E] (b)(6) wrote:

Jon, yes, absolutely, I will be happy to fo so. Please get me all materials/info asap. D

Sent from my iPhone

David M Morens

OD, NIAID, NIH

On Jan 17, 2021, at 13:18, Jon Epstein (b)(6) wrote:

Hi David,

I hope you're doing well. I'm applying to (b)(6)

(b)(6)

(b)(6)

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The application deadline is Jan 20th, but I'm trying to find out when the reference letters are due.

Sorry for the last minute request, and I'll absolutely understand if you're unable to do it.

Thanks, in advance, for considering.

Cheers,

Jon

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

(b)(6) (direct)
(mobile)

web: ecohealthalliance.org

Twitter: [@epsteinjon](https://twitter.com/epsteinjon)

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

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From: Jon Epstein
Sent: Mon, 1 Feb 2021 09:11:03 -0500
To: Morens, David (NIH/NIAID) [E]
Cc: Taubenberger, Jeffery (NIH/NIAID) [E]
Subject: Re: bioRxiv: A novel SARS-CoV-2 related coronavirus in bats from Cambodia

Hi David,
Yes, thanks. They were linked in with the PREDICT team. This is an important addition to the Rhinolphus host/ SARS-CoV-2 related virus story, which will no doubt continue to expand as more results come out from the NIAID centers.

Cheers,
Jon

Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
New York

(e) (b)(6)
(o) [redacted]
(m) [redacted]
@epsteinjon

On Tue, Jan 26, 2021, 7:20 PM Morens, David (NIH/NIAID) [E] (b)(6) wrote:

Jon, are you aware of our niaid field group in Cambodia? The site has Rhinophilus bats and humans with sarbecovirus antibodies. They have been doing dengue work but have recently started doing a few coronavirus studies

Sent from my iPhone
David M Morens
OD, NIAID, NIH

Begin forwarded message:

From: "Morens, David (NIH/NIAID) [E]" (b)(6)
Date: January 26, 2021 at 19:15:29 EST
To: "Manning, Jessica (NIH/NIAID) [E]" (b)(6), "Taubenberger, Jeffery

(NIH/NIAID) [E]" (b)(6)

Subject: Fwd: bioRxiv: A novel SARS-CoV-2 related coronavirus in bats from Cambodia

Sent from my iPhone
David M Morens
OD, NIAID, NIH

Begin forwarded message:

From: "Folkers, Greg (NIH/NIAID) [E]" (b)(6)

Date: January 26, 2021 at 18:59:37 EST

Subject: bioRxiv: A novel SARS-CoV-2 related coronavirus in bats from Cambodia

A novel SARS-CoV-2 related coronavirus in bats from Cambodia

Vibol Hul, Deborah Delaune, [View ORCID Profile](#)Erik A. Karlsson, [View ORCID Profile](#)Alexandre Hassanin, Putita Ou Tey, Artem Baidaliuk, Fabiana Gambaro, Vuong Tan Tu, Lucy Keatts, Jonna Mazet, Christine Johnson, Philippe Buchy, Philippe Dussart, Tracey Goldstein, [View ORCID Profile](#)Etienne Simon-Loriere, Veasna Duong

doi: <https://doi.org/10.1101/2021.01.26.428212>

This article is a preprint and has not been certified by peer review [[what does this mean?](#)].

- [Abstract](#)
- [Info/History](#)
- [Metrics](#)
- [Preview PDF](#)

Abstract

Knowledge of the origin and reservoir of the coronavirus responsible for the ongoing COVID-19 pandemic is still fragmentary. To date, the closest relatives to SARS-CoV-2 have been detected in *Rhinolophus* bats sampled in the Yunnan province, China. Here we describe the identification of SARS-CoV-2 related coronaviruses in two *Rhinolophus shameli* bats sampled in Cambodia in 2010. Metagenomic sequencing identified nearly identical viruses sharing 92.6% nucleotide identity with SARS-CoV-2. Most genomic regions are closely related to SARS-CoV-2, with the exception of a small region corresponding to the spike N terminal domain. The discovery of these viruses in a bat species not found in China indicates that SARS-CoV-2 related viruses have

a much wider geographic distribution than previously understood, and suggests that Southeast Asia represents a key area to consider in the ongoing search for the origins of SARS-CoV-2, and in future surveillance for coronaviruses.

Competing Interest Statement

Philippe Buchy is currently an employee of GSK vaccines Asia-Pacific.

Paper in collection **COVID-19 SARS-CoV-2 preprints from medRxiv and bioRxiv**

Disclaimer: Any third-party material in this email has been shared for internal use under fair use provisions of U.S. copyright law, without further verification of its accuracy/veracity. It does not necessarily represent my views nor those of NIAID, NIH, HHS, or the U.S. government.

From: Morens, David (NIH/NIAID) [E]
Sent: Mon, 18 Jan 2021 22:21:27 +0000
To: Jon Epstein
Subject: Re: Request for support (b)(6) letter
Attachments: Epstein NIH BioSketch R24 2021.pdf

TY. I will be on it tomorrow. Today am (b)(6) D

Sent from my iPhone
David M Morens
OD, NIAID, NIH

On Jan 18, 2021, at 17:15, Jon Epstein (b)(6) wrote:

Attaching a current NIH biosketch - this may be more useful than my full CV.
-Jon

On Mon, Jan 18, 2021 at 5:04 PM Jon Epstein (b)(6) wrote:
(b)(6) have been able to get vaccinated.
(b)(6)

Stay safe :)

On Mon, Jan 18, 2021 at 5:00 PM Morens, David (NIH/NIAID) [E] (b)(6) wrote:

That should be all i need, if not i will get back to you. It is due by Wednesday night

(b)(6) No one i know at nih has been vaccinated, only the ill patients, plus the folks taking care of covid patients plus the nih police and fire fighters

D
Sent from my iPhone
David M Morens
OD, NIAID, NIH

On Jan 18, 2021, at 16:54, Jon Epstein (b)(6) wrote:

perfect - and sincerely appreciated.
I've sent you both my CV and the short essay they requested, which highlights a few things. If you want anything else, let me know.
Cheers,
Jon

p.S. (b)(6)

On Mon, Jan 18, 2021 at 4:50 PM Morens, David (NIH/NIAID) [E] (b)(6) wrote:

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Sent from my iPhone
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OD, NIAID, NIH

On Jan 18, 2021, at 16:41, Jon Epstein (b)(6) wrote:

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Meanwhile, here's the short paragraph they asked me for (below), and my CV, if you want to use those.

Cheers,
Jon

Describe

(b)(6)

250
words

(b)(6)

(b)(6)

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Thanks, in advance, for considering.

Cheers,
Jon

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Vice President for Science and Outreach

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520 Eighth Avenue, Ste. 1200

New York, NY 10018

(b)(6) (direct)
(b)(6) (mobile)

web: ecohealthalliance.org

Twitter: [@epsteinjon](https://twitter.com/epsteinjon)

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

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Withheld pursuant to exemption

(b)(6)

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Page 055 of 190

Withheld pursuant to exemption

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From: Morens, David (NIH/NIAID) [E]
Sent: Mon, 18 Jan 2021 22:12:04 +0000
To: Jon Epstein
Bcc: Morens, David (NIH/NIAID) [E]
Subject: Re: Request for support (b)(6) letter

U2! All we have to do is (b)(6) and then get thru a few more months of shit, and life as we knew it will start to return. Not soon enough for me... d

Sent from my iPhone
David M Morens
OD, NIAID, NIH

On Jan 18, 2021, at 17:05, Jon Epstein (b)(6) wrote:

(b)(6) have been able to get vaccinated.
(b)(6)

Stay safe :)

On Mon, Jan 18, 2021 at 5:00 PM Morens, David (NIH/NIAID) [E] (b)(6) wrote:

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(b)(6)

(b)(6)

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From: Morens, David (NIH/NIAID) [E]
Sent: Mon, 18 Jan 2021 21:50:06 +0000
To: Jon Epstein
Bcc: Morens, David (NIH/NIAID) [E]
Subject: Re: Request for support (b)(6) letter
Attachments: Jonathan H Epstein full CV 2021.pdf

Jon, yes i did get the request although it said almost nothing. I will forward what i got when i get to a computer probably tomorrow am. No need to go overboard on helping to draft. My way is to get a cv and perhaps a half page list of most significant things, or whatever materials you have, and then i draw from that and personalize it. I like to make these kinds of letters sound spontaneous and and thoughtful, not like they were written by a cheering machine. D

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(b)(6)

(b)(6)

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(b)(6)

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Page 085 of 190

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From: Jon Epstein
Sent: Sun, 17 Jan 2021 14:15:19 -0500
To: Morens, David (NIH/NIAID) [E]
Subject: Re: Request for support (b)(6) letter

Brilliant! Thank you. I'll initiate the request through the application, then send you materials, likely tonight.
-Jon

On Sun, Jan 17, 2021 at 1:52 PM Morens, David (NIH/NIAID) [E] (b)(6) wrote:

Jon, yes, absolutely, I will be happy to fo so. Please get me all materials/info asap. D

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OD, NIAID, NIH

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From: Morens, David (NIH/NIAID) [E]
Sent: Fri, 1 Apr 2016 10:29:26 +0000
To: William B. Karesh
Cc: Anthony Ramos
Bcc: Morens, David (NIH/NIAID) [E]
Subject: Re: Zika (!)

guys

let me know if there are any glitches

i am down in (b)(6) but back on weekend

d

David M Morens MD
NIAID, NIH
Sent from my iPhone

On Mar 31, 2016, at 16:30, William B. Karesh (b)(6) wrote:

Thanks !!

On Mar 31, 2016, at 3:32 PM, Anthony Ramos (b)(6) wrote:

David and Billy,

Dr. Fauci's office is going to send me a PDF of the slides for the purpose of sharing. When I receive it I will send to you Billy.

Anthony

Anthony M. Ramos
Senior Director, Marketing and Development

EcoHealth Alliance
460 West 34th Street – 17th floor
New York, NY 10001

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(b)(6) (mobile)

1.212.380.4465 (fax)
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 Thu, Mar 31, 2016 at 3:18 PM, William B. Karesh (b)(6) wrote:
David, Thanks so much again for helping make last night happen. Hope all is well (b)(6).

Not sure if you know Bob Huffman from EoP S&T - see note below, but he was asking if he could get a copy of the slide deck.

Anthony has it on his computer from last night, but we would not share it without permission.

BK

Begin forwarded message:

From: "Huffman, Robert V CIV USARMY HQDA ASA ALT (US)"

(b)(6)

Subject: Zika (!)

Date: March 31, 2016 at 2:59:44 PM EDT

To: "William B. Karesh" (b)(6)

Billy, good afternoon. Thanks so much for a superb and riveting program last evening. It was good seeing you, and I also thoroughly enjoyed the preceding (and post-briefing) networking event. All around great night.

Do you know if a copy of Dr. Fauci's slides are available? Frankly, I wasn't overly concerned about Zika prior to his talk, but the information presented did elevate my concerns and interest.

Best Rgds,
bob

Robert V. Huffman, P.E.
Deputy, Biosurveillance Strategy & Policy, Strategic Operations Directorate (SOD)
Joint Program Executive Office for Chemical and Biological Defense (JPEO CBDP)

Executive Secretary, Disease Prediction and Forecasting Working Group
Subcommittee on Biological Defense Research and Development
Committee on Homeland and National Security
National Science and Technology Council
The White House

Office: (b)(6) | Blackberry: (b)(6)

(b)(6)

Medical Countermeasure Systems BioDefense Therapeutics (MCS-BDTX)
10109 Gridley Road, Bldg 314, 2nd Floor | Fort Belvoir, VA, 22060
www.jpeocbd.osd.mil

From: Morens, David (NIH/NIAID) [E]
Sent: Wed, 4 Mar 2020 19:58:49 +0000
To: Robert Kessler
Cc: Peter Daszak; Tara Hoda; Aleksei Chmura; Alison Andre
Subject: RE: Cosmos Club EcoHealth Alliance Event


Thanks!




David M. Morens, M.D.

CAPT, United States Public Health Service
Senior Advisor to the Director
Office of the Director
National Institute of Allergy and Infectious Diseases
National Institutes of Health
Building 31, Room 7A-03
31 Center Drive, MSC 2520
Bethesda, MD 20892-2520

 (b)(6) (assistants: Kimberly Barasch; Whitney Robinson)

 301 496 4409

 (b)(6)

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From: Robert Kessler (b)(6)
Sent: Wednesday, March 4, 2020 2:35 PM
To: Morens, David (NIH/NIAID) [E] (b)(6)
Cc: Peter Daszak (b)(6); Tara Hoda (b)(6); Aleksei

Chmura (b)(6); Alison Andre (b)(6)
Subject: Re: Cosmos Club EcoHealth Alliance Event




Thanks David, that's too bad. We'll be having another event in July sometime and we'll keep you in mind for that. The date's not yet finalized but I will let you know.

Thanks,
Robert

On Wed, Mar 4, 2020 at 2:22 PM Morens, David (NIH/NIAID) [E] (b)(6) wrote:
Hi Peter, I'd love to do that but as things stand now, I am scheduled to be at UCLA from 5/27-5/29 giving a keynote lecture and then various stuff with faculty and students over the next couple days. Everything is of course up in the air with this coronavirus, but I am on the hook for that 3 day event. Always love to get together with you guys, so yes, you can count on me in the future



David M. Morens, M.D.

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From: Peter Daszak (b)(6)
Sent: Monday, March 2, 2020 4:57 PM
To: Morens, David (NIH/NIAID) [E] (b)(6)
Cc: Robert Kessler (b)(6); Tara Hoda (b)(6); Aleksei Chmura (b)(6); Alison Andre (b)(6)
Subject: Cosmos Club EcoHealth Alliance Event

Hi, David,

We'd really love to have you speak at our upcoming Cosmos Club Event on 27th May. Our main speaker will be Mike Osterholm and having you give an official NIAID statement on the outbreak would be terrific!

If you are not free to do this in May, we could set up something for our next event in July?

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
460 West 34th Street – 17th Floor
New York, NY 10001

Tel. (b)(6)

Website: www.ecohealthalliance.org

Twitter: [@PeterDaszak](https://twitter.com/PeterDaszak)

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

--

Robert Kessler

Communications Manager

he/him

EcoHealth Alliance
460 West 34th Street Ste. 1701
New York, NY 10001

(b)(6) (direct)
(b)(6) (mobile)

www.ecohealthalliance.org

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation.

From: Morens, David (NIH/NIAID) [E]
Sent: Wed, 1 Jul 2020 01:19:55 +0000
To: Bloom, Marshall (NIH/NIAID) [E]
Bcc: Taubenberger, Jeffery (NIH/NIAID) [E]; Peter Daszak; Howard Markel
Subject: Re: great article

Marshall, very kind of you! I will check and see what versions we have of the images, and send those. The photo of the Rembrandt is dark I think. I have not seen the original of that painting, at least not that I recall, but I think it was done in dark shadow, like many Rembrandt paintings and with heavy impasto. D

Sent from my iPhone
David M Morens
OD, NIAID, NIH

On Jun 30, 2020, at 20:51, Bloom, Marshall (NIH/NIAID) [E] (b)(6) wrote:

David,
The perspective you all wrote for mBio is just terrific!
Is there any chance you could send me clean images of the figures?
Thanks very much,
Marshall

Marshall E. Bloom, M.D.
RML Associate Director for Scientific Management
Division of Intramural Research
Chief, Biology of Vector-borne Viruses Section
Laboratory of Virology
Rocky Mountain Laboratories
National Institute of Allergy and Infectious Diseases
National Institutes of Health
903 South 4th Street
Hamilton, MT 59840

PHO: (b)(6)

Cell: 4

email: (b)(6)

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From: Morens, David (NIH/NIAID) [E]
Sent: Fri, 19 Jun 2020 12:36:40 +0000
To: Ellen Carlin
Cc: Sarah Babcock
Subject: Re: I've arrived!

You are a rock star! I always knew it! D

Sent from my iPhone
David M Morens
OD, NIAID, NIH

> On Jun 19, 2020, at 08:22, Ellen Carlin (b)(6) wrote:

>

> I'm in a video piece with Dr. Fauci! https://www.washingtonpost.com/video/health/worried-about-a-second-wave-of-coronavirus-were-still-in-the-first/2020/06/18/35d25e0d-863f-4735-9915-a88773bfd06f_video.html

>

> I need to remember to look at the pinpoint camera on the top of my computer when doing interviews. It's so awkward.

>

> Hope you guys are well.

>

> Ellen

>

From: Morens, David (NIH/NIAID) [E]
Sent: Sun, 19 Apr 2020 18:21:38 +0000
To: Akpa, Esther (NIH/NIAID) [E] (b)(6); (b)(6);
(b)(6); Babcock Sarah (b)(6); (b)(6);
Ellen Carlin; Chertow, Jessica (NIH/NHLBI) [E] (b)(6); James T. Douglas
(b)(6); Naomie Gathua (b)(6); Bob Holman (b)(6);
(b)(6); Reck, Linda (b)(6)

From Allison Imrie, 04/19/20:

I don't forward chain emails at other times but these are unusual times and this may bring some new ideas-

Ok everyone this will be fun to get new recipes to try. The toughest part of this is having emails for people since I communicate through the phone or texting, not so much via email so please try and keep this going gives us something new to do besides drinking and watching TV :)

"Going back to old times with a recipe exchange! As the world is social distancing right now, many of us are experimenting in our kitchens to help pass the time. So you have been invited to be a part of a #QuarantineCooking recipe exchange!

Please send a recipe to the person whose name is in position #1 (even if you don't know them) and it should be something quick, easy and without rare ingredients. Actually, the best one is the one you know in your head and can type right now. **Don't agonize over it...** It is the recipe you make when you are short on time.

After you've sent your recipe to the person in position #1 below (and only to that person), copy this email into a new email, move my name to the top and put your name in position #2. Only my and your name should show when you send your email. Send to 20 friends via BCC.

You should receive 36 recipes. It's fun to see where they come from! Seldom does anyone drop out because we all need new ideas. The turnaround is fast, as there are only 2 names on the list and you only have to do this once.

In the meantime, stay safe, stay healthy, and STAY HOME.

Happy #QuarantineCooking!

1. Allison Imrie

(b)(6)


2. David Morens

(b)(6)


David

David M. Morens, M.D.

CAPT, United States Public Health Service
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From: Morens, David (NIH/NIAID) [E]
Sent: Wed, 25 Mar 2020 16:30:44 +0000
To: Laura Spinney
Bcc: Taubenberger, Jeffery (NIH/NIAID) [E] (b)(6); Peter Daszak (b)(6)
Subject: RE: It takes a whole world to create a new virus, not just China | Laura Spinney | Opinion | The Guardian

Laura, thanks, very nice! Nice title, too! Davd

From: Laura Spinney (b)(6)
Sent: Wednesday, March 25, 2020 12:22 PM
To: Morens, David (NIH/NIAID) [E] (b)(6)
Subject: It takes a whole world to create a new virus, not just China | Laura Spinney | Opinion | The Guardian

Hello David,
I'm not sure if you'll approve of my overall argument, but I quoted your great NEJM piece with JT here, where it put a part of it better than I could have.
All the best,
Laura

<https://www.theguardian.com/commentisfree/2020/mar/25/new-virus-china-covid-19-food-markets>

It takes a whole world to create a new virus, not just China

[Laura Spinney](#) Wed 25 Mar 2020 15.31 GMT

Viruses such as Covid-19 wouldn't emerge in food markets if it wasn't for factory farming, globalised industry and rapid urbanisation



A hog farm in Iowa. ‘The factory farms that produce our food today ratchet up the virulence of flu viruses.’ Photograph: Ben Brewer/Reuters

When I get stressed, a patch of annoying red eczema appears on the inside of my upper right arm. The doctor gives me some cream to rub on it, but I also know that to stop it coming back I have to deal with the underlying problem.

Too much information, you’re thinking, but let me make the analogy. The reason we shouldn’t call the Sars-CoV-2 virus causing global misery the “Chinese virus” is the same reason I shouldn’t blame my eczema on my upper arm: there is clearly a superficial weakness there, but the real cause lies elsewhere.

All the evidence gathered to date suggests that the now notorious Chinese “wet markets” – places selling live and dead animals for human consumption – provide an opportunity for coronaviruses to jump easily from animals to people. It happened with the Sars-CoV virus in 2002-3 – which was contained before it caused a pandemic – and it has happened again with its close relative, Sars-CoV-2.

But to understand why the emergence of such zoonoses – human infections of animal origin – has accelerated in recent decades, you have to understand the forces putting those viruses in our path. They are political and economic. They have to do with the rise of industrial-scale farming concerns in China and the resulting marginalisation of millions of smallholder farmers. In order to survive, those farmers have moved into the production of more exotic species – animals that were once eaten only for subsistence. But the bigger operations have pushed the farmers out geographically too, as they have taken up more prime farming land. The smallholders have been forced closer to uncultivable zones such as forests, where bats – reservoirs for coronaviruses – lurk. The stars have aligned, and not in a good way, to channel bat viruses through intermediate mammalian hosts such as pangolins, and into humans.

Even so, to play devil’s advocate for a moment, the problem could still be regarded as uniquely Chinese. But there are two reasons why that’s not true. First, with the opening up of China, its agribusiness has ceased to be wholly Chinese-owned. It is a big recipient

of foreign direct investment. Second, as the American pandemic expert, David Morens, and his colleagues pointed out last month in the New England Journal of Medicine, we've been watching a similar drama unfold over a much longer timescale with influenza – the disease that has caused more pandemics in the history of humanity than any other. Flu viruses that infect animals, including poultry and pigs, have periodically spilled over into humans ever since we domesticated those animals millennia ago. But the factory farms that produce our food today ratchet up the virulence of those flu viruses just before they spill over. This ratcheting up has been documented in Europe, Australia and the US more than it has in poor or emerging economies, and it's what gave rise to the last flu pandemic in 2009. The first cases of that pandemic were recorded in California, but nobody calls it the American flu – and it's right that they don't, if only because American farms aren't wholly American-owned either. China, for one, has invested in them. It's not just the industries that produce our food that are creating the conditions in which new zoonoses emerge. Logging, mining, road-building and rapid urbanisation are also contributing, and the profits from those are shared internationally too. “We have created a global, human-dominated ecosystem that serves as a playground for the emergence and host-switching of animal viruses,” wrote Morens et al. The resulting diseases are suffered locally at first, as is reflected in their names – Ebola and Zika virus diseases and Bolivian hemorrhagic fever, to name just three – but the irony is that some of them, such as HIV and Covid-19, go on to become global. It's hard not to see a terrible natural justice in that.

In 2015, the World Health Organization issued guidelines on how to name diseases, which stipulated that such names should not single out particular human populations, places, animals or food. Names that commit those sins often turn out to be wrong anyway, but by the time that becomes clear the damage has already been done. Gay-related immune deficiency or GRID, the first name given to Aids, stigmatised the gay community while stymying research into how the disease affected other groups. President Trump's labelling of Sars-CoV-2 as the “Chinese virus” is also unhelpful. At a time when the main centres of Covid-19 infection are outside China, and Americans and Europeans could be learning valuable lessons from the Chinese, he is exchanging insults with Chinese politicians who have accused him of racism and hinted – just as preposterously – that the US military brought the virus to China. The slanging match suits Trump, distracting from his mishandling of the epidemic at home, but it does the rest of us no favours.

That doesn't mean China shouldn't be held accountable for its shortcomings. Americans know where their weak points are – they include agricultural fairs, where pigs and

humans come together – and they police them ferociously. Their infectious disease experts can detect a virus circulating in a herd and generate a vaccine to it within hours. The Chinese have got better at this lately. They now vaccinate their poultry flocks against a dangerous flu virus, H7N9, which first infected humans in 2013, for example. But nearly 20 years after Sars-CoV spilled over in a wet market, those places still appear to be a liability.

Controlling that animal-human interface is obviously important, but it shouldn't blind us to the bigger problem, which is those globalised industries. Economists use the term “tragedy of the commons” to describe a shared resource – common grazing land, say – that is spoiled by individuals acting in their own self-interest. It has been applied to the climate crisis, but as University of British Columbia geographer Luke Bergmann and his colleagues have pointed out, it doesn't quite fit what has happened here. In the case of these industries, it would be more accurate to say that they have excluded the nearly 8 billion of us who depend on the commons from participating in their governance. Yet we are bearing the costs of their industrial exploitation, in the form of pandemic disease.

We have our share of responsibility, as individuals, in the foods we choose to eat and the lifestyle choices we make generally. There are a lot of us on this planet and sustaining us is costly. But as has become increasingly clear, these industries have decoupled themselves from consumer choice; they're driving it rather than responding to it.

It's time we took back the commons, which means voting for politicians who will hold those industries accountable, rather than ones who deflect the blame. We need leaders who understand that the treatment for this particular eruption cannot only be topical, it has to be systemic too.

- Laura Spinney is a science journalist, novelist and author of *Pale Rider: The Spanish Flu of 1918 and How it Changed the World*

Laura Spinney
Writer & science journalist

Paris, France

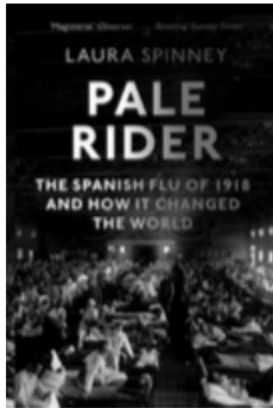
Tel: (b)(6)

Mob: (b)(6)

Skype: (b)(6)

(b)(6)

www.lauraspinney.com




From: Morens, David (NIH/NIAID) [E]
Sent: Mon, 23 Mar 2020 13:06:03 +0000
To: Ellen Carlin
Subject: RE: March 24 - Invitation for 5-minute plenary update


OK, that's fine, just wanted to be sure since nothing is up and running hewre at NIAID. Not only that, but it's a ghost town.


David

David M. Morens, M.D.

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From: Ellen Carlin (b)(6)
Sent: Monday, March 23, 2020 9:03 AM
To: Morens, David (NIH/NIAID) [E] (b)(6)
Subject: Re: March 24 - Invitation for 5-minute plenary update

Thanks so much, David—John is doing it, so we’ve got the NIH covered. Thank you so much for thinking to circle back. Go take care of the many other things on your plate...

On Mar 23, 2020, at 8:35 AM, Morens, David (NIH/NIAID) [E] (b)(6) wrote:

Ellen, as of yet I haven’t gotten clearance but I see John M is doing it whether he has clearance or not. I’m willing to do that if you still need me, and if not that is fine. Things are all out crazy here, the no-clearance things is just that everything but crisis management is falling through the cracks. Let me know,

<image001.gif>

David M. Morens, M.D.

CAPT, United States Public Health Service
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<image002.jpg>

From: Ellen Carlin (b)(6)
Sent: Wednesday, March 18, 2020 12:59 PM
To: Morens, David (NIH/NIAID) [E] (b)(6)
Subject: Re: March 24 - Invitation for 5-minute plenary update

David—thanks so much. I can’t tell you how much I know everyone is on the run, NIH especially, and really appreciate you considering.

Ellen


On Mar 18, 2020, at 12:47 PM, Morens, David (NIH/NIAID) [E] (b)(6) wrote:

Ellen, I am on the run at the moment but will do a quick reply now. I would be happy to do it if I can. Since you asked Tony it is already in the system and his assistants might already be looking for a replacement, so I'll check on that. I meet with Tony in about an hour. Also, these things need to be cleared with HHS, whoever does it. Again, I'll follow up


<image001.gif>

David M. Morens, M.D.

CAPT, United States Public Health Service
Senior Advisor to the Director
Office of the Director
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<image002.jpg>

From: Ellen Carlin (b)(6)
Sent: Wednesday, March 18, 2020 10:25 AM
To: Morens, David (NIH/NIAID) [E] (b)(6)
Cc: Phyllis A. Arthur (b)(6); Gregory Frank (b)(6); Mascola, John (NIH/VRC) [E] (b)(6)
Subject: March 24 - Invitation for 5-minute plenary update

Dear David,

I hope this email finds you well during these trying times. Does it feel like the world is a different place entirely since I saw you a month ago??

By now you will have received an invitation to BIO's multi-stakeholder COVID-19 Collaboration Virtual Summit that will take place March 24-25, 2020 (agenda attached). I am working with BIO in their efforts to ensure that the government is connected to the companies and researchers who are working on products and technologies that could counter the COVID outbreak, and to identify any challenges that could delay progress.

We are writing to ask if you would provide **five minutes of remarks during the opening plenary on "U.S. Government and NGO Response, Current Development Partnerships, and R&D Gaps" on Tuesday March 24 from 11:00-11:40 pm**. We had asked Dr. Fauci but he is quite understandably otherwise engaged. My next thought was you and I recognize that you are probably just as busy. But we are very much hoping for NIH representation; BARDA, DOD JPEO, and CEPI speakers are confirmed for that session. The meeting will be held via GoToMeeting and you can join from your home or office.

Thank you for considering lending your expertise to ensure robust discussion and actionable outcomes from the meeting. We look forward to your RSVP, and really appreciate your consideration during this very busy time.

Many thanks,

Ellen

From: Morens, David (NIH/NIAID) [E]
Sent: Mon, 17 Sep 2018 19:26:42 +0000
To: 'Ellen Carlin'
Subject: RE: Invitation to keynote at NMNH, Oct 23


OK, sounds good, I will put a few things together.... Have fun at the WH today!


David

David M. Morens, M.D.

CAPT, United States Public Health Service
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 (b)(6) (assistants: Meaghan Vance; Logan Salmon)

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From: Ellen Carlin (b)(6)
Sent: Monday, September 17, 2018 8:31 AM
To: Morens, David (NIH/NIAID) [E] (b)(6)
Subject: Re: Invitation to keynote at NMNH, Oct 23

Hi David! Always good to hear from you. I will be anxious to hear about DRC if NIH gets involved.

Thank you as always for your generosity of time! We are excited to have you join us for this workshop. I can answer all your questions either by email or hop on a call.

Timing: I think the 12:15-1:30 is a typo/holdover from an old draft. The talk can be as short or as long as you like. What if we planned 30 minutes followed by 15 minutes of questions?

Topic: Totally understand if you can't make the prior sessions. What I always appreciated from you is that you bring field experience to your work in science and science policy. I think that's the perspective that would be most valuable here. So your suggestion to look to past epidemics and focus on challenges is exactly right. Tell us a story. We will have a lot of technical talks on modeling and human behavior—we'd love to hear about your own experience working with humans in pandemics, and maybe some things you learned from their behavior and how the diseases spread.

I am headed to the White House this afternoon for a preview of the National Biodefense Strategy, set for release tomorrow. You may have already seen it or worked on it. I am anxious to see it myself.

Thanks again so much, and speak with you soon,
Ellen

On Sep 14, 2018, at 3:31 PM, Morens, David (NIH/NIAID) [E] (b)(6) wrote:

Hi Ellen,

I should be in town then, although just for a few days between meetings in Texas and New Orleans.

I can probably do something but have a few questions about topic, placement, length and so on.

You have me doing the closing keynote with the title "where do we go from here", but that title implies summing up what all the previous speakers have already said, which I may not be the best person to do. But we can discuss.

One thought that comes to mind I might be able to do is look at older and recent past pandemics and outbreaks and comment on the challenges posed by behavioral things, e.g., during the Ebola epidemics running away from their homes to hide in other villages, thereby spreading the disease.


Also the time length (1h 15 m) suggests not a long talk but rather a shorter one, with discussion.


No I am not off chasing Ebola this time. Yet. NIH is just beginning to get into it, but there are some turf sensitivities, so we are kinda lying low.


<image001.gif>

David M. Morens, M.D.

CAPT, United States Public Health Service
Senior Advisor to the Director
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<image002.jpg>

From: Ellen Carlin (b)(6)

Sent: Thursday, September 13, 2018 9:20 AM

To: Morens, David (NIH/NIAID) [E] (b)(6)

Subject: Invitation to keynote at NMNH, Oct 23

Hi David,

I hope this note finds you well! Are you in DRC these days?

If you will be stateside at the end of October, I would like to invite you to provide the closing keynote at a workshop on behavioral risk modeling to be held October 22-23, 2018 at the National Museum of Natural History in Washington, DC. The draft agenda is attached. The workshop has been developed by the U.S. Pandemic Prediction and Forecasting Science and Technology (PPFST) working group, and with my Smithsonian hat I have been helping to get it off the ground.

As the keynote, you would have broad leeway in your remarks. The workshop, *Behavioral Risk Modeling for Pandemic Prevention and Response*, will explore the human behavioral element of disease transmission models and how they can be improved to better inform preparedness and response. The working group seeks to understand the degree to which models for high-consequence infectious diseases account for behavioral factors; technical and policy challenges that are limiting the development of such models; and the extent to which modeling programs supported by Federal Departments and Agencies incorporate or plan to incorporate behavioral dynamics. The workshop will draw on expert input from a variety of disciplines needed to develop and implement useful models of behavioral risk. Findings will inform recommendations to the National Science and Technology Council.

As you may know, the PPFST was established in 2013 as an advisory group under the NSTC, the Cabinet-level Council established by Executive Order in 1993 that is the principal means within the Executive Branch to coordinate science and technology policy across the federal research and development enterprise. Its purpose is to coordinate priorities and activities to accelerate the development of infectious disease outbreak prediction and forecasting capabilities. The working group will host this workshop in partnership with other interagency and external groups, including the Department of Anthropology of the National Museum of Natural History.

Thank you very much for your consideration!

Sincerely,

Ellen

From: Ellen Carlin
Sent: Thu, 13 Sep 2018 09:20:25 -0400
To: Morens, David (NIH/NIAID) [E]
Subject: Invitation to keynote at NMNH, Oct 23
Attachments: PPFST workshop agenda draft 9.12.18.docx

Hi David,

I hope this note finds you well! Are you in DRC these days?

If you will be stateside at the end of October, I would like to invite you to provide the closing keynote at a workshop on behavioral risk modeling to be held October 22-23, 2018 at the National Museum of Natural History in Washington, DC. The draft agenda is attached. The workshop has been developed by the U.S. Pandemic Prediction and Forecasting Science and Technology (PPFST) working group, and with my Smithsonian hat I have been helping to get it off the ground.

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Thank you very much for your consideration!

Sincerely,

Ellen

Workshop: Behavioral Risk Modeling for Pandemic Prevention and Response

**Hosted by the National Science and Technology Council and the
Pandemic Prediction and Forecasting Science and Technology Working Group**

October 22-23, 2018

**National Museum of Natural History
Q?rius Auditorium, First Floor
Washington, DC 20013**

Draft Agenda

DAY 1

- 8:15-8:45** **Arrivals, coffee and light breakfast**
- 8:45-9:00** **Introductions**
*Invited: Representative from Office of Science and Technology Policy (or
National Security Council), Executive Office of the President*
- 9:00-9:45** **Human Behavior and Pandemics: What Don't We Know?**
James Holland Jones, Stanford University
- SESSION I: HUMAN BEHAVIOR AND PANDEMICS**
- 9:45-10:15** **How the Spread of Behavior Influences the Spread of Diseases**
*Damon Centola, Associate Professor of Communication, University of
Pennsylvania*
- 10:15-10:45** **Land Use Change as a Human Behavioral Risk Factor**
*Invited: Peter Leimgruber, Director of the Conservation Ecology Center,
Smithsonian Institution*
- 10:45-11:00** **Coffee break**
- 11:00-11:30** **Using Social Media to Inform USG Disaster Preparedness and
Response**
*Latasha Allen, Office of the Assistant Secretary for Preparedness and
Response, U.S. Department of Health and Human Services*
- 11:30-12:30** **Lunch**

SESSION II: BEHAVIORAL RISK MODELING FOR IMPROVING PANDEMIC PREVENTION AND RESPONSE

- 12:30-1:00** **How the USG Currently Applies Behavioral Dynamics and Disease Modeling to Pandemics**
Invited: TBD, Centers for Disease Control and Prevention
- 1:00-1:30** **Predictive Modeling of Human Behavioral Pandemic Risk: Challenges and Opportunities**
Invited: Yasha Feferholtz, Senior Research Scientist, EcoHealth Alliance
- 1:30-2:00** **Behavioral Intervention Modeling to Mitigate Pandemic Risk**
Ben Althouse, Institute for Disease Modeling
- 2:00-2:30** **Applied Modeling for Pandemic Preparedness and Decision-Making**
TBD
- 2:30-3:00** **Coffee and refreshments break**

SESSION III: BREAKOUTS

- 3:00-4:00** **Group Breakouts**
- **Group A:** Define three major gaps in the knowledge base for effective models
 - **Group B:** Develop three recommendations for improving predictive models
 - **Group C:** Develop three recommendations for improving intervention models
- 4:00-4:15** **Closing Remarks for Day 1**
JP Chretien, PPFST working group

DAY 2

8:15-8:45 Arrivals, coffee and light breakfast

8:45-9:00 **Introductions and Recap of Day 1**
JP Chretien, PPFST working group

SESSION IV: INTERVENTIONS

9:00-9:45 **Nine Years of PREDICT: Lessons for Behavioral Modeling Interventions**
Invited: Dennis Carroll, U.S. Agency for International Development

9:45-10:30 **Behavioral Risk Surveillance: Entry Points for Interventions**
Leilani Francisco, Senior Research Scientist, EcoHealth Alliance and Global Director for Behavioral Risk Surveillance, PREDICT

SESSION V: GROUP FINDINGS AND RECOMMENDATIONS

10:30-11:30 **Panel discussion**
Representative from each of Group A, B, and C
Invited: Moderated by Dylan George, In-Q-Tel

11:30-12:15 **Lunch**

12:15-1:30 **Closing Keynote: Where Do We Need to Go?**
TBD

1:30-1:45 **Conclusions and Next Steps**
JP Chretien (or other representative), Office of Science and Technology Policy, Executive Office of the President

Coffee, continental breakfast, and lunch will be served

From: Ellen Carlin
Sent: Wed, 18 Mar 2020 20:52:56 -0400
To: Mascola, John (NIH/VRC) [E]
Cc: Morens, David (NIH/NIAID) [E]; Phyllis A. Arthur; Gregory Frank; Austin, Sarah (NIH/NIAID) [E]; Suhana, Tina (NIH/VRC) [E]; Graham, Barney (NIH/VRC) [E]; Ledgerwood, Julie (NIH/NIAID) [E]
Subject: Re: March 24 - Invitation for 5-minute plenary update

Dear John,

Many thanks for the confirmation. We know this is an extraordinary time, and we very much appreciate you be willing to participate in this important event.

We will follow up in the near term with dial-in logistics and a final agenda. Please don't hesitate to be in touch in the meantime if you have any questions for us.

Sincerely,
Ellen

On Mar 18, 2020, at 7:57 PM, Mascola, John (NIH/VRC) [E] (b)(6) wrote:

Dear Ellen,

It is certainly a busy time and we are all adjusting.

I can contribute to the virtual meeting and provide brief remarks.

Best regards,
John

From: Ellen Carlin (b)(6)
Sent: Wednesday, March 18, 2020 10:25 AM
To: Morens, David (NIH/NIAID) [E] (b)(6)
Cc: Phyllis A. Arthur (b)(6); Gregory Frank (b)(6); Mascola, John (NIH/VRC) [E] (b)(6)
Subject: March 24 - Invitation for 5-minute plenary update

Dear David,

I hope this email finds you well during these trying times. Does it feel like the world is a different place entirely since I saw you a month ago??

By now you will have received an invitation to BIO's multi-stakeholder COVID-19 Collaboration Virtual Summit that will take place March 24-25, 2020 (agenda attached). I am working with BIO in their efforts to ensure that the government is connected to the companies and researchers who are working on

products and technologies that could counter the COVID outbreak, and to identify any challenges that could delay progress.

We are writing to ask if you would provide **five minutes of remarks during the opening plenary on "U.S. Government and NGO Response, Current Development Partnerships, and R&D Gaps" on Tuesday March 24 from 11:00-11:40 pm**. We had asked Dr. Fauci but he is quite understandably otherwise engaged. My next thought was you and I recognize that you are probably just as busy. But we are very much hoping for NIH representation; BARDA, DOD JPEO, and CEPI speakers are confirmed for that session. The meeting will be held via GoToMeeting and you can join from your home or office.

Thank you for considering lending your expertise to ensure robust discussion and actionable outcomes from the meeting. We look forward to your RSVP, and really appreciate your consideration during this very busy time.

Many thanks,

Ellen

<BCCI Virtual Summit AGENDA 17Mar2020 - Public v5.docx>

From: Ellen Carlin
Sent: Wed, 18 Mar 2020 10:24:56 -0400
To: Morens, David (NIH/NIAID) [E]
Cc: Phyllis A. Arthur; Gregory Frank; Mascola, John (NIH/VRC) [E]
Subject: March 24 - Invitation for 5-minute plenary update
Attachments: BCCI Virtual Summit AGENDA 17Mar2020 - Public v5.docx

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Many thanks,

Ellen



BIO Coronavirus Collaboration Initiative Summit
March 24-25, 2020
Virtual Meeting

Summit Goals

1. Inform industry of the latest data on COVID-19, the current status of projects already underway, and the knowledge gaps and technical and policy challenges that are important to the development of medical countermeasures.
2. Discuss the best approaches to the development of therapeutics, vaccines, diagnostics and other tools to respond to the COVID-19 global outbreak.
3. Promote future industry collaboration as well as partnerships with governmental and non-governmental partners.

Schedule at a Glance

Tuesday, March 24th

- 10:00 a.m. – 11:45 a.m.: Plenary Session
- 12:30 p.m. – 3:00 p.m.: Breakout Session - *Treatment*

Wednesday, March 25th

- 10:00 a.m. – 12:30 p.m.: Breakout Session - *Prevention*
- 1:00 p.m. – 3:30 p.m.: Breakout Session – *Diagnostics*

****** Instructions for joining the webinars will be emailed to participants prior to the Summit******

Plenary Session

Tuesday, March 24th

| | |
|-------------------------|---|
| 10:00 a.m. – 10:10 a.m. | Opening Remarks & Welcome <ul style="list-style-type: none">• <i>Jim Greenwood, CEO, BIO</i>• <i>Dr. George Scangos, CEO, Vir Biotechnology</i> |
| 10:10 a.m. – 10:30 a.m. | Opening Remarks <ul style="list-style-type: none">• <i>Ambassador Deborah Birx, MD [invited]</i>• <i>Robert Kadlec, MD, HHS Assistant Secretary for Preparedness and Response (ASPR) [invited]</i> |
| 10:30 a.m. – 11:00 a.m. | Panel 1: Coronavirus Virology, Epidemiology, and Clinical Presentation <ul style="list-style-type: none">• <i>Dr. Ralph Baric, UNC Gillings School of Global Public Health [invited]</i>• <i>Centers for Disease Control and Prevention (CDC) [invited]</i> |
| 11:00 a.m. – 11:40 a.m. | Panel 2: U.S. Government and NGO Response, Current Development Partnerships, and R&D Gaps <ul style="list-style-type: none">• <i>National Institutes of Health (NIH) [invited]</i>• <i>Dr. Rick Bright, Director, Biomedical Advanced Research & Development Authority (BARDA), HHS [confirmed]</i>• <i>Mr. Doug Bryce, Joint Program Executive Officer, Joint Program Executive Office for Chemical, Biological, Radiological, and Nuclear Defense (JPEO-CBRND), Department of Defense (DOD) [confirmed]</i>• <i>TBD, Coalition for Epidemic Preparedness Innovations (CEPI) [confirmed]</i>• <i>Bill & Melinda Gates Foundation [invited]</i> |
| 11:40 a.m. – 11:45 a.m. | Charge to Breakout Groups <ul style="list-style-type: none">• <i>Dr. George Scangos, CEO, Vir Biotechnology</i> |

Breakout Session Schedule

Tuesday, March 24th

| | |
|------------------------|--|
| 12:30 p.m. – 3:00 p.m. | Treatment <ul style="list-style-type: none">• Moderators: <i>Dr. Gerald Parker, Associate Dean for Global One Health, Texas A&M College of Veterinary Medicine and Biomedical Sciences</i> |
|------------------------|--|

Wednesday, March 25th

| | |
|-------------------------|---|
| 10:00 a.m. – 12:30 p.m. | Prevention <ul style="list-style-type: none">• Moderators: |
| 1:00 p.m. – 3:30 p.m. | Diagnostics <ul style="list-style-type: none">• Moderators: <i>Dr. Luciana Borio, Vice President, Technical Staff, In-Q-Tel</i> |

From: William B. Karesh
Sent: Thu, 11 Aug 2016 13:19:30 +0000
To: Morens, David (NIH/NIAID) [E]
Subject: Re: NEW YORK DAILY NEWS: Raising our biodefenses now

Thanks - LoL. No bar hopping with (b)(6) but I have been enjoying talking with him from time to time.

BK

William B. Karesh, D.V.M
Executive Vice President for Health and Policy

EcoHealth Alliance
460 West 34th Street - 17th Floor
New York, NY 10001 USA

(b)(6) (direct)
+1.212.380.4465 (fax)
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 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 Aug 11, 2016, at 6:54 AM, Morens, David (NIH/NIAID) [E] (b)(6) wrote:

Billy, great article! Have you been bar-hopping with (b)(6)? he doesn't seem the bar-hopping type.....


<image001.gif>

David M. Morens, M.D.
CAPT, United States Public Health Service

Senior Advisor to the Director
Office of the Director
National Institute of Allergy and Infectious Diseases
National Institutes of Health
Building 31, Room 7A-03
31 Center Drive, MSC 2520
Bethesda, MD 20892-2520

 (b)(6) (assistants: Kelley, Meaghan)

 301 496 4409

 (b)(6)

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<image003.jpg>

From: Folkers, Greg (NIH/NIAID) [E]
Sent: Wednesday, August 10, 2016 11:29 PM
Subject: NEW YORK DAILY NEWS: Raising our biodefenses now

Raising our biodefenses now

BY [Joe Lieberman](#) And [Dr. William Karesh](#)

NEW YORK DAILY NEWS

Wednesday, August 10, 2016, 5:00 AM

With the news from government officials that the Zika virus has now established itself in Florida and mosquitoes are transmitting it among people, we are reminded that yet another infectious disease is moving faster than our response to it. And our elected leaders in Washington left for the summer before finding common ground to deal with it.

Nearly six months have passed since the President requested \$1.9 billion in emergency Zika funds. Before it recessed, Congress considered offering \$1.1 billion in a bill so laden with poison pills that the President has threatened to veto it. This frustrating inability to reach an agreement has cost lives. More fundamentally, it reflects a reactionary mind-set.

We argue here for a simple yet paradigm-shifting approach grounded in prediction and prevention. Its fundamental tenet is this: Instead of arguing over cost offsets, instead of cities like New York having to pull money from other urgent public health needs, we can actually use the money we already invest each year in baseline budgets to reduce disease impacts and buffer the economic jolts they cause.

In 2003, the emergence of a previously unknown virus, SARS, cost the global economy \$40 billion. Influenza continues to pose a perennial threat to people and animals alike: A huge avian flu outbreak among poultry in Indiana and other states racked up staggering costs amounting to a \$5.5 billion hit — from a disease limited to poultry. We are already seeing similar financial shocks related to tourism and trade behavior with Zika's arrival in the Americas.

The good news is that just as you can now map your genes for \$100, you can sequence the entire genetic code of a virus for little more than that. For less than the cost of last year's bird flu outbreak, and for one-tenth of the cost of dealing with SARS, scientists now have the ability to identify 98% of hidden but threatening viruses through a new initiative called the Global Virome Project, proposed by scientists working with the U.S. government (including one of us, Dr. Karesh).

This effort would fund the sampling of animals and people from global hotspots where 75% of diseases are emerging, and analyze them for unknown viruses. Identifying the existence and location of previously unknown viruses that can cause outbreaks would allow us to assess their relative risk, and plan accordingly. The government, through the U.S. Agency for International Development's PREDICT program, has already been testing the feasibility of this approach, and results are extremely encouraging.

Cost-sharing with other countries, or groups like the World Bank, over a 10-year time frame means that pennies per person could save thousands of lives and hundreds of billions of dollars. Economist Jamison Pike of EcoHealth Alliance and colleagues at the University of Wyoming showed that if we begin enacting sensible strategies during this decade, we could save close to \$400 billion in the decades to come. That's a roughly 1,000-to-1 return on a well-planned annual investment in prevention.

Instead of persistent blindsides and time-consuming funding debates, this paradigm shift would give us the lead on emerging diseases, and even help prepare us for bioterrorism. This approach is consistent with the recommendations, now nearly a year old, of the bipartisan Blue Ribbon Study Panel on Biodefense on which we both serve.

In an encouraging move, a House bill proposed just before Congress left for vacation would pay for future emergencies through a public health emergency response fund, much the way the Federal Emergency Management Agency has access to emergency disaster money. The World Bank has also proposed a public-private financing initiative to help meet the response gap on a global level. We support these necessary efforts, but they provide little benefit to Americans at risk right now, or to the global millions caught in infectious disease crises.

We cannot ignore the need for emergency response, but we can reduce its costs through preventive efforts on the front end. What will the human and economic costs of Zika be? We don't know yet. But we do know that Zika's risk might have been revealed in advance had we put in place the kind of preventive programs a decade ago that we still need today.

Lieberman was chairman of the Senate Committee on Homeland Security and Governmental Affairs. He currently co-chairs the bipartisan Blue Ribbon Study Panel on Biodefense. Karesh is a doctor of veterinary medicine, executive vice president of health and policy at EcoHealth Alliance and an ex officio member of the biodefense panel.

From: Morens, David (NIH/NIAID) [E]
Sent: Sun, 5 Jun 2016 22:24:21 +0000
To: Kevin Olival, PhD
Cc: (b)(6)
Subject: RE: Viruses | Free Full-Text | Filoviruses in Bats: Current Knowledge and Future Directions | HTML
Attachments: Singh Ruzek VHF Book ch7.pdf

Guys, this is the Jens Kuhn review I mentioned on baTS AND FILOVIRUSES, IT'S AT THE END OF THE PAPER.....

David

David M. Morens, M.D.
CAPT, United States Public Health Service
Senior Advisor to the Director
Office of the Director
National Institute of Allergy and Infectious Diseases
National Institutes of Health
Building 31, Room 7A-03
31 Center Drive, MSC 2520
Bethesda, MD 20892-2520
B (b)(6) (assistants: Kelley, Meaghan)
(301 496 4409
3 (b)(6)

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-----Original Message-----

From: Kevin Olival, PhD [mailto:(b)(6)]
Sent: Friday, June 03, 2016 6:39 PM
To: Morens, David (NIH/NIAID) [E] (b)(6)
Subject: Viruses | Free Full-Text | Filoviruses in Bats: Current Knowledge and Future Directions | HTML

Cheers,
Kevin

<http://www.mdpi.com/1999-4915/6/4/1759/htm>

7 Role of Rodents and Bats in Human Viral Hemorrhagic Fevers

*Victoria Wahl-Jensen, Sheli R. Radoshitzky,
Fabian de Kok-Mercado, Shannon L. Taylor,
Sina Bavari, Peter B. Jahrling, and Jens H. Kuhn*

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7.1 RODENTS

The reservoir hosts of those hemorrhagic fever viruses that are not transmitted by arthropods or bats are assigned to the mammalian order Rodentia (rodents), which includes some 2000 different species. Its superfamily Muroidea (hamsters, gerbils true mice, and rats) includes over 1300 species (Wilson and Reeder, 2005). Of the hemorrhagic fever viruses, only those of the family *Arenaviridae* (arenaviruses) and the bunyaviral genus *Hantavirus* (hantaviruses) infect rodents, and all those rodents are muroid.

7.1.1 ARENAVIRUSES

The family *Arenaviridae* includes a single genus, *Arenavirus*, currently comprising 25 recognized species (Charrel et al., 2003; Clegg, 2002; Erickson et al., 2006; Jay et al., 2005; Lecompte et al., 2007;

Oldstone, 2002; Salvato et al., 2011). Based on antigenic properties and sequence phylogeny, arenaviruses have been divided into two distinct groups: The Old World arenaviruses include viruses indigenous to Africa, and the New World arenaviruses include viruses indigenous to the Americas (Bowen et al., 1996; Clegg, 2002; Rowe et al., 1970).

Most arenaviruses are not known to cause human disease, but several arenaviruses have been identified as the etiological agents of viral hemorrhagic fevers (VHFs) with case-fatality rates as high as 30%. Lassa virus (LASV) is an Old World arenavirus that causes Lassa fever (LF) in West Africa. More than 300,000 LASV infections (most of which do not manifest as overt VHFs) are reported in endemic areas per year with several thousand deaths (McCormick and Fisher-Hoch, 2002). Another Old World arenavirus, Lujo virus (LUJV), has been recently isolated from severe cases of undiagnosed viral hemorrhagic fevers in southern Africa (Zambia) (Briese et al., 2009). Machupo (MACV), Guanarito (GTOV), Junín (JUNV), and Sabiá (SABV) viruses are New World arenaviruses that cause Bolivian (BHF), “Venezuelan” (“VHF”), Argentinian (AHFV), and “Brazilian” hemorrhagic fevers, respectively (Buchmeier et al., 2006). Another virus, Chapare virus (CHPV), also causes VHF, but this disease has not yet received a name (Delgado et al., 2008). Among these arenaviruses, JUNV is the most important pathogen causing annual outbreaks in a progressively expanding region in north central Argentina, with almost five million individuals at risk of infection (Enria et al., 2008). There is a remarkable rodent specificity seen among arenaviruses in nature. Field studies strongly support the concept of only a single major reservoir rodent host for each virus (Salazar-Bravo et al., 2002b). Non-reservoir rodents might at times develop chronic infection and viremia, such as has been observed following experimental MACV infection of golden hamsters (*Mesocricetus auratus*) (Johnson et al., 1965). Rodents of the superfamily Muroidea are the natural hosts of arenaviruses (with the possible exception of Tacaribe virus, which might be transmitted by bats, and CHPV, LUJV, and SABV, for which no reservoirs have yet been identified). Old World arenaviruses are found in rodents of the muroid family Muridae, subfamily Murinae (Old World rats and mice), in sub-Saharan Africa, whereas New World arenaviruses are found in rodents of the muroid family Cricetidae, subfamily Sigmodontinae (New World rats and mice), in specialized ecological niches in South and North America. The geographic distribution of each arenavirus is determined by the range of its corresponding rodent host (Clegg, 2002; Salazar-Bravo et al., 2002b). Current evidence suggests a long-term “diffuse coevolution” between the arenaviruses and their rodent hosts. According to this model, a parallel phylogeny between the viruses and their corresponding rodent host(s) allows for host switches between rodents of closely related taxa (Hugot et al., 2001; Salazar-Bravo et al., 2002b). Arenaviruses establish chronic infections in their respective reservoirs accompanied by chronic viremia or viremia without clinical signs of disease (Fullhorst et al., 1999; Johnson et al., 1965; Sabattini et al., 1977; Walker et al., 1975). The chronic carrier state in rodents usually results from exposure to infectious virus early in ontogeny or later in life through aggressive or venereal behavior (Coetzee, 1975; Mills et al., 1992; Webb et al., 1975). Humans become infected through contact with infected rodent reservoirs or inhalation of aerosolized virus from contaminated rodent excreta or secretions and from rodents caught in mechanical harvesters and probably via consumption of rodent meat (Charrel and de Lamballerie, 2003; Maiztegui, 1975; TerMeulen et al., 1996). In fact, AHF, BHF, and “VHF” are typically seasonal diseases and outbreak frequency peaks during the harvest season with the majority of infected cases being male agricultural workers. BHF outbreak frequency peaks during April–July, AHF during the corn-harvesting season (March–June), and “VHF” between November and January. Direct human-to-human transmission, though possible, is probably not the principal mode of disease dissemination.

7.1.1.1 Lassa Virus

The Natal mastomys (*Mastomys natalensis*) is the natural reservoir host of LASV (Lecompte et al., 2006; Monath et al., 1974). The Natal mastomys is widely distributed in sub-Saharan Africa, breeds to high numbers, and is semi-commensal, i.e., lives both in the wild and in and around human dwellings and houses, which the rodents seek out especially during the rainy season (Coetzee, 1975;

Isaacson, 1975; Keenlyside et al., 1983; McCormick et al., 1987; Monath et al., 1974). Rainfall and to lesser extent temperature variability influence the prevalence of LASV (Fichet-Calvet and Rogers, 2009). For instance, the prevalence of LASV is higher during the rainy season than during the dry season (Fichet-Calvet et al., 2007). The reproductive activity of Natal mastomys is also highest during the rainy season (Fichet-Calvet et al., 2008). LASV can be found in Natal mastomys of all age groups, but LASV prevalence increases with age (Fichet-Calvet et al., 2007). Rainfalls could therefore lead to increased breeding of Natal mastomys and thereby increase the likelihood of LF outbreaks (Fichet-Calvet et al., 2008; Sluydts et al., 2007). The absence of rain, on the other hand, could decrease Natal mastomys populations because of lack of food, which could then force the rodents to enter human homes, especially into grain storage areas and kitchens. This would then again increase the risk of LASV transmission to humans. The Natal mastomys is the most common rodent found in the sub-Saharan region. Curiously, LF cases seem to be restricted to focal areas, however (Demby et al., 2001). A survey to examine the distribution of LASV, conducted in households and bush sited across the savannah, forest, urban, and coastal regions of Guinea, found a LASV prevalence in Natal mastomys ranging from 0% to 9% per region examined (Demby et al., 2001). The distribution and prevalence of LASV-infected rodents did not appear to localize to any one particular region but rather resembled focal spots by clustering in houses (Demby et al., 2001). A recent evolutionary sequence analysis of LASV suggests that the virus has appeared between 750 and 900 years ago in Nigeria but only recently spread to western Africa (150–250 years). The study identified a close relationship between civil war–related mass movements of refugees into new areas that were subsequently environmentally changed (deforestation), a decline in Natal mastomys populations in these areas due to these environmental disruptions, and an increase in LF cases due to increased human contact with rodents (including consumption) (Lalis et al., 2012).

7.1.1.2 Machupo Virus

The big laucha (*Calomys callosus*) is the principal host for MACV. The virus was recovered repeatedly from this small pastoral and peridomestic mouse (Johnson et al., 1966). Little information has been published about the ecology or natural history of this rodent. Although its exact geographic range has not been determined, available evidence indicates that the big laucha is distributed through the grasslands and along the forest edges from San Joaquín (lowlands and open biomes of eastern Bolivia) south to northern Argentina, in the northern portion of Paraguay, as well as in the continuous western fringe of Mato Grosso State in Brazil (Olds, 1988). It is preadapted for peridomestic living; it readily invades houses and gardens, where it lives in much the same manner as the house mouse (*Mus musculus*), and reaches population densities under these circumstances that are never observed in the absence of man (Mercado, 1975). During the 1960s, when the first known BHF outbreaks occurred, human settlements were almost invariably located in either of two types of ecological settings in the BHF epidemic region. The first included port villages, located on elevated riverbanks in gallery forest, where domestic rodents, if present, included usually roof rats (*Rattus rattus*) and house mice, with small numbers of rice rats (*Oryzomys bicolor*). Lauchas were not found in this ecological setting, presumably for lack of an avenue of suitable habitat between neighboring grasslands and the houses surrounded by forest. No human cases of BHF have been reported from port villages. The second ecological setting involved elevated sites between river systems, on which the richest agricultural developments were located in clearings in the climax forests. Such elevated areas were known locally as “Alturas,” and their elevation was sufficient to escape inundation during all except the most severe flood conditions. Farmhouses were usually located at the edge of the forest overlooking the grass-covered marshlands or “savannas.” Lauchas usually infested such farm villages. This was the ecological setting characteristic of all villages and isolated settlements from which human cases of BHF have been reported (Kuns, 1965). MACV induces a viremic immunotolerant infection in suckling lauchas and a split response in animals more than 9 days of age (Justines and Johnson, 1969; Webb et al., 1975). The “immunocompetent” response of 50% of the mice is characterized by clearance of viremia, minimal or absent viruria,

and presence of circulating neutralizing antibodies. The other “immunotolerant” mice develop persistent viremia, viruria, little or no neutralizing antibodies, anemia, and splenomegaly. MACV antigen can be detected in most tissues of these animals, including the reproductive organs (Justines and Johnson, 1969; Webb et al., 1975), and virus can be isolated from blood, spleen, and kidneys (Johnson et al., 1965; Kuns, 1965). The long-term effects of tolerant infection include mild runting, reduced survival rate, and almost total sterility among females, largely caused by virus infection of embryos. Selective breeding experiments in lauchas demonstrated that a complex polygenic inheritance accounts for the split response following MACV infection, suggesting a host genetic component as a determinant (Justines and Johnson, 1969; Webb et al., 1975). In these experiments, the infection of newly born lauchas could occur neonatally through the milk, and adult mice were infected through sexual transmission of MACV, suggesting that horizontal transmission through venereal encounters might be an important natural mechanism for virus maintenance (Webb et al., 1975). These studies also predict a model for MACV maintenance in its reservoir: virus infection would be more common in larger wild colonies of lauchas where increasing venereal transmission occurs, and infected colonies would eventually pass through a phase of reduced population with near complete, tolerant infection as young infected females are rendered sterile.

7.1.1.3 Junín Virus

The drylands laucha (*Calomys musculus*), a wild rodent that inhabits crop (corn, wheat, and soybeans) fields, pastures, and stable linear habitats (adjacent roadsides and fence lines), is the reservoir of JUNV (Sabattini and Gonzalez, 1967; Sabattini et al., 1977). It is rarely captured in or around houses. The populations of these rodents reach maximum densities in autumn in Argentina, coinciding with the harvest of the principal summer crops. Furthermore, the patchy spatial distribution of these rodents has been suggested to account for the focal distribution of AHF. The transmission to humans is believed to occur predominantly by inhaling aerosolized viral particles from contaminated soil and plant litter, which are disturbed during the mechanized harvesting process (Carballal et al., 1988; Maiztegui, 1975). Both horizontal and vertical transmissions have been reported as possible maintenance mechanisms of JUNV (Sabattini et al., 1977). Drylands lauchas infected at birth with JUNV exhibit decreased survival, body growth, and fertility, whereas animals that are inoculated with the virus as adults are usually asymptomatic and do not show altered body weight, reproduction, and survival (Vitullo et al., 1987; Vitullo and Marani, 1987; Vitullo and Merani, 1990). Furthermore, 50% of drylands lauchas infected as adults (90–120 days) develop persistent infections with JUNV isolated from urine, saliva, blood, or brain (and infection observed in brain, kidney, and spleen). The others develop serum antibodies and appear to clear the virus within 21 days after infection. The virus cannot transgress the placenta and reach the embryos (Vitullo and Merani, 1990). This suggests that vertical transmission might contribute, to some extent, to the maintenance of infection. In terms of a natural population of drylands lauchas, it may be assumed that animals vertically infected (during lactation), if unable to transfer the infection satisfactorily to the next generation, contribute toward intra-generation infection by horizontal transmission. Horizontally infected adults may secure the intergeneration transmission by both vertical and horizontal means. Under these circumstances, JUNV maintenance may arise from an equilibrium between both modes of transmission, with the horizontal route representing the main route resulting in viral persistence in nature and vertical transmission being an added option for intergeneration transfer that may support the infection when population numbers are reduced and horizontal transmission is precluded (Sabattini et al., 1977; Vitullo and Merani, 1988; Vitullo et al., 1987). A 30 month field study in the epidemic area of AHF estimated the total prevalence of JUNV infection to be 10.9% in drylands lauchas. Serum antibody and viral antigen were detected in blood and saliva of these rodents. JUNV-infected animals were predominantly males in the older age and heavier body mass classes. Seropositive males were twice as likely to have body scars as the overall population. JUNV-infected animals were also strongly associated with the relatively rare roadside and fence-line habitats (Mills et al., 1991, 1992, 1994). These observations implicate horizontal transmission as the primary mode

of infection in drylands laucha populations and suggest that aggressive encounters among adult, male lauchas in relatively densely populated roadside and fence-line habitats are an important mechanism of transmission of JUNV within its reservoir population. The high rate of virus production in salivary glands of drylands lauchas, as well as virus isolation from saliva of infected reservoirs (Peralta et al., 1979; Sabattini et al., 1977), makes JUNV transmission following a bite highly likely. Furthermore, laboratory studies with drylands lauchas showed that the transmission of JUNV was generally horizontal, taking place between rodents in close contact with each other (Sabattini et al., 1977). There are some differences in the maintenance mechanism of JUNV and MACV. First, horizontal venereal transmission does not seem to be predominant in JUNV transmission, as it would not account for the greater prevalence of infection in male drylands lauchas. Second, while viral infection is hypothesized to be an important driving force in reservoir population dynamics in the MACV big laucha model, JUNV infection in drylands lauchas should have a much less severe effect. This is because in contrast to MACV-infected female mice, which abort (Webb et al., 1975), chronically JUNV-infected rodent females, when infected as adults, have a normal number of pups (Vitullo and Merani, 1990). Finally, all pups born to MACV viremic female mice in the laboratory are infected neonatally through the milk (Webb et al., 1975), whereas JUNV-infected female rodents transmit the virus to only half of their pups (Vitullo and Merani, 1990; Vitullo et al., 1987).

7.1.1.4 Guanarito Virus

Experimental work identified the nocturnal short-tailed zygodont (*Zygodontomys brevicauda*) as the reservoir of GTOV. Alston's cotton rats (*Sigmodon alstoni*) were indicated as a secondary host, and fulvous colilargos, Guaira spiny rats, and roof rats (*Oligoryzomys fulvescens*, *Proechimys guairae* and *R. rattus*, respectively) were found to be seropositive (Tesh et al., 1993). GTOV could be isolated from throat swabs, urine, spleens, lungs, or kidneys of infected animals, and antibodies were found in the sera (Milazzo et al., 2011). Short-tailed zygodonts are native to the plains of western Venezuela and can reach high densities in tall grassy (weedy) areas found in pastoral and agricultural areas along roadsides and fence lines and in the naturally occurring savannah that dominates the landscape of the "VHF" endemic region (Fulhorst et al., 1997; Fulhorst et al., 1999; Salazar-Bravo et al., 2002b; Tesh et al., 1993). The presence of GTOV-infected short-tailed zygodonts in Apure, Barinas, Cojedes, and Guárico indicates that GTOV was enzootic in Venezuela's Portuguesa State long before GTOV was discovered in 1989. As such, the emergence of "VHF" was likely a consequence of demographic and/or ecological changes in rural areas of Portuguesa State that eventually resulted in a significant increase in the frequency of contact between humans and GTOV-infected rodents (Fulhorst et al., 2008). However, during four years of rodent trapping in the region of "VHF," neither short-tailed zygodonts nor Alston's cotton rats were ever found within houses or farm buildings (de Manzione et al., 1998). Presumably, human infection therefore occurs outdoors. Thus, one might expect persons having frequent contact with rodent-infested grassland habitats to be at higher risk of contracting "VHF." The laboratory infection of short-tailed zygodonts with GTOV produces chronic viremia characterized by persistent shedding of infectious virus in oral and respiratory secretions and urine without clinical signs of disease through day 208 post-inoculation (Fulhorst et al., 1999). The analyses of field and laboratory data suggest that horizontal transmission is the dominant mode of GTOV transmission in short-tailed zygodonts, as most GTOV infections in these mice are acquired in an age-dependent manner. Therefore, the chronic carrier state in short-tailed zygodonts most likely results from exposure to infectious virus later in life through aggressive or venereal behavior such as allogrooming, mating, intraspecies aggression, and other activities that entail close physical contact. Evidence also suggests that male and female mice contribute equally to GTOV transmission (Milazzo et al., 2011).

7.1.1.5 Conclusion

LF, BHF, AHF, and "VHF" are all examples of natural nidality; zoonoses within the host reservoir occur focally and have an incomplete pattern of overlap with the host species range. Natal mastomys,

big lauchas, drylands lauchas, and short-tailed zygodonts, the hosts of LASV, MACV, JUNV, and GTOV, respectively, are found in larger distribution areas than the endemic areas of BHF, AHF, and “VHF” (Demby et al., 2001; Fulhorst et al., 1997; Mills et al., 1992; Weaver et al., 2000). At least in the case of BHF, it has been demonstrated that the population of big lauchas responsible for the maintenance and transmission of MACV represent an independent monophyletic lineage, different from that in other areas of South America (Salazar-Bravo et al., 2002a), which could explain the phenomenon of natural nidality for BHF. Interestingly, although drylands lauchas are found in most of central and northwestern Argentina, a gradient of infection in these rodents has been described in JUNV surveys across the boundaries of AHF endemic–epidemic regions. The prevalence of JUNV infection in drylands lauchas is highest in endemic regions and is reported to be nonexistent or low outside the endemic zone. Nonetheless, JUNV has been isolated from rodents in areas where human cases have not been reported (deVillafañe et al., 1977; Garcia et al., 1996; Mills et al., 1991). Similarly, some GTOV variants were isolated from locations outside of the endemic–epidemic regions (outlying locations in Cojedes, Barinas, and Apure States of Venezuela) and yet were found to belong to genotypes that included variants isolated from human cases of “VHF” from areas surrounding Guanarito. This suggests that pathogenic GTOV variants occur in these outlying areas, but do not frequently infect people and/or cause inapparent disease there. Furthermore, “VHF” does not appear to be associated with a specific GTOV genotype that is restricted to a particular rodent host (Weaver et al., 2000). Most of the rodents associated with arenaviruses, such as those assigned to the genera *Mus*, *Mastomys*, and *Calomys*, are found in grassland/brush habitats and frequently come in contact with human dwellings and therefore humans. Contact opportunities are increased when rodents infest field crops or invade storage areas for grains. The association of rodents with agricultural practices often results in cyclic reproductive patterns linked to the harvesting of crops, and the invasion of barns and other storage areas increases when rodent food opportunities decrease.

7.1.2 HANTAVIRUSES

Hantaviruses represent a diverse group of viruses within a separate genus (*Hantavirus*) of the family *Bunyaviridae*, each carried by a specific rodent, bat or eulipotyphlan host (Heyman et al., 2011; Klempa et al., 2003; Okumura et al., 2007; Pensiero et al., 1992; Vapalahti et al., 1996). Rodent-borne hantaviruses are associated with two disease syndromes with varying degrees of severity: hemorrhagic fever with renal syndrome (HFRS) or hantavirus pulmonary syndrome (HPS). Of the two syndromes, only HFRS is considered a viral hemorrhagic fever and will be discussed here. Human infections with HFRS-causing hantaviruses are exclusively zoonotic, with transmission occurring through contact with or inhalation of excreted or secreted virus from rodents. Vascular leakage, acute thrombocytopenia, and kidney dysfunction are associated with HFRS (Lee et al., 1999; Zaki and Nolte, 1999). Those viruses that cause HFRS in humans are listed in Table 7.1. Four hantaviruses cause the majority of cases of HFRS: Hantaan virus (HTNV), Seoul virus (SEOV), Dobrava–Belgrade virus (DOBV), and Puumala virus (PUUV). The most prevalent and lethal HFRS-associated hantavirus is HTNV (>100,000 cases/year, mostly in Asia) with a case-fatality rate of 10%–15%. The host reservoirs for HFRS-causing viruses are assigned to the muroid family Muridae, subfamily Murinae, and the muroid family Cricetidae, subfamily Arvicolinae (lemmings, voles, and muskrats). Assigned to the subfamily Murinae are the reservoir hosts for DOBV, HTNV, and SEOV. PUUV is the only HFRS-causing virus harbored by an arvicoline rodent. There are no vaccines or specific antiviral drugs licensed by the U.S. Food and Drug Administration to treat or prevent HFRS, but vaccines of varying quality and efficacy are available in countries other than the United States. For instance, inactivated virus vaccines against HFRS are licensed for use in China and South Korea, which may account for the reduced incidence of HFRS in these countries in the past 10 years.

TABLE 7.1
Hantaviruses Causing HFRS

| Virus (Abbreviation) | Case-Fatality Rate (%) | Rodent (Species) | Geographic Location |
|---|-------------------------------|--|--|
| Puumala virus (PUUV) | 0.1–0.4 | Bank vole (<i>Myodes glareolus</i>) | Eurasia |
| Dobrava–Belgrade virus (DOBV) genotype Sochi | >6 | Caucasus field mouse (<i>Apodemus ponticus</i>) | Russia |
| Dobrava–Belgrade virus (DOBV) genotype Dobrava | 10–12 | Yellow-necked field mouse (<i>Apodemus flavicollis</i>) | Slovenia, Croatia, Serbia, Montenegro, Hungary, Slovakia, Bulgaria, Greece |
| Dobrava–Belgrade virus (DOBV) genotype Saaremaa | ? | Striped field mouse (<i>Apodemus agrarius</i>) | Estonia, Slovakia, Slovenia, Hungary, Denmark |
| Dobrava–Belgrade virus (DOBV) genotype Kurkino | 0.3–0.9 | Striped field mouse (<i>A. agrarius</i>) | Germany, Slovakia, Russia, Hungary, Slovenia, Croatia, Denmark, mainland Estonia |
| Tula virus (TULV) | Not known | Common vole (<i>Microtus arvalis</i>), field vole (<i>Microtus agrestis</i>), East European vole (<i>Microtus levis</i>) | Europe |
| Amur/Soochang virus (ASV) | ? | Korean field mouse (<i>Apodemus peninsulae</i>) | Far Eastern Russia |
| Hantaan virus (HTNV) | ≥10 | Striped field mouse (<i>A. agrarius</i>) | Asia, Eastern Russia |
| Seoul virus (SEOV) | <1 | Brown rat (<i>Rattus norvegicus</i>), roof rat (<i>R. rattus</i>) | Worldwide |

7.1.2.1 Brief History of Hemorrhagic Fever with Renal Syndrome

Although described in the Soviet and Japanese literature since the late 1930s, the western world became aware of HFRS for the first time during an outbreak of what was then referred to as Korean hemorrhagic fever (KHF) that began in 1951 during the United States–Korean War. KHF had affected nearly 3000 United Nations troops by 1954 and exhibited a case-fatality rate of 7% (Johnson, 2001). Despite extensive investigations and reports on this outbreak, the etiologic agent was not identified at that time. Indeed, the mystery agent for KHF remained elusive until HTNV, named for the river that runs near the border of today's North and South Korea, was isolated in 1978 by Lee Ho-wang and colleagues (Lee et al., 1978). Shortly following the discovery of HTNV, other hantaviruses were identified in Eurasia (Brummer-Korvenkontio et al., 1980; Brummer-Korvenkontio et al., 1982; Gresikova et al., 1984).

7.1.2.2 Epidemiology

In general, the infection of the natural hantavirus reservoir hosts results in a chronic carrier state without pronounced pathology or signs of disease. However, in-depth histological studies identified lesions within the lungs of North American deer mice (*Peromyscus maniculatus*) infected with HPS-causing Sin Nombre virus (SNV) and white-footed deer mice (*Peromyscus leucopus*) infected with HPS-causing New York virus (NYV) (Lyubsky et al., 1996; Netski et al., 1999). There is also a report that PUUV-infected animals are less likely to survive winter, suggesting infection has a negative effect on host fitness (Kallio et al., 2007). Disease in humans occurs when persons are exposed to contaminated rodent feces, urine, or saliva. The most common mode of transmission is thought to be the inhalation of aerosolized rodent droppings; however, contact with open wounds, rodent bites, and ingestion of contaminated material are also possible modes of transmission. The ingestion of virus as a mode of infection is not well documented; however, laboratory hamsters can be readily infected through the gut (gavage needle) with the HPS-associated Andes virus (ANDV), supporting

the possibility that hantaviruses could be transmitted by the ingestion of contaminated food or the consumption of rodents (Hooper et al., 2008). In humans, hantaviruses cause disease in the young and old, male and female. In most studies, HFRS occurred predominantly in working-age males. The preponderance of the disease in this population is likely related to occupational exposure. The epidemiologic studies of HFRS report increased incidence of hantavirus disease in persons working or sleeping in environments inhabited by rodents, which include agricultural workers, forest workers, and soldiers (Abu Sin et al., 2007; Mulic and Ropac, 2002; Sinclair et al., 2007; Vapalahti et al., 2003). In many regions, hantavirus disease has a seasonal peak. For example, most of the cases in the 2005 outbreaks in Europe occurred in June and July (Heyman et al., 2007). The geographic range of HFRS is shown in Figure 7.1 and compared to the geographic range of the rodent hosts for HFRS-causing hantaviruses. Although disease has not been detected in all of these regions, the presence of the rodent reservoirs indicates that the potential for hantavirus disease exists. HFRS has been documented in China, the Korean peninsula, Russia, Northern Europe/Scandinavia, and Southern Europe/Balkans. Approximately 40 countries have reported hantavirus disease, the presence of virus, or the serological evidence of infection, whereas several other countries have reported rare and sporadic HFRS in port cities that can probably be attributed to SEOV infections spread by rats carried port to port on ships.

7.1.2.3 China, Korea, and Far Eastern Russia

HFRS is a significant public health concern in China and has been a notifiable disease there since 1950. During the period of 1950–2007, a total of 1,557,622 cases of HFRS in humans and 46,427 deaths (3%) were reported in China (Fang et al., 2006; Kariwa et al., 2007; Yan et al., 2007; Zhang et al., 2010). Most of the severe cases that occur in rural areas are caused by HTNV, whereas SEOV is the major cause of a less severe form of HFRS carried by anthropophilic urban species of rodents. Although HFRS cases have been found in 29 Chinese provinces, the disease remains most prevalent in Shāndōng, Hēilóngjiāng, Jílín, Liáoníng, Héběi, Jiāngsū, Zhèjiāng, Ānhuī, Hénán, Jiāngxī, Húběi, Húnán, Shǎnxī, Sichuān, and Guìzhōu provinces (Zhang et al., 2010).

South Korea reported 3039 cases of HFRS between 1997 and 2006 (DisWeb, 2003). During that time, there has been a trend of increasing numbers of cases with more than 400 cases per year for the last 3 years. Based on its geographic location, it is very likely that North Korea has a significant number of HFRS cases; however, as is the case for many countries, the number of HFRS cases is not readily available. One review from 1996 reported 316 HFRS cases in North Korea since 1961 (Lee, 1996).

In Far Eastern Russia, there were 4442 cases of HFRS between 1978 and 1997 (Tkachenko et al., 1998). ASV, HTNV, and SEOV are causative agents of HFRS in Far Eastern Russia. Several other countries in the area, including Australia, Fiji, Hong Kong, India, Indonesia, Japan, Malaysia, Mongolia, Myanmar, Singapore, Sri Lanka, Taiwan, Thailand, and Vietnam, have reported rare or sporadic cases of HFRS or sero-epidemiological evidence that hantaviruses exist and can cause infections (reviewed in Kariwa et al., 2007). The major viruses that cause HFRS in the Far East are HTNV and SEOV.

7.1.2.4 Western Russia and Eastern Europe

HFRS has been a reportable disease in Russia since 1978. In a review of HFRS in Russia, E. Tkachenko reports that between 1978 and 1997, there were 109,082 cases in western Russia (Tkachenko et al., 1998). Specific regions of Russia have reported relatively large outbreaks. The Bashkiria region in particular has regularly reported high numbers of cases, including epidemics in 1993 and 1997, where the numbers of cases approached 150 and 287 cases/1,000,000 population, respectively (Niklasson et al., 1993; Tkachenko et al., 1998). In 2007, there were outbreaks of greater than 3000 cases in the vicinity of Voronezh and Lipetsk (Dybas, 2007). As in China and Korea, most of the HFRS cases in Russia occur in rural areas; however, there can be epidemics in urban areas, as was the situation in the 1997 Bashkiria outbreak (Tkachenko et al., 1998). In western Russia, most of the HFRS is caused by PUUV, carried by bank voles (*Myodes glareolus*). Case-fatality rates indicate

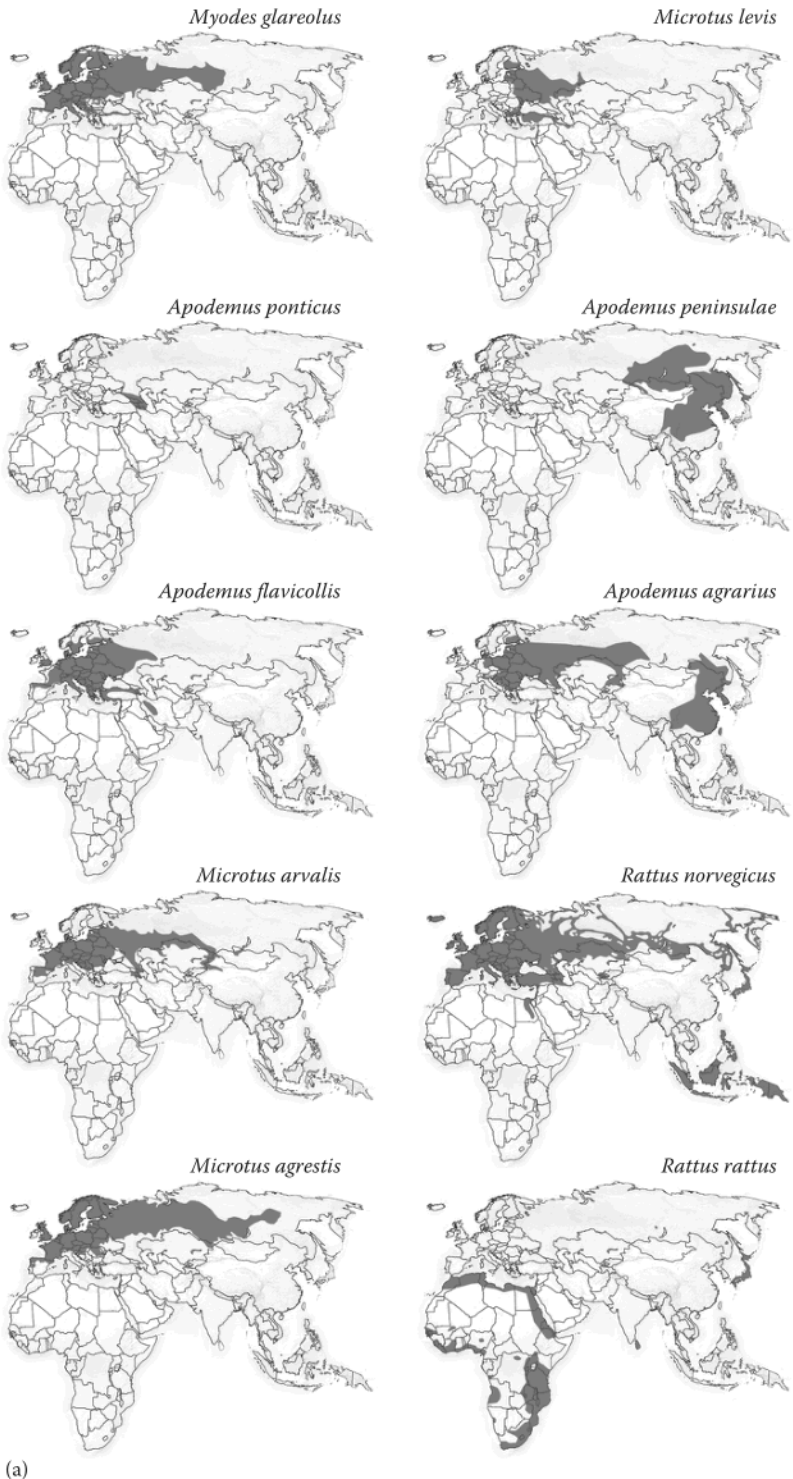
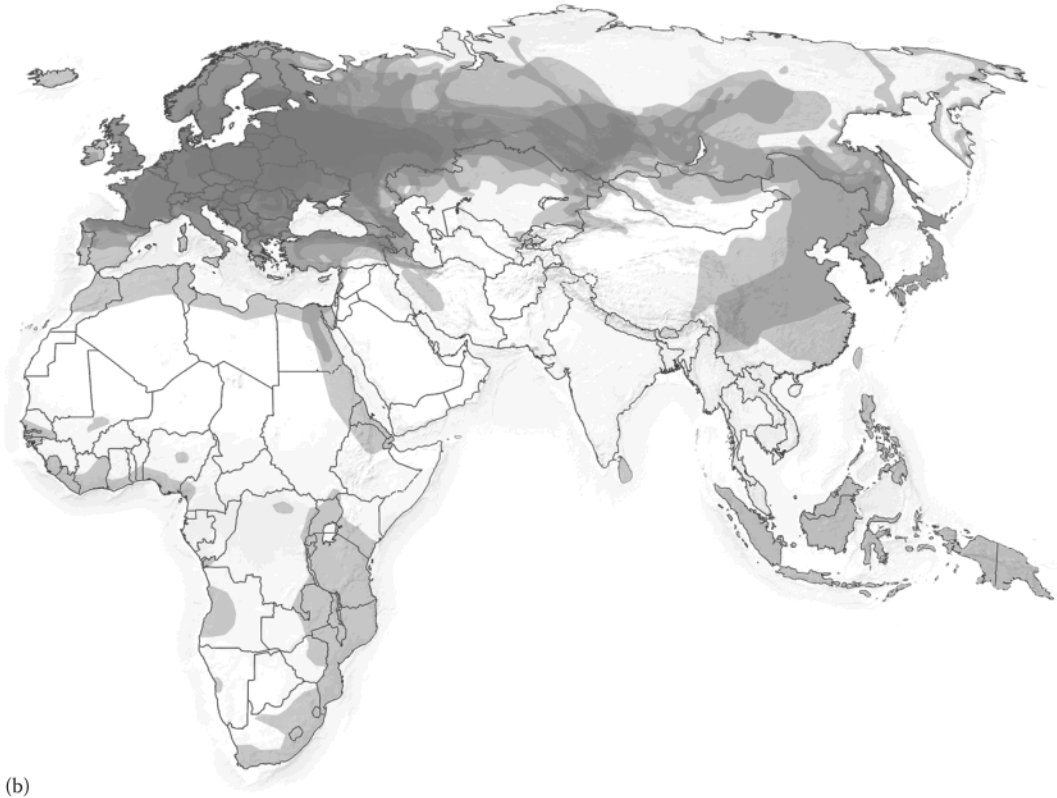


FIGURE 7.1 Distribution of rodents that are associated with HFRS is shown in individual (a) as well as a single composite map (b). All data used to generate maps were obtained from IUCN 2012. (From IUCN, The IUCN red list of threatened species, version 2012.1, 2012, <http://www.iucnredlist.org>.)

(continued)



(b)
FIGURE 7.1 (continued) Distribution of rodents that are associated with HFRS is shown in individual (a) as well as a single composite map (b). All data used to generate maps were obtained from IUCN 2012. (From IUCN, The IUCN red list of threatened species, version 2012.1, 2012, <http://www.iucnredlist.org>.)

that strains of PUUV in Russia, such as strain K27 isolated from a fatal human case, cause a more severe form of disease (0.4% case fatality) than the strains of PUUV found in Finland and Sweden (0.1% case fatality) (Tkachenko et al., 1998). Several other countries in Eastern Europe, including Belarus, Estonia, Georgia, Latvia, Lithuania, Poland, Romania, and Ukraine, have reported rare or sporadic cases of HFRS or serologic evidence that pathogenic hantaviruses are endemic (reviewed in Avsic-Zupanc, 1998; Tkachenko et al., 1999; Vapalahti et al., 2003).

7.1.2.5 Northern and Central Europe/Scandinavia

A review published in 2003 indicated that 12 countries in Europe reported five or more cases of HFRS per year (Vapalahti et al., 2003). Other countries in Europe with rare or sporadic cases of HFRS or seroepidemiologic evidence of infection include Austria, Czech Republic, Great Britain, Portugal, and Switzerland (Lee, 1996; Vapalahti et al., 2003). It is likely that HFRS in Europe is underdiagnosed because the disease is relatively mild as compared to HFRS in Asia. A study in Belgium reported that the seroprevalence was at 3.8%, well above the number of diagnosed cases (van der Groen et al., 1983). Finland and Sweden have the most cases (1000 or more/year, respectively) followed by Germany, France, and Belgium each with ≈ 100 cases/year. These national numbers mask the health problem HFRS causes in specific geographic regions. For example, the number of cases in northern Sweden is much higher than in the south. Most of the cases are in Vasterbotten County where the incidence is normally ≈ 23.5 cases/100,000 (Settergren et al., 1988). In Finland, the number of cases in the province of Mikkeli was 70 cases/100,000, mostly in farmers (Vapalahti et al., 1999). PUUV and DOBV are believed to cause most of the cases of HFRS in Northern Europe and Scandinavia.

Recently, HFRS has become more of a health concern in Europe. In 2005, there was a relatively large series of outbreaks in Belgium, France, the Netherlands, Luxembourg, and Germany (1114 cases), caused by PUUV (Heyman et al., 2007). In Germany, many of the cases occurred in relatively large cities, including Osnaburg and Cologne, where the annual incidence was 8.5 and 4.2 cases/100,000, respectively (AbuSin et al., 2007). In 2007, Sweden experienced an almost 10-fold increase in the annual number of HFRS cases (Pettersson et al., 2008). Vasterbotten County accounted for 800 of the 2200 cases, with two fatalities. In Europe and elsewhere, there is a suspected link between climate change, food-source production, reservoir population, and incidence of human disease. Climate conditions that result in increased production of food source (e.g., mast years resulting in high yields of oak and beechnuts) can, in turn, result in an increase in reservoir population and an increase in the incidence of human disease (Heyman et al., 2007; Vapalahti et al., 2003). Although HFRS in Europe has not resulted in high numbers of fatalities, this disease does have a substantial impact on the health-care system because many patients are hospitalized and some require hemodialysis.

7.1.2.6 Southern Europe/Balkans

There are approximately 100 HFRS cases per year reported in the Balkans (Avsic-Zupanc, 1998), including Albania, Bosnia, Bulgaria, Croatia, Greece, Macedonia, Montenegro, Serbia, and Slovenia. The military conflicts in the area of former Yugoslavia resulted in increased numbers of HFRS cases, as would be expected based on the increased numbers of military personnel and displaced civilians serving, working, and sleeping outdoors (Avsic-Zupanc, 1998). Severe cases of HFRS in the Balkans are usually caused by DOBV (Avsic-Zupanc et al., 1992). PUUV is also circulating in this region and has been associated with disease (Lundkvist et al., 1997).

7.1.2.7 Prospects for the Future

As climatic changes affect the environment, we can expect to see changes in rodent populations and distributions. It is likely that these changes will alter the ways in which humans come in contact with hantaviruses and these changes could result in changes in the rates and distribution of HFRS cases. Moreover, changes in interactions between rodents of different species could, theoretically, increase the possibility that different hantaviruses might coinfect the same rodent host and produce reassortant progeny viruses. There is an evidence that hantaviruses have reassorted in nature (Henderson et al., 1995; Li et al., 1995). Reassortant viruses could exhibit altered biological properties including virulence, as is the case for influenza viruses (genetic shift). Thus, the threat posed by naturally occurring hantavirus disease is dynamic and must be carefully monitored.

7.2 BATS

The mammalian order Chiroptera includes over 1000 established bat species (Nowak and Walker, 1994; Wilson and Reeder, 2005). One arenavirus (Downs et al., 1963) and several hantaviruses (Jung and Kim, 1995; Sumibcay et al., 2012; Weiss et al., 2012) are associated with bats in nature, but none of these agents have been identified as human pathogens. Filoviruses (order *Mononegavirales*, family *Filoviridae*) are the only VHF-causing pathogens for which a bat association has been plausibly documented.

7.2.1 FILOVIRUSES

Filoviruses are the etiological agents of geographically isolated severe VHFs among human and other ape populations (Kuhn, 2008). The most current filovirus classification distinguishes three separate genera based on molecular and genomic properties. Two viruses, Marburg virus (MARV) and Ravn virus (RAVV), are assigned to the genus *Marburg virus*; five viruses, Bundibugyo virus (BDBV), Ebola virus (EBOV), Reston virus (RESTV), Sudan virus (SUDV), and Tai Forest virus (TAFV), belong to the genus *Ebolavirus*. Finally, Lloviu virus (LLOV) is the sole member of the

genus *Cuevavirus* (Adams and Carstens, 2012; Kuhn et al., 2010, 2011). With the exception of RESTV and LLOV, all filoviruses have been identified as the causes of human VHF.

Natural disease outbreaks among humans and animals indicate that filoviruses are endemic in equatorial Africa (MARV, RAVV, BDBV, EBOV, SUDV, TAFV), the Philippines (RESTV), and southern Europe (LLOV) (Kuhn, 2008; Negrodo et al., 2011). Numerous surveys of collected human and animal sera suggest that filoviruses are also endemic in regions from where disease outbreaks have not yet been reported, but the results of many of these studies are considered controversial (Kuhn, 2008). However, ecological niche studies support the idea that the natural filovirus distribution is broader than the areas of recorded disease outbreaks (Peterson et al., 2004, 2006). Interestingly, these studies also imply that marburgviruses and ebolaviruses circulate in different ecological zones. Marburgviruses have thus far only been detected in arid woodlands, whereas ebolaviruses seem to be endemic in humid rain forests. Furthermore, marburgvirus disease outbreaks were often associated with people visiting or working in caves, whereas such a connection has not been made in the case of ebolavirus disease outbreaks (Peterson et al., 2004, 2006).

The limited number and temporal separation of filovirus disease outbreaks and the rapidly fatal disease these viruses cause in primates (Kuhn, 2008) indicate that they are maintained in nature in organisms other than primates over long periods of time. Since all other viruses known to cause VHF in humans are known to be arthropod-borne (arboviruses) or rodent-borne, it was quickly hypothesized that this would be the case for filoviruses as well. However, the natural filovirus reservoirs proved elusive despite numerous animal sampling studies (Kuhn, 2008).

In 1996, Swanepoel et al. reported a study during which several types of plants and animals were inoculated with EBOV to evaluate whether they could support virus replication and therefore aid in the identification of the filovirus reservoir hosts. Surprisingly, sustained EBOV replication was detected in the absence of clinical signs in individual wild-caught little free-tailed bats (*Chaerephon pumilus*), Angolan free-tailed bats (*Mops condylurus*), and Wahlberg's epauletted fruit bats (*Epomophorus wahlbergi*) after subcutaneous infection of $10^{4.6}$ ffu EBOV. EBOV antigen could be detected in lung endothelial cells of one insectivorous bat. More importantly, EBOV could be recovered from the feces of a Wahlberg's epauletted fruit bat on day 21 post-infection, and viral titers of $10^{4.6}$ – $10^{7.0}$ ffu/ml and $10^{2.0}$ – $10^{6.5}$ ffu/ml were detected in the sera and pooled viscera of several of these bats, respectively. EBOV isolation was successful up to day 12 (Angolan free-tailed bats), day 14 (little free-tailed bats), and day 21 post-infection (Wahlberg's epauletted fruit bats), and the study was terminated soon thereafter (Swanepoel et al., 1996). Bats had been collected before these experiments in areas affected by ebolavirus disease outbreaks, but filoviruses were never isolated or otherwise detected (Table 7.2). However, as this was the first study that experimentally proved that sustained replication of filoviruses is possible in animals in the absence of clinical signs, bats became the prime suspects for harboring filoviruses in nature.

Approximately 20% of all mammalian species have bats as their members (Teeling et al., 2005). Traditionally, bats (order Chiroptera) have been divided into two major clades, the megabats (suborder Megachiroptera) and the microbats (suborder Microchiroptera). Megabats, often also referred to as fruit bats or flying foxes, are typically frugivorous or nectarivorous, often quite large, and do not use echolocation, whereas microbats are typically insectivorous, generally smaller, and use echolocation for orientation (Simmons, 2005). This division and the monophyly of individual suprageneric taxa are, however, currently hotly debated (Agnarsson et al., 2011; Simmons, 2005). Bats have long been known to carry viruses, including important human pathogens, such as rabies virus (Calisher et al., 2006, 2008; Laminger and Prinz, 2010; Messenger et al., 2003; Wang et al., 2011; Wong et al., 2007). However, they had not been associated with the transmission of VHF.

A study performed around Kikwit in Zaire (today Democratic Republic of the Congo), which in 1995 was the epicenter of one of the largest human ebolavirus disease outbreaks thus far recorded (317 cases, 245 deaths), revealed the presence of bats belonging to at least 18 different species in that area alone (van Cakenberghe et al., 1999). This exemplifies the vast diversity of bats in general and implies that it will not be easy to pinpoint particular bats as filovirus hosts.

TABLE 7.2
Bats Screened for Filoviruses with Negative Results

| Bat Species (Vernacular Name) | Type of Bat | Sampling Location (Year) | Number Screened | Assay | Reference |
|---|---|---------------------------|-----------------|---|-----------------------|
| <i>Casinycteris argynnis</i> (golden short-palated fruit bat) | Frugivorous (megachiropteran pteropodid) | ~Kikwit, Zaire (1995) | 2 | Filovirus isolation, ELISA (EBOV) | Leirs et al. (1999) |
| <i>C. argynnis</i> (golden short-palated fruit bat) | Frugivorous (megachiropteran pteropodid) | Gabon and COG (2005–2006) | 2 | qRT-PCR (MARV), nested PCR (MARV), ELISA (MARV) | Towner et al. (2007) |
| <i>Chaerephon ansorgei</i> (Ansorge's free-tailed bat) | Insectivorous (microchiropteran molossid) | ~ Kikwit, Zaire (1995) | 121 | Filovirus isolation, ELISA (EBOV) | Leirs et al. (1999) |
| <i>Chaerephon major</i> (lapped-eared free-tailed bat) | Insectivorous (microchiropteran molossid) | ~ Tandala, Zaire (1976) | 26 | Filovirus isolation, IFA (EBOV) | Breman et al. (1999) |
| <i>Chaerephon pumilus</i> (little free-tailed bat) | Insectivorous (microchiropteran molossid) | ~ Kikwit, Zaire (1995) | 213 | Filovirus isolation, ELISA (EBOV) | Leirs et al. (1999) |
| <i>Chalinolobus</i> sp. (wattled bat) | Insectivorous (microchiropteran vespertilionid) | ~ Tandala, Zaire (1976) | 15 | Filovirus isolation, IFA (EBOV) | Breman et al. (1999) |
| <i>Coleura afra</i> (African sheath-tailed bat) | Insectivorous (microchiropteran emballonurid) | Gabon (2009–2010) | 31 | qRT-PCR (MARV), nested PCR (MARV) | Maganga et al. (2011) |
| <i>Eidolon helvum</i> (African straw-colored fruit bat) | Frugivorous (megachiropteran pteropodid) | ~ Tandala, Zaire (1976) | 6 | Filovirus isolation, IFA (EBOV) | Breman et al. (1999) |
| <i>E. helvum</i> (African straw-colored fruit bat) | Frugivorous (megachiropteran pteropodid) | Gabon and COG (2005–2006) | 35 | qRT-PCR (MARV), nested PCR (MARV), ELISA (MARV) | Towner et al. (2007) |
| <i>E. franqueti</i> (Franquet's epauletted fruit bat) | Frugivorous (megachiropteran pteropodid) | ~ Tandala, Zaire (1976) | 21 | Filovirus isolation, IFA (EBOV) | Breman et al. (1999) |
| <i>E. franqueti</i> (Franquet's epauletted fruit bat) | Frugivorous (megachiropteran pteropodid) | ~ Kikwit, Zaire (1995) | 2 | Filovirus isolation, ELISA (EBOV) | Leirs et al. (1999) |
| <i>E. franqueti</i> (Franquet's epauletted fruit bat) | Frugivorous (megachiropteran pteropodid) | Gabon and COG (2005–2006) | 296 | qRT-PCR (MARV), nested PCR (MARV), ELISA (MARV) | Towner et al. (2007) |
| <i>Eptesicus</i> sp. (house bat) | Insectivorous (microchiropteran vespertilionid) | ~ Tandala, Zaire (1976) | 22 | Filovirus isolation, IFA (EBOV) | Breman et al. (1999) |
| <i>Hipposideros caffer</i> (Sundevall's leaf-nosed bat) | Insectivorous (microchiropteran hipposiderid) | Gabon (2009–2010) | 521 | qRT-PCR (MARV), nested PCR (MARV) | Maganga et al. (2011) |

(continued)

TABLE 7.2 (continued)
Bats Screened for Filoviruses with Negative Results

| Bat Species (Vernacular Name) | Type of Bat | Sampling Location (Year) | Number Screened | Assay | Reference |
|---|---|---------------------------|-----------------|---|-----------------------|
| <i>Hipposideros cyclops</i> (cyclops leaf-nosed bat) | Insectivorous (microchiropteran hipposiderid) | ~ Tandala, Zaire (1976) | 52 | Filovirus isolation, IFA (EBOV) | Breman et al. (1999) |
| <i>H. gigas</i> (giant leaf-nosed bat) | Frugivorous (megachiropteran pteropodid) | Gabon and COG (2005–2006) | 1 | qRT-PCR (MARV), nested PCR (MARV), ELISA (MARV) | Towner et al. (2007) |
| <i>H. gigas</i> (giant leaf-nosed bat) | Frugivorous (megachiropteran pteropodid) | Gabon (2009–2010) | 233 | qRT-PCR (MARV), nested PCR (MARV) | Maganga et al. (2011) |
| <i>H. ruber</i> (Noack's leaf-nosed bat) | Insectivorous (microchiropteran hipposiderid) | ~ Tandala, Zaire (1976) | 17 | Filovirus isolation, IFA (EBOV) | Breman et al. (1999) |
| <i>Hypsignathus</i> (hammer-headed fruit bat) | Frugivorous (megachiropteran pteropodid) | ~ Yambuku, Zaire (1976) | 1 | Filovirus isolation | Germain (1978) |
| <i>H. monstrosus</i> (hammer-headed fruit bat) | Frugivorous (megachiropteran pteropodid) | Gabon and COG (2005–2006) | 56 | qRT-PCR (MARV), nested PCR (MARV), ELISA (MARV) | Towner et al. (2007) |
| <i>Megaloglossus woermanni</i> (Woermann's long-tongued fruit bat) | Frugivorous (megachiropteran pteropodid) | ~ Kikwit, Zaire (1995) | 43 | Filovirus isolation, ELISA (EBOV) | Leirs et al. (1999) |
| <i>M. woermanni</i> (Woermann's long-tongued fruit bat) | Frugivorous (megachiropteran pteropodid) | Gabon and COG (2005–2006) | 37 | qRT-PCR (MARV), nested PCR (MARV), ELISA (MARV) | Towner et al. (2007) |
| <i>Micropteropus pusillus</i> (Peters's lesser epauletted fruit bat) | Frugivorous (megachiropteran pteropodid) | ~ Kikwit, Zaire (1995) | 78 | Filovirus isolation, ELISA (EBOV) | Leirs et al. (1999) |
| <i>M. pusillus</i> (Peters's lesser epauletted fruit bat) | Frugivorous (megachiropteran pteropodid) | Gabon and COG (2005–2006) | 149 | qRT-PCR (MARV), nested PCR (MARV), ELISA (MARV) | Towner et al. (2007) |
| <i>Miniopterus inflatus</i> (greater long-fingered bat) | Insectivorous (microchiropteran vespertilionid) | Gabon (2009–2010) | 186 | qRT-PCR (MARV), nested PCR (MARV) | Maganga et al. (2011) |
| <i>Miniopterus minor</i> (least long-fingered bat) | Insectivorous (microchiropteran vespertilionid) | ~ Kikwit, Zaire (1995) | 2 | Filovirus isolation, ELISA (EBOV) | Leirs et al. (1999) |
| <i>M. condylurus</i> (Angolan free-tailed bat) | Insectivorous (microchiropteran molossid) | ~ Tandala, Zaire (1976) | 54 | Filovirus isolation, IFA (EBOV) | Breman et al. (1999) |
| <i>M. condylurus</i> (Angolan free-tailed bat) | Insectivorous (microchiropteran molossid) | ~ Kikwit, Zaire (1995) | 10 | Filovirus isolation, ELISA (EBOV) | Leirs et al. (1999) |

| | | | | | |
|--|---|---------------------------|-----|---|-----------------------|
| <i>Mops congicus</i> (Congo free-tailed bat) | Insectivorous (microchiropteran molossid) | ~ Tandala, Zaire (1976) | 20 | Filovirus isolation, IFA (EBOV) | Breman et al. (1999) |
| <i>Mops niveiventer</i> (white-bellied free-tailed bat) | Insectivorous (microchiropteran molossid) | ~ Kikwit, Zaire (1995) | 3 | Filovirus isolation, ELISA (EBOV) | Leirs et al. (1999) |
| <i>Mops (Xiphonycteris) nanulus</i> (dwarf free-tailed bat) | Insectivorous (microchiropteran molossid) | ~ Tandala, Zaire (1976) | 15 | Filovirus isolation, IFA (EBOV) | Breman et al. (1999) |
| <i>M. (Xiphonycteris) nanulus</i> (dwarf free-tailed bat) | Insectivorous (microchiropteran molossid) | ~ Kikwit, Zaire (1995) | 14 | Filovirus isolation, ELISA (EBOV) | Leirs et al. (1999) |
| <i>Mops (Xiphonycteris) thersites</i> (railer free-tailed bat) | Insectivorous (microchiropteran molossid) | ~ Tandala, Zaire (1976) | 69 | Filovirus isolation, IFA (EBOV) | Breman et al. (1999) |
| <i>Mops (Xiphonycteris) thersites</i> (railer free-tailed bat) | Insectivorous (microchiropteran molossid) | ~ Kikwit, Zaire (1995) | 1 | Filovirus isolation, ELISA (EBOV) | Leirs et al. (1999) |
| <i>M. torquata</i> (little collared fruit bat) | Frugivorous (megachiropteran pteropodid) | Gabon and COG (2005–2006) | 264 | qRT-PCR (MARV), nested PCR (MARV), ELISA (MARV) | Towner et al. (2007) |
| <i>Myopterus whiteleyi</i> (bini winged-mouse bat) | Insectivorous (microchiropteran molossid) | ~ Kikwit, Zaire (1995) | 2 | Filovirus isolation, ELISA (EBOV) | Leirs et al. (1999) |
| <i>Myotis bocagii</i> (rufous myotis) | Insectivorous (microchiropteran vespertilionid) | ~ Tandala, Zaire (1976) | 17 | Filovirus isolation, IFA (EBOV) | Breman et al. (1999) |
| <i>M. bocagii</i> (rufous myotis) | Insectivorous (microchiropteran vespertilionid) | ~ Kikwit, Zaire (1995) | 22 | Filovirus isolation, ELISA (EBOV) | Leirs et al. (1999) |
| <i>Neoromicia nanus</i> (banana pipistrelle) | Insectivorous (microchiropteran vespertilionid) | ~ Tandala, Zaire (1976) | 73 | Filovirus isolation, IFA (EBOV) | Breman et al. (1999) |
| <i>N. nanus</i> (banana pipistrelle) | Insectivorous (microchiropteran vespertilionid) | ~ Kikwit, Zaire (1995) | 2 | Filovirus isolation, ELISA (EBOV) | Leirs et al. (1999) |
| <i>Neoromicia somalicus</i> (Somali serotine) | Insectivorous (microchiropteran vespertilionid) | ~ Kikwit, Zaire (1995) | 1 | Filovirus isolation, ELISA (EBOV) | Leirs et al. (1999) |
| <i>Neoromicia tenuipinnis</i> (white-winged serotine) | Insectivorous (microchiropteran vespertilionid) | ~ Kikwit, Zaire (1995) | 1 | Filovirus isolation, ELISA (EBOV) | Leirs et al. (1999) |
| <i>Nycteris hispida</i> (hairy slit-faced bat) | Insectivorous (microchiropteran nycterid) | ~ Kikwit, Zaire (1995) | 2 | Filovirus isolation, ELISA (EBOV) | Leirs et al. (1999) |
| <i>Nycteris</i> sp. (slit-faced bat) | Insectivorous (microchiropteran nycterid) | ~ Tandala, Zaire (1976) | 14 | Filovirus isolation, IFA (EBOV) | Breman et al. (1999) |
| <i>Rhinolophus</i> sp. (horseshoe bat) | Insectivorous (microchiropteran rhinolophid) | Gabon (2009–2010) | 17 | qRT-PCR (MARV), nested PCR (MARV) | Maganga et al. (2011) |

(continued)

TABLE 7.2 (continued)
Bats Screened for Filoviruses with Negative Results

| Bat Species (Vernacular Name) | Type of Bat | Sampling Location (Year) | Number Screened | Assay | Reference |
|--|---|---------------------------|-----------------|---|----------------------|
| <i>Saccolaimus peli</i> (Pel's pouched bat) | Insectivorous (microchiropteran emballonurid) | ~ Tandala, Zaire (1976) | 9 | Filovirus isolation, IFA (EBOV) | Breman et al. (1999) |
| <i>Scotophilus dinganii</i> (yellow-bellied house bat) | Insectivorous (microchiropteran vespertilionid) | ~ Kikwit, Zaire (1995) | 20 | Filovirus isolation, ELISA (EBOV) | Leirs et al. (1999) |
| <i>Scotophilus</i> sp. (yellow bat) | Insectivorous (microchiropteran vespertilionid) | ~ Tandala, Zaire (1976) | 10 | Filovirus isolation, IFA (EBOV) | Breman et al. (1999) |
| <i>Chaerephon chapini</i> (pale free-tailed bat) | Insectivorous (microchiropteran molossid) | ~ Tandala, Zaire (1976) | Total of 23 | Filovirus isolation, IFA (EBOV) | Breman et al. (1999) |
| <i>Hipposideros commersoni</i> (Commerson's leaf-nosed bat) | Insectivorous (microchiropteran hipposiderid) | | | | |
| <i>Hipposideros</i> sp. (leaf-nosed bat) | Insectivorous (microchiropteran hipposiderid) | | | | |
| <i>H. monstrosus</i> (hammer-headed fruit bat) | Frugivorous (megachiropteran pteropodid) | | | | |
| <i>Kerivoula lanosa</i> (lesser woolly bat) | Insectivorous (microchiropteran vespertilionid) | | | | |
| <i>M. woermanni</i> (Woermann's long-tongued fruit bat) | Frugivorous (megachiropteran pteropodid) | | | | |
| <i>Mops</i> sp. (free-tailed bat) | Insectivorous (microchiropteran molossid) | | | | |
| <i>M. torquata</i> (little collared fruit bat) | Frugivorous (megachiropteran pteropodid) | | | | |
| <i>Taphozous (Taphozous) mauritanus</i> (Mauritian tomb bat) | Insectivorous (microchiropteran emballonurid) | | | | |
| Unspecified microbats | Insectivorous | Gabon and COG (2005–2006) | 15 | qRT-PCR (MARV), nested PCR (MARV), ELISA (MARV) | Towner et al. (2007) |

COD, Republic of the Congo; bats for which a connection with filoviruses could be established in other studies are printed bold.

More and more scientific evidence accumulated in recent years supports the hypothesis that bats are indeed at least involved in the sustenance of filoviruses, if not being their reservoir hosts. The first set of data that revealed a direct link between bats and filoviruses was published in 2005 (Leroy et al., 2005). Specifically, the data indicated that at least three types of bats were in contact with EBOV during the 2002–2003 ebolavirus disease outbreaks in Gabon and Republic of the Congo, as anti-EBOV IgG antibodies could be detected by ELISA in sera of 8 of 117 collected Franquet's epauletted fruit bats (*Epomops franqueti*), 4 of 17 collected hammer-headed fruit bats (*Hypsignathus monstrosus*), and 4 of 58 collected little collared fruit bats (*Myonycteris torquata*). Intriguingly, Leroy et al. were also able to detect short fragments of what appeared to be filovirus polymerase (L) genes using nested RT-PCT in liver and spleen tissues from 5 of 117 Franquet's epauletted fruit bats, 4 of 21 hammer-headed fruit bats, and 4 of 141 little collared fruit bats. The team did, however, not succeed in isolating filoviruses from these animals (Leroy et al., 2005) despite the fact that filoviruses grow rapidly in most mammalian cell cultures (Kuhn, 2008). A follow-up study in the same area confirmed the serological results and established an overall 5% anti-EBOV IgG seroprevalence in bats belonging to all three species when they were collected during ebolavirus disease outbreaks among humans (2003–2005) (Pourrut et al., 2007). In 2007, Towner et al. published data that revealed the presence of anti-MARV IgG and MARV VP40, VP35, and NP gene-specific RNA sequences in 4 out of 283 Egyptian rousettes (*Rousettus aegyptiacus*) that were caught in Gabon and Republic of the Congo, but not in numerous bats of other species, including those suggested previously with EBOV endemicity (Table 7.2; Towner et al., 2007). Others detected MARV-specific genomic (VP35 and VP40 gene) fragments in 9 out of 1257 bats of the same species collected between 2009 and 2010 in Gabon (Maganga et al., 2011). These studies not only implicated a fourth type of bat in filovirus transmission but also suggested that MARV, which had not previously been known to cause disease outbreaks in these geographic locations, may be present in Gabon and Republic of Congo. A large serological survey arrived at the same results and extended the possible host spectrum of filoviruses even further. In 2009, Pourrut et al. reported anti-MARV IgG in Egyptian rousettes and hammer-headed fruit bats collected in these two countries and anti-EBOV IgG not only in Franquet's epauletted fruit bats, hammer-headed fruit bats, and little collared fruit bats but also in Egyptian rousettes, Angolan free-tailed bats, and Peters's lesser epauletted fruit bats (*Micropteropus pusillus*). Filovirus genomic fragments were not detected, and filoviruses were not isolated from samples (Pourrut et al., 2009). However, in 2009, Towner et al. reported the isolation of infectious MARV (two times) and RAVV (three times) from Egyptian rousettes caught in Kitaka Cave, Uganda, the place of a limited cluster of human MARV/RAVV infections in 2007 (Towner et al., 2009). In 2010, Kuzmin et al. reported the detection of MARV NP gene fragments in Egyptian rousettes collected around Kitum Cave in Kenya, where MARV and RAVV infections were reported in 1980 and 1987. Also in 2010, Hayman et al. reported anti-EBOV IgG in an African straw-colored fruit bat (*Eidolon helvum*) collected in Ghana (where filovirus disease outbreaks have not been reported) (Hayman et al., 2010). The same team later also reported the presence of anti-EBOV antibodies in three Franquet's epauletted fruit bats, four Gambian epauletted fruit bats (*Epomophorus gambianus*), and two hammer-headed fruit bats and anti-RESTV antibodies in two Gambian epauletted fruit bats and one hammer-headed fruit bat. A single Gambian epauletted fruit bat tested positive for antibodies against both EBOV and RESTV (Hayman et al., 2012). Other studies revealed the presence of anti-RESTV IgG in Geoffrey's rousettes (*Rousettus amplexicaudatus*) in the Philippines, where RESTV is known to be endemic (Taniguchi et al., 2011), and the detection of a previously entirely unknown filovirus, LLOV, in deceased Schreiber's long-fingered bats (*Miniopterus schreibersii*) in caves of Southern Europe (Negredo et al., 2011).

Together, the findings of all these studies raise many questions. MARV and RAVV disease outbreaks have almost always been associated with people visiting or working in caves or mines (Adjemian et al., 2011; Bausch et al., 2006; Centers for Disease Control and Prevention, 2009; Johnson et al., 1996; Peterson et al., 2006; Smith et al., 1982; Timen et al., 2009; Towner et al., 2009).

Egyptian rousettes are strictly cavernicolous, and MARV and RAVV isolation succeeded from individual bats captured in a cave that was implicated in human infections (Towner et al., 2009). Therefore, the hypothesis of Egyptian rousettes being marburgvirus hosts stands on relatively solid ground. On the other hand, ebolavirus disease outbreaks have never been associated with caves and usually occur in areas of tropical rainforest, rather than arid woodlands (Peterson et al., 2004, 2006). It is difficult to interpret the finding of anti-EBOV IgG, anti-MARV IgG, and genomic fragments in Egyptian rousettes in Gabon and Republic of the Congo, in particular, because marburgvirus disease outbreaks have never been reported from these countries. This could mean that marburgviruses are endemic in Gabon and Republic of the Congo, as some speculate (Maganga et al., 2011). But if this is the case, then it is surprising that human cases of MARV or RAVV infection have not been detected in these countries. It seems unlikely that they have been overlooked given that ebolavirus disease outbreaks are recorded in these countries on a regular basis—clinically, the diseases caused by marburgviruses and ebolaviruses cannot be differentiated upon presentation. It is of course possible that people in these countries do not get in contact with Egyptian rousettes.

Vice versa, if Egyptian rousettes are ebolavirus reservoirs based on the described IgG findings, one cannot help but wonder why there have not been any ebolavirus disease outbreaks in Uganda or Kenya, where marburgviruses are endemic. Egyptian rousettes are frugivorous animals that are widely distributed over Africa, the Middle East, and even Southwest Asia. Are EBOV, MARV, and RAVV endemic in these countries and just have never been reported (or never caused human infections)? One explanation could be that not all Egyptian rousettes carry filoviruses. For instance, Egyptian rousettes are currently assigned to six different *R. aegyptiacus* subspecies. Bats of the subspecies *aegyptiacus* are found in Egypt only; those of the subspecies *arabicus* are found exclusively in Iran, Pakistan, and southern Arabia, and those of the subspecies *tomensis* and *princeps* live in São Tomé and Príncipe. Only animals assigned to the subspecies *leachii* and *unicolor* are widely distributed across Africa (Benda et al., 2008). If filoviruses would be able to only infect animals of the latter two subspecies, then this would explain the absence of human filovirus infections outside of Africa. At the same time, if marburgviruses and ebolaviruses would preferentially infect animals of the one or the other subspecies, then this could possibly explain the different human case distributions. Subspecies specificity could also play a major role in the possible association of other filoviruses with bats. For instance, Geoffrey's rousettes, the presumed hosts of RESTV, are assigned to five different subspecies (Csorba et al., 2008). Maybe a species-specific association restricts RESTV to the Philippines. Or RESTV is endemic all over Southeast Asia—the range of Geoffrey's rousettes—and has just not been detected yet outside of the Philippines.

One must exert caution when speculating about an association of ebolaviruses and bats. It needs to be stressed that in contrast to marburgviruses, ebolaviruses have thus far not been isolated from any bat in the wild, and in three cases (BDBV, SUDV, TAFV), not even epidemiological links to bats have been uncovered. Instead, the hypothesis of bats being hosts of ebolaviruses is based on antibody detection in the case of two ebolaviruses (EBOV, RESTV), the detection of genomic RNA fragments in the case of one EBOV, and a speculated epidemiological link between an ebolavirus disease outbreak and the consumption of fruit bats in the Democratic Republic of the Congo (Grard et al., 2011; Leroy et al., 2009). Interestingly, anti-EBOV IgG was discovered in bats of various species, not only those of the species *R. aegyptiacus* (Table 7.3). This could mean that in contrast to what is known about the single host/single virus relationship found in the case of arenaviruses and hantaviruses, individual filoviruses may be able to colonize several hosts belonging to different genera at the same time. Likewise, bats belonging to one particular species could be reservoirs of filoviruses belonging to different species.

In the case of Franquet's epauletted fruit bats, hammer-headed fruit bats, and little collared fruit bats, only anti-EBOV IgG or EBOV genomic RNA fragments could be detected in individual animals, but never both together in the same individual animal (Leroy et al., 2005). The performers of the study hypothesized that IgG-positive animals were once infected but had cleared the infection, whereas RNA-positive animals had been infected recently, but had not then mounted an immune

TABLE 7.3
Evidence for an Association of Filoviruses with Bats

| Filovirus | Suspected Bat Host (Species) | Supporting Data for Bat Association | Bat Geographic Distribution | Known Filovirus Endemicity (Based on Disease Outbreaks and Virus Isolation/Full Genome Detection) |
|-----------|---|--|--|---|
| BDBV | N/A | N/A | N/A | Uganda |
| EBOV | African straw-colored fruit bat | Anti-EBOV IgG (Hayman et al., 2010) | Sub-Saharan Africa | Democratic Republic of the Congo, Gabon, Republic of the Congo |
| | Angolan free-tailed bat | Anti-EBOV IgG (Pourrut et al., 2009) | Sub-Saharan Africa | |
| | Egyptian rousette | Anti-EBOV IgG (Pourrut et al., 2009) | Africa Middle East Southwest Asia | |
| | Franquet’s epauletted fruit bat | Anti-EBOV IgG (Hayman et al., 2012; Leroy et al., 2005; Pourrut et al., 2007; Pourrut et al., 2009) RT-PCR positive for EBOV L gene fragment (Leroy et al., 2005) | Equatorial Africa | |
| | Gambian epauletted fruit bat | Anti-EBOV IgG (Hayman et al., 2012) | Angola, Benin, Cameroon, Côte d’Ivoire, | |
| | Hammer-headed fruit bat | Anti-EBOV IgG (Hayman et al., 2012; Leroy et al., 2005; Pourrut et al., 2007; Pourrut et al., 2009) RT-PCR positive for EBOV L gene fragment (Leroy et al., 2005; Pourrut et al., 2009) | Democratic Republic of the Congo, Gabon, Ghana, Guinea, Nigeria, Republic of the Congo | |
| | Little collared fruit bat | Anti-EBOV IgG (Leroy et al., 2005; Pourrut et al., 2007, 2009) RT-PCR positive for EBOV L gene fragment (Leroy et al., 2005) | Central Africa, West Africa | |
| | Peters’s lesser epauletted fruit bat | Anti-EBOV IgG (Pourrut et al., 2009) | Equatorial Africa | |
| LLOV | Schreiber’s long-fingered bat | Complete genome detection (Negredo et al., 2011) | Caucasus, North and West Africa, Southwestern Europe | France, Portugal, Spain |

(continued)

TABLE 7.3 (continued)

Evidence for an Association of Filoviruses with Bats

| Filovirus | Suspected Bat Host (Species) | Supporting Data for Bat Association | Bat Geographic Distribution | Known Filovirus Endemicity (Based on Disease Outbreaks and Virus Isolation/Full Genome Detection) |
|-----------|---|--|--|---|
| MARV | Egyptian rousette | Anti-MARV IgG (Pourrut et al., 2009; Towner et al., 2007) | Africa Middle East Southwest Asia | Angola, Democratic Republic of the Congo, Kenya, Uganda, Zimbabwe |
| | Hammer-headed fruit bat | RT-PCR positive for VP35, VP40, and NP gene fragment (Kuzmin et al., 2011; Maganga et al., 2011; Towner et al., 2007) Virus isolation (Towner et al., 2009) Anti-MARV IgG (Pourrut et al., 2009) | Angola, Benin, Cameroon, Côte d'Ivoire, Democratic Republic of the Congo, Gabon, Ghana, Guinea, Nigeria, Republic of the Congo | |
| RAVV | Egyptian rousette | Virus isolation (Towner et al., 2009) | Africa Middle East Southwest Asia | Democratic Republic of the Congo, Kenya, Uganda |
| RESTV | Gambian epauletted fruit bat Geoffroy's rousette | Anti-RESTV IgG (Hayman et al., 2012) Anti-RESTV IgG (Taniguchi et al., 2011) | Equatorial Africa Cambodia, East Timor, Indonesia, Malaysia, Myanmar, Papua New Guinea, Philippines, Thailand, Vietnam | Philippines |
| | Hammer-headed fruit bat | Anti-RESTV IgG (Hayman et al., 2012) | Côte d'Ivoire, Guinea, Ghana, Benin, Nigeria, Cameroon, Angola, Republic of the Congo, Democratic Republic of the Congo, Gabon | |
| SUDV | N/A | N/A | N/A | South Sudan, Uganda |
| TAFV | N/A | N/A | N/A | Côte d'Ivoire |

N/A, not applicable; bats for which a connection with filoviruses could not be established in other studies (Table 7.1) are printed bold.

response (Leroy et al., 2005). It is possible that filoviruses infect a bat only for a short period of time and are then transmitted to a co-roosting bat before the immune system of the first bat eliminates it. Especially in large cohorts of bats (hundreds of thousands of individuals), developing sterilizing immunity in individuals may not cause a bottleneck for efficient filovirus transmission. But in such a case, one would expect IgG antibodies in a large percentage of bats of a colony, which thus far has not been demonstrated (Kuzmin et al., 2011). On the other hand, if the natural maintenance of arenaviruses and hantaviruses is any indication, one would expect a more time-stable filovirus–bat relationship in the form of a subclinical persistent infection of a host. Also, one should not forget that all the studies published thus far on bats and filoviruses do not specifically address the order of events during a human outbreak, i.e., it is also possible that bats become infected with filoviruses because of an ongoing epizootic/epidemic, rather than being the factor that started it. A study by Biek et al., for instance, revealed that the EBOV-specific L gene fragments from the Franquet’s epauletted fruit bats, hammer-headed fruit bats, and collected little collared fruit bats “appear to be direct descendents of viruses seen during previous outbreaks,” i.e., this study revealed a direct connection between the few detected sequences and the EBOV known from human outbreaks (Biek et al., 2006). If these bats were the natural reservoirs of EBOV, then one could expect EBOV diversity to be by broader, with some sequences having only indirect connections to known viruses. Biek et al. offered a hypothesis why this does not necessarily have to be the case: a unknown event could have led to an extremely small population of infected bats, thereby selecting only a particular genetic EBOV lineage. But the authors and others also came to the conclusion that it is possible that a circulating disease outbreak–causing virus was introduced into the bat population (Biek et al., 2006; Kuzmin et al., 2011). Such a scenario is also supported by the finding of Pourrut et al. that 5% of sampled Franquet’s epauletted fruit bats, hammer-headed fruit bats, and collected little collared fruit bats contained anti-EBOV IgG when they were collected during human ebolavirus disease outbreaks in either epidemic or nonepidemic regions but considerably lower (0.9%) in bats collected between ebolavirus disease outbreaks (Pourrut et al., 2007).

An alternative to the hypothesis that bats are the natural reservoir hosts of filoviruses is that bats may be merely in close contact with that host. For instance, bat ectoparasites such as winged or wingless bat flies (families Streblidae and Nycteribiidae) or other arthropods could be primary filovirus hosts (Monath, 1999). If that were the case, genomic RNA fragments could be detected in bats that had been bitten by infected arthropods, and IgG antibodies could be detected in bats that had been bitten in the past. Virus isolation could be possible if a bat was caught right around the time of the bite. Bat ectoparasites could also migrate from bats of one species to those of another, especially among co-roosting populations, and thereby explain why bats of different species tested positive for anti-EBOV IgG. If a filovirus-infected arthropod is not bat specific, but rather feeds on bats only occasionally, then this could explain the rarity of filovirus disease outbreaks. Arthropod-transmitted filoviruses could also better explain the discovery of LLOV in Spain (Negredo et al., 2011). LLOV was discovered after massive die-offs of Schreiber’s long-fingered bats in Spain, France, and Portugal. Koch’s postulates could not yet be fulfilled, which leaves the door open for three scenarios. One, these bats are subclinically and persistently infected with LLOV (natural reservoir hosts), and some of them died due to something unrelated to LLOV infection. Two, these bats became sick because of unknown reasons and this sickness allowed LLOV to infect them. And, finally, three, LLOV infected the bats and killed them. The second and third scenario would suggest that at least these bats are not reservoirs of LLOV.

The last intriguing question is how filoviruses are transmitted to humans from bats, if indeed bats are filovirus reservoir hosts or at least amplifying hosts. In the case of marburgviruses, humans probably simply come into direct contact with bats or their secretions or excreta in colonized caves or mines. In the case of ebolaviruses, and the absence of the cave connection, transmission is much less clear. Hunting of bats and subsequent slaughtering and food preparation and/or consumption could further transmission of filoviruses to humans, but convincing data supporting this hypothesis are lacking despite the fact that certain types of bats are part of the general human diet in many

African countries. Alternatively, nonhuman primates, which are often epidemiologically linked to ebolavirus disease outbreaks (Kuhn, 2008), could get in close contact with bats when feasting in fruit trees, thereby becoming intermediary hosts until they get killed by humans for food. Pourrut et al. pointed out that ebolavirus disease outbreaks occur most often at the end of the dry season, coinciding with the birthing season of many frugivorous bats. As fruit are scarce around that time in the forest, bats and nonhuman primates may forage in the same trees and even on the same fruit, thereby furthering transmission (Pourrut et al., 2006). This then, would leave the question open how insectivorous bats, which also have been associated with filovirus disease outbreaks (Angolan free-tailed bats, Schreiber's long-fingered bats) fit into filovirus epidemiology/epizootiology. Most likely, many other factors need to be evaluated to understand why filovirus disease outbreaks are rare despite an abundance of hosts. If bats truly are filovirus hosts, bat roost population size (hundreds of thousands of animals vs. few individuals), migration patterns (short vs. long range), roosting location (caves vs. forest or savannah), and even age and sex may be important factors. Laboratory studies will be necessary to better understand why certain bats can maintain filovirus replication without developing disease (Omatsu et al., 2007), how filoviruses could establish persistent infections and under which circumstances they could emerge from their hosts (Strong et al., 2008), and how filoviruses interact with bat cells (Jordan et al., 2009, 2012; Krähling et al., 2010; Kuhl et al., 2011).

DISCLAIMER

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From: Morens, David (NIH/NIAID) [E]
Sent: Tue, 24 May 2016 17:50:02 -0400
To: (b)(6)
Cc: Johnson Karl
Subject: bat questions

Hi Jon

when we spoke a few weeks ago about the role of bats in ebola i mentioned rhat Karl Johnson and I and colleagues were discussing the complicated bat data in the context of penning an wbola review

In following up on a suggestion of Karl's, is it possible that ebola viruses "bloom" in pregnant females? and we also wonder whether there migjt be seasonalty or other patterns when these bat species breed

The larger question is: are there any factors (such as sex or fighting between males) that might account for waxing and waning of viral infection? Otherwise, the epidemiology is hard to reconcile

Thanks, and i hope you will be coming down for the seminar on, what is it, the 3rd? Get Peter to put you up at the (b)(6) and relax and take in DC

thanks as always

david

David M Morens MD
NIAID, NIH
Sent from my iPhone

From: Morens, David (NIH/NIAID) [E]
Sent: Sun, 5 Jun 2016 22:15:42 +0000
To: Kevin Olival, PhD
Subject: RE: Viruses | Free Full-Text | Filoviruses in Bats: Current Knowledge and Future Directions | HTML

Thanks, I am going to find and send you the Jens Kuhn thing I mentioned. to you and Jon
david

David M. Morens, M.D.
CAPT, United States Public Health Service
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-----Original Message-----

From: Kevin Olival, PhD [mailto:(b)(6)]
Sent: Friday, June 03, 2016 6:39 PM
To: Morens, David (NIH/NIAID) [E] (b)(6)
Subject: Viruses | Free Full-Text | Filoviruses in Bats: Current Knowledge and Future Directions | HTML

Cheers,
Kevin

<http://www.mdpi.com/1999-4915/6/4/1759/htm>

From: Kevin Olival, PhD
Sent: Mon, 6 Jun 2016 13:49:19 +0000
To: Morens, David (NIH/NIAID) [E]
Cc: Jon Epstein
Subject: Re: Viruses | Free Full-Text | Filoviruses in Bats: Current Knowledge and Future Directions | HTML

No worries, let me know if you have any questions about it.

Kevin J. Olival, PhD

Associate Vice President for Research

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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.

On Jun 5, 2016, at 6:51 PM, Morens, David (NIH/NIAID) [E] (b)(6)
wrote:

And I hadn't seen you8rs, which I just printed out here at work. I probably won't get to read it tonight but will soon.

Thasnks,

david

David M. Morens, M.D.
CAPT, United States Public Health Service
Senior Advisor to the Director

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-----Original Message-----

From: Kevin Olival, PhD [mailto:(b)(6)]
Sent: Sunday, June 05, 2016 6:50 PM
To: Morens, David (NIH/NIAID) [E] (b)(6)
Cc: Jon Epstein (b)(6)
Subject: Re: Viruses | Free Full-Text | Filoviruses in Bats: Current Knowledge and Future Directions | HTML

Thanks David, and great to see you Friday night! Don't think I've seen this chapter!

Best,
Kevin

On Jun 5, 2016, at 6:24 PM, Morens, David (NIH/NIAID) [E] (b)(6)
wrote:

Guys, this is the Jens Kuhn review I mentioned on baTS AND FILOVIRUSES, IT'S AT THE END OF THE PAPER.....

David

David M. Morens, M.D.
CAPT, United States Public Health Service Senior Advisor to the
Director Office of the Director National Institute of Allergy and

Infectious Diseases National Institutes of Health Building 31, Room
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31 Center Drive, MSC 2520

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-----Original Message-----

From: Kevin Olival, PhD [mailto:(b)(6)]

Sent: Friday, June 03, 2016 6:39 PM

To: Morens, David (NIH/NIAID) [E] (b)(6)

Subject: Viruses | Free Full-Text | Filoviruses in Bats: Current
Knowledge and Future Directions | HTML

Cheers,

Kevin

<http://www.mdpi.com/1999-4915/6/4/1759/htm>
<Singh Ruzek VHF Book ch7.pdf>

From: Jon Epstein
Sent: Fri, 11 Dec 2020 15:56:30 -0500
To: Morens, David (NIH/NIAID) [E]
Cc: Peter Daszak ((b)(6)); Keusch, Gerald T
Subject: Re: FW: NYT [Opinion]: The Virus and Bats /They probably spread the virus that's killing humans. We almost certainly spread the fungus that's killing them.

Thanks, David. David Quammen is such a great storyteller and one of the best at describing the issues around zoonotic disease emergence and the role of people, more so than wildlife, as the main driver. It's refreshing to see an article in the paper focused on the importance of bats, rather than just as a source of SARS-COV-2.

Cheers,
Jon

On Fri, Dec 11, 2020 at 12:54 PM Morens, David (NIH/NIAID) [E] ((b)(6)) wrote:


Guys, great story, congrats!




David M. Morens, M.D.
CAPT, United States Public Health Service

Senior Advisor to the Director
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From: Folkers, Greg (NIH/NIAID) [E] (b)(6)

Sent: Friday, December 11, 2020 11:54 AM

Subject: NYT [Opinion]: The Virus and Bats /They probably spread the virus that's killing humans. We almost certainly spread the fungus that's killing them.

The Virus and Bats

They probably spread the virus that's killing humans. We almost certainly spread the fungus that's killing them.

By David Quammen

Mr. Quammen is the author of "Spillover: Animal Infections and the Next Human Pandemic."

- Dec. 11, 2020



Credit...Wesley Allsbrook

The order of animals known as Chiroptera, the bats, enjoys a mixed reputation among humans. I'm putting this politely: They have been calumniated and abused for centuries.

Some people, mainly from the comfort of distance and ignorance, find bats repellent and spooky. Some people fear them, with or without rational grounds. Bats are sometimes slaughtered in large numbers, defenseless at their collective roosts, when people deem them menacing, inconvenient, noxious or desirable as food.

The idea of bat soup or roasted bat may induce cringes in sensitive Western eaters, but that's no consolation to the tens of thousands of flying foxes (as the largest of the Old World fruit bats are known) that have been legally hunted for meat and sport in Malaysia in recent years. Or to the Mariana fruit bat, pushed toward oblivion not just by habitat loss in Guam and neighboring islands, but also by the introduction of a tree snake that preys upon them and a tradition among the local Chamorro people of eating them as a celebratory

meal. Almost 200 bat species around the world are threatened with extinction.



A young grey-headed flying fox in Victoria, Australia. Ancient literature and folklore record a long list of anti-bat beliefs. Some people also blame bats for carrying dangerous pathogens, including, potentially, the precursor of the new coronavirus. Credit...Annette Ruzicka

And this pattern of antipathy will only be made worse by the Covid-19 pandemic — given molecular evidence showing bats as the likely origin of the new coronavirus — unless we recognize the merits and beauties of these creatures, as well as the biases against them.

Ancient literature and folklore record a long list of anti-bat beliefs: that they were turncoats in the primordial battle between Birds and Beasts, that they curdled the eggs of storks, that they gouged bites out of hams hung for curing, that they entangled themselves in women's hair, that they were accomplices to Satan in his effort to seize control of human nature, that bat blood could serve as an antidote to snakebite and all manner of other silly stuff.

The association of vampirism with bats, though, is no myth. Three species of small, sneaky New World bats are adapted to feeding exclusively on blood from birds and oblivious mammals — originally wildlife, but now also cows, horses and humans asleep with their feet exposed. The most conspicuous of them is the common vampire bat, Desmodus rotundus, known from Uruguay to Mexico and especially abundant in

southeastern Brazil. These sanguinivorous bats have heat sensors in their noses for locating capillary concentrations, sharp incisors for slicing flesh, anticoagulant saliva — the whole deal. Like furry mosquitoes.

The “rotundus” (portly) in their scientific name reflects the fact that after they’ve crept across the ground to nip the ankles of cattle and drink blood, they become so fat from a night’s meal (burp), that they must piss away the plasma, retaining the red cells, before they can be airborne and get back to their roost. From there it’s a short flight to “Dracula.”



A vampire bat, *Desmodus rotundus*. Bat viruses spill into humans; they don’t climb into us. And the spilling generally happens when we intrude upon bats in their habitats. Credit...Stephen Dalton/Avalon, via Alamy

Some people also blame bats for the dangerous pathogens they carry — including, potentially, the precursor of the new coronavirus, SARS-CoV-2. That virus may have gotten into us from one of the several kinds of horseshoe bat from southern China. If so, the fateful event probably had more to do with what some human wanted from bats than with what some bat wanted from humans.

Bat viruses *spill* into humans; they don’t *climb* into us. They don’t seek us out. And the spilling generally happens when we intrude upon bats in their habitats, excavating their guano for fertilizer,

capturing them, killing them or transporting them live to markets, or otherwise initiating a disruptive interaction.

Scientists haven't yet discovered (and they may never) just which such encounter brought this coronavirus to humanity. But you can be confident that it didn't happen because some Chinese rufous horseshoe bat flew into Wuhan and bit a poor man on the toe.

II.

The most lethal of bat-borne viruses, for humans, is rabies, now recognized as one member of a diverse group called the lyssaviruses (as in Lyssa, the Greek goddess of frenzy and rage), most of them associated with bats. Humans have been aware of rabies at least since Democritus, in the fifth century B.C. We've seen it in our dogs, sometimes driven mad, like Old Yeller, and occasionally in an unlucky person who got bit. The fatality rate for rabies, absent prompt post-exposure vaccination, is nearly 100 percent, and the disease still kills tens of thousands of people each year.

But from what original source did rabies get into dogs or raccoons or skunks or the other carnivores from whose saliva it drips into a bite wound? The first clue to that mystery came in 1911, when rabies virus was reported among bats by an Italian scientist in Brazil, Antonio Carini, who noted the odd detail that it didn't seem to make the bats sick. That suggested a long relationship between the bats and the virus, which had perhaps reached a mutual accommodation: a secure habitat for the virus, no symptoms for the host.

Although rabies was the topic that dominated research in this field for much of the 20th century, a few other bat-borne viruses turned up, mostly as incidental discoveries by scientists studying something else. Rio Bravo virus, for instance, found among some California bats in 1954 and related to the yellow fever virus, was one. Tacaribe virus, carried by both bats and mosquitoes in Trinidad, was another. These viruses yielded scientific papers but not newspaper headlines, because they weren't causing human deaths.

Soon, too, there appeared some new killer viruses, though without (at first) any clear linkage to bats. Marburg virus as well as the most lethal and infamous of the Ebolas, now known as Zaire ebolavirus, caused gruesome illness and death with their first recognized outbreaks among humans, during the late 1960s and 1970s. But their confirmed (Marburg) or probable (Zaire ebolavirus) connections to bats as reservoirs were not established by science until later.

Then, in 1994, a strange new bug spilled out of certain flying foxes in eastern Australia, burned its way horrifically through a stable of racehorses and killed one of the three men who had labored, shoulder-deep in bloody froth, to save those horses. A second man, a stable hand, got very sick but survived. The third man was a tall veterinarian named Peter Reid.

“That’s it,” Dr. Reid told me, a dozen years later, as we sat in his car amid a sprawl of new tract houses near Brisbane, gazing at a solitary fig tree left standing in a traffic circle. “That’s the bloody tree.” The suburb, in 1994, was a horse pasture. The bats came for the figs. The first infected horse shaded herself beneath this tree,

feeding on grass splashed with virus-laced bat feces. From her it passed to the other horses and to the men.

That virus got the name Hendra, after the Brisbane suburb where the horse deaths occurred. This was before it became politically unacceptable to name a nasty new virus after a place.

Nipah virus, in 1998, in Malaysia, also emerged from bats, also passed through an amplifier host (pigs), also killed people and also was named for a place: the village of Sungai Nipah, home to a 51-year-old pig farmer from whose cerebrospinal fluid the virus was first isolated.

The original SARS virus appeared shortly thereafter, in 2002. It, too, arose from a bat, passed possibly through palm civets, and began sickening people in Shenzhen, China. It spread alarmingly fast to other countries in 2003, with several superspreading events and a high fatality rate, but it was controlled thanks to strong public health measures, and it killed “only” 774 people.

The SARS outbreak of 2002-03 was a galvanizing event for disease scientists, who recognized that it could have brought about a disastrous pandemic if just a few factors had differed: a slower response by public health officers, disorganized efforts of containment, or maybe a similar coronavirus but capable of spreading from asymptomatic cases. (Does all that sound familiar? It should.) Discovery of the bat-SARS link two years later moved bat-virus research, according to the eminent virologist Charles H. Calisher, “from serendipitous, fragmented, and local, to well-planned, methodical, and global,” with attention focused ever more strongly on bats as the reservoirs from which many nefarious viruses have emerged.

That's a long list of animosities, scurrilities, grudges and indictments. So what can be said for bats, these feared and detested creatures?

Plenty can be said for them.

III.

To grasp the majesty of bats, start by imagining this: You are on a small cargo boat, chartered for 25 bucks, puttering southward across open sea among the small islands east of Komodo, in central Indonesia. There are scarcely any villages, scarcely any people, and certainly no hotels in this remote, austere bit of the archipelago. It's twilight and you're hurrying toward a safe anchorage at the lee of one of these islands, where you and the boat captain and his two sons, who constitute his crew, can sleep the night. Just before dark, a great flock of fruit bats comes out of the west, flying high, maybe a thousand of them, each as large as a raven.

Most likely they are Sunda fruit bats, *Acerodon mackloti*, a species endemic to Indonesia, and whatever viruses they may carry have not yet caused any known harm to people. Their wings flap in easy rhythm as they move in procession, full of purpose, like migrating geese, toward their nocturnal feeding grounds on some island eastward. The dipping sun warms the sky with a last peach-colored wash. The moon is a thin crescent, and the bats cross it in silhouette, minding their own business. They are magnificent.

The Sunda fruit bat is just one of what scientists tally as more than 1,400 living species of bat. That's more than any other mammalian order except the rodents and constitutes about 20 percent

of all mammals. Think of it: One in every five mammals on earth, by count of species, is a bat. They must be doing something right.



A colony of fruit bats flying above the rainforest in West Sumatra, Indonesia. Almost 200 bat species around the world are threatened with extinction. Credit...Leisa Tyler/LightRocket, via Getty Images

By another standard, bats are more diverse even than rodents if you consider the variousness of their ecological, physiological and behavioral traits, as well as the sheer count of species. They live on every continent except Antarctica, from north of the Arctic Circle to Tierra del Fuego, and on some of the world's most remote islands. Their diets include insects, small mammals, reptiles, amphibians, fish taken by skimming over water, fruit, flowers, nectar, pollen, leaves, scorpions and blood.

Some of them migrate, traveling long distances for seasonal food or mild temperatures. Some of them hibernate, notably in caves, to avoid the hardships of winter. Many bats of the temperate zones are also capable of daily torpor, reducing their body temperature and oxygen consumption while they are inactive, to save energy.

When they perk up again and take flight, their metabolic rate can increase quickly by a factor of 14. All of these traits relate to the two great adventures that evolution opened to early bats: They colonized the air and they embraced the dark. Nowadays they sleep by day and fly by night.

They were the first, and are still the only, mammals capable of powered flight. That's big: By opening a third spatial dimension to them, a vast new realm of activity scarcely explored by other mammals, flight may be what enabled such extraordinary diversification.

Another factor is the duration of their lineage. The earliest known bat fossil dates to about 50 million years ago, and because it resembles a modern bat, the dawning of bats must have occurred well before that. The earliest flying squirrel may not have appeared until 30 million or 40 million years later, by which time bats were the mammalian masters of the air.

To function at night, performing the aerial dives and swoops necessary to catch flying insects, without going hungry or continually knocking themselves silly against tree limbs or rock walls, they acquired another crucial capacity: echolocation. They became able to blast out pulses of high-frequency sound, some of them through their noses, like silent screams, and receive back the echoes with acutely sensitive ears. This allows their brains to assemble dynamic images of the size, shape, distance and motion of the zigzagging moths and plummeting katydids that are their prey.

Certain of the nostril shriekers, including the horseshoe bats and the leaf-nosed bats, developed elaborate nasal structures that help focus their sonic pulses. Some others, by evolutionary increments, grew huge ears. Tomes's long-eared bat, native to forests in Central and South America, has combined both — towering, wide ears shaped like the spinnaker on a yacht, plus a nose like the prow of a Viking ship. This makes for a face of peculiar distinction — I would say, a face only a mother could love, except that chiroptophiles love it, too — while the poor little animal is just trying to locate dinner.



A horseshoe bat. Thanks to elaborate nasal structures, it can blast out pulses of high-frequency sound, like silent screams, and receive back the echoes. This allows the bat to assemble dynamic images of the size, shape, distance and motion of the zigzagging moths and plummeting katydids it preys on. Credit...Charles M. Francis/Bat Conservation International

Bat superlatives are both wide and long: Besides showing great collective diversity, bats also have high life expectancy. If an infant bat gets past its first birthday, it has a good prospect of surviving to 7 or 8. Much longer than a mouse. On average, according to one study, a bat lives more than three times as long as a nonflying mammal about the same size, and some can reach 30 years, even in the wild.

This longevity is not just because of torpor and hibernation, giving long periods of rest. Even non-hibernating bats live to be old, possibly in part because flight allows them escape from predators, possibly also because escape from predators, lengthening life, has given Darwinian natural selection the time and reasons to eliminate negative mutations that might cause congenital disease in middle-aged bats — a positive feedback loop. But these are guesses that invite more investigation.

Another conundrum now at the forefront of bat research, with potential medical value for humans, is how their immune systems tolerate viral infection with such aplomb. Bats carry many viruses, and yet they generally don't suffer symptoms themselves.

In at least some cases, the concentration of virus in their blood tends to be low. They don't mount the same inflammatory responses as other mammals, which is good for their longevity, because excessive inflammatory responses can be dangerous, sometimes overwhelming the body with a reaction worse than the cause. The sequencing of the genomes of several bat species has revealed that they carry about half as many immunity-related genes as a human does.

Why would evolution dampen down immune reactions in bats? One hypothesis is that it's a trade-off for flight: Flying entails such physiological stress that an alert immune system might react against unstable molecules produced by the animal's own exertion. In this view, it's better for the bat to ignore the presence of viruses than to suffer autoimmune symptoms from flying. So, could bats

help medical researchers understand autoimmune disease in humans? That's an open question.

IV.

Although the earliest bats were small insect-eaters, the big fruit bats diverged at least 35 million years ago, when chance and evolutionary opportunity led them to abandon echolocation (mostly) for good eyesight, and agile insectivory for vegetarianism and bulk. The largest are the flying foxes, stately creatures with broad wingspans, dog-like faces, molars for crushing fruit pulp and, in some species, long tongues for lapping up nectar.



A grey-headed flying fox in Melbourne, Australia. One in every five mammals on earth, by count of species, is a bat. They must be doing something right. Credit...Annette Ruzicka

A few of them are lovely, russet-bodied with umber wings, occasionally a golden collar. They roost mainly in trees, such as the tall karois surrounding a certain derelict warehouse, in southern Bangladesh, where a wildlife veterinarian named Jonathan Epstein, along with his field crew and me, in 2009 found a roosting colony of 4,000 to 5,000 Indian flying foxes. Dr. Epstein had come to trap some of these animals and sample them for Nipah virus.

On the first afternoon, as Dr. Epstein's two agile net-riggers climbed high into one tree, the bats stirred, woke and, spooked, rose into the sky, one after another, with what seemed calm caution, to escape the disturbance. Soon, the whole flock was airborne, circling out to the northeast, then back in, out again, back, riding the thermals with minimal wing beats, like flotsam going around in a great river eddy. I gawked up in awe and Dr. Epstein reminded me — I can't remember if it was then or later — that a wide-open gape beneath a caldron of such bats might be a good way to get a mouthful of Nipah-laced guano.

In the wee hours of the night we returned, climbed a rickety bamboo ladder to the warehouse roof, wearing masks and goggles and gloves and headlamps, and were in position when the first bat — now returning from its nocturnal foraging — hit the net. Dr. Epstein, hands protected in welder's gloves from the sharp claws and teeth, held the animal in a firm grip behind its neck while a colleague untangled it. That one went into a cloth bag, and so had, by dawn, five others. Then, in a makeshift field lab, Dr. Epstein and his crew took blood samples and cheek swabs from the bats, now anesthetized, being careful not to hurt them.



Dr. Jonathan Epstein and his team capturing an Indian flying fox in Bangladesh in 2015 as part of a long-term study to understand Nipah virus and how it jumps from bats to humans. Credit...Eco Health Alliance 2020

At full daylight, we all marched outside. By now a small crowd of people, adults and children, had gathered to watch the strange business. Dr. Epstein released each animal gently: He raised an arm high, letting the bat free its wings and legs and then drop of its own accord, catching itself with wing beats just above ground, and then slowly flap away. With one of his crew members translating, Dr. Epstein addressed the gathering: “You’re very fortunate to have so many bats.” They pollinate plants, they spread seeds, they generate fruit trees, he explained. Implied but unmentioned was this message: If you leave them alone, if you keep your distance, you probably won’t get Nipah-virus disease.

Dr. Epstein — one of those cross-trained experts with a veterinary degree, a Ph.D. in ecology and a master’s in public health — is now a vice president at [EcoHealth Alliance](#), a research and conservation

organization devoted to animal and human health. He reminded me during a recent conversation, as he had those villagers in Bangladesh, of the benefits ledger for bats.



“Bats are too important to lose,” said Dr. Epstein, a vice president at EcoHealth Alliance, a research and conservation organization devoted to animal and human health. Credit...Karsten Moran for The New York Times

They play a huge role in the perpetuation of tropical hardwood forests. They eat a vast tonnage of insects each year. In Thailand, wrinkle-lipped bats provide protection against a major rice pest. In Indonesia, other bats reduce the insect burden on shade-grown cacao. A single colony of big brown bats in the American Midwest, by consuming 600,000 cucumber beetles in a year, prevents 33 million cucumber beetle larvae from feeding on the next year’s crop. Mexican free-tailed bats eat cotton bollworm moths in Texas. By one estimate, from 2011, bat predation on insects was saving \$23 billion annually for agriculture in the United States. The global total is incalculable. “Bats are too important to lose,” Dr. Epstein said.

V.

Yet they *are* being lost in many parts of the world, because of habitat destruction and direct killing — and, at a cataclysmic rate in North America over the past 14 years, because of a new problem: a contagious disease. It's called white-nose syndrome, and it's caused by a pathogenic fungus that seems to have arrived from Europe. In this case, humans are the vector, and bats are the victims.

Winifred Frick is the chief scientist of Bat Conservation International and has studied white-nose syndrome almost from the start. The disease first showed itself at a tourist-destination cave west of Albany, N.Y., in February 2006, where a caver photographed some hibernating bats with powdery white fuzz on their muzzles, like frost on the beard of a skier. A year later, biologists for New York State found thousands of dead bats with similar growths in another cave nearby. By 2008, Dr. Frick, among others, was at work on the problem, which grew into a crisis for the hibernating bats of North America.



Dr. Winifred Frick, the chief scientist of Bat Conservation International. “You can almost think of them as being like little cold Petri dishes,” Dr. Frick said of hibernating bats exposed to white-nose syndrome, a deadly fungus. Credit...Cayce Clifford for The New York Times

“It spread really rapidly,” she told me recently by Skype, walking on her treadmill as we spoke. I knew Dr. Frick already as a multitasking scientist a decade ago, having met her when a group of us shared dinner in a grand venue at the close of an international bat conference in Berlin and she brought along her 4-month-old son, Darwin. By now, white-nose syndrome is in 33 U.S. states and Canadian provinces, she told me, having caused a 90 percent decline in the known populations of three bat species, plus losses among at least four others. Millions of bats have died.

One of the three hardest-hit species, the northern long-eared bat, she said, was “totally gone,” within three years, from some areas where it used to hibernate. North America’s hibernating bat populations could be nearly or completely wiped out.

The fungus thrives in cold, damp environments such as caves, and it takes hold on bats during their periods of torpor and hibernation, when their immune systems are inattentive, not just to viruses but also to other infections. “You can almost think of them as being like little cold Petri dishes,” Dr. Frick said. The fungus grows robustly, causes irritation and rouses the bats in midwinter, whereupon they fly out, expend crucial fat reserves searching for insect food that isn’t there and die.



Bats with white-nose syndrome. It's caused by a pathogenic fungus that seems to have arrived from Europe. In this case, humans are the vector, and bats are the victims. Credit...Michael Schirmacher/Bat Conservation International

The same fungus is commonly found on bats in Europe, but with relatively mild effect and no evidence of mass mortality, possibly because it's long familiar and those populations have adapted. How did it get to North America? No one knows for sure, Dr. Frick said. "We don't have a smoking gun," but "the most parsimonious explanation is that it came over on somebody's boots." An invisible smudge of the fungal spores, on the footwear of a casual tourist or a serious caver lately returned from spelunking in northeastern France or Germany, could have been enough. Bats don't fly between Europe and America, but people do.

I'm sure you see the analogy here, the gruesome symmetry that brings consolation to no one: Covid-19 is a disease catastrophe for humans, with its likely origin in bats, triggered by human action; white-nose syndrome is a disease catastrophe for bats, with its origin who knows where, triggered again by human action. We humans are one species, abundant and wondrous and powerful. Bats are many species, diverse and wondrous and vulnerable.

That puts some responsibility upon us. Our lives and our health are entangled with theirs. If we could speak to bats, offering armistice, seeking concord, I'd suggest six words for a start: "Thank you. No hard feelings. Sorry."



Credit...Annette Ruzicka

David Quammen is an author and journalist whose books include "Spillover: Animal Infections and the Next Human Pandemic."

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

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Twitter: [@epsteinjon](https://twitter.com/epsteinjon)

EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation

From: Morens, David (NIH/NIAID) [E]
Sent: Sun, 26 Jul 2020 00:22:48 +0000
To: Jon Cohen
Cc: Joel Breman; Gerald Keusch; Peter Daszak; Taubenberger, Jeffery (NIH/NIAID) [E]
Subject: Re: Another Great article, thanks!

Thanks for your great stuff! Really. David

Sent from my iPhone
David M Morens
OD, NIAID, NIH

> On Jul 25, 2020, at 20:04, Jon Cohen <jcohen@aaas.org> wrote:

>

> Yes, I read. Many thanks to all of you. I'm going to see if I can add a link in my article.

>

> All the best,

>

> Jon

>

>> On Jul 25, 2020, at 4:36 PM, Morens, David (NIH/NIAID) [E] (b)(6) wrote:

>>

>> [EXTERNAL EMAIL]

>>

>> Jon, Joel Breman, President of Am Soc Trop Med Hyg, called me today to ask me to bring to your attention the two publications, out this past Wednesday, in the ASTMH journal, which defend the work Of Peter and Chinese colleagues in a background review and a companion go-with editorial. Each of these papers is authored by senior internationally recognized experts And provide evidence in accord with your reporting. David

>>

>> Sent from my iPhone

>> David M Morens

>> OD, NIAID, NIH

>

From: Jon Epstein
Sent: Fri, 31 Mar 2017 20:15:01 -0400
To: Morens, David (NIH/NIAID) [E]
Subject: Re: favor?

David,
I'd be more than happy to. Especially as she's a friend of yours, and even if not, I'd be happy to help.

Have her email me.

Cheers,
Jon

On Mar 31, 2017 5:25 PM, "Morens, David (NIH/NIAID) [E]" (b)(6)
wrote:

Hi Jon, this is a little out of the ordinary, but would you be willing to email with or speak with an internationally famous novelist about bats?

It's a friend, Hanya Yanagihara, who is planning her next novel to be about an outbreak of a deadly pandemic in New York City. She and I spoke and communicated plot issues last year but now I am fuzzy on the details. She is just back from a European book tour for the last book, and wants to get back to the new novel. Her uncle, Ric Yanagihara, was one of nobellist Carleton Gajdusek's top researchers, you may know him. He discovered one of the hantaviruses with Carleton. Anyway, Hanya lives in NYC; her last book, an international bestseller called *A Little Life*, won the Kirkus Award and was a finalist for the Mann Booker, the top prize in literature, and was favored to win. But didn't. She's a very good writer and very smart, but has no science training to speak of.


If you are willing to let her email I'll punch that button, but if not, I undersdtand.


David


David M. Morens, M.D.

CAPT, United States Public Health Service

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From: Morens, David (NIH/NIAID) [E]
Sent: Thu, 5 Aug 2021 12:09:13 +0000
To: Jason Gale
Cc: (b)(6)
(b)(6) Garry, Robert F; (b)(6)
Subject: Re: draft

Great piece!!!!!! Kudos to you! dmm

Sent from my iPhone
David M Morens
OD, NIAID, NIH

On Aug 5, 2021, at 07:37, Jason Gale (BLOOMBERG/ NEWSROOM:) <j.gale@bloomberg.net> wrote:

Hi guys. Please keep this to yourselves. Thanks for trusting me with your perspectives and thoughts. Here's what I drafted. Every editor involved (and there's a bunch!) has a different idea on what the story should say at the top. I can't say I love this iteration, but it's bound to change anyway! (The original was a lot more colorful). Always glad to get your thoughts. Thanks again. Jason

By Jason Gale
(Bloomberg) --

The origin story of Covid-19 in China remains a mystery more than 18 months into the pandemic. Conjecture the virus escaped from a maximum security biology lab in Wuhan has piqued the interest of foreign intelligence services, despite no supporting evidence that's surfaced publicly.

A more plausible theory, some scientists contend based on past coronavirus outbreaks, is that an infected animal brought the virus to a Wuhan seafood and produce market, where many of the early cases of Covid-19 were traced back to in late 2019. Chinese authorities have shot down that theory as steadfastly as the lab-leak hypothesis, insisting there were never any wild animals sold at the market.

Yet a just-published study by researchers in China and at the University of Oxford containing photographic evidence of Wuhan's wildlife trade suggests otherwise. Minks, civets, raccoon dogs and other mammals known to harbor SARS-CoV-2 and related coronaviruses were sold for food and as pets in plain sight in shops across Wuhan for years, including the Huanan Seafood Wholesale Market, considered ground zero of the global health crisis.

The evidence, collected by a scientist working at a research lab affiliated with China's Ministry of Education, gathered dust for a year and a half, buried under layers of bureaucracy and obfuscation. The delay allowed Chinese officials to weave alternative narratives in which the virus could not have possibly evolved in an animal market, and that the threat was likely imported from elsewhere. Meanwhile, controversial speculation that the virus had escaped from a nearby lab gained traction.

"It is unclear why earlier initiatives within China to locate source animals for SARS-CoV-2 were curtailed, and now appear unfortunately to have stopped," said Robert F. Garry, a professor of microbiology and immunology at Tulane

University's School of Medicine in New Orleans. "Instead, the focus is on highly implausible origins scenarios. If we continue to place politics over science, humanity will again be unprepared for the next emergence of a pandemic virus."

The U.S. Intelligence Community is slated to report its own findings later by Aug. 24, but Garry and others say that with only circumstantial evidence remaining, scientists are unlikely to get to the bottom of what caused the outbreak. They are left wondering whether among the dozens of species of exotic animals sold live across Wuhan, animals existed that may have acted as intermediate hosts between the pandemic strain and its closest known relative -- a virus collected from a bat cave in Yunnan province nine years ago. Quickly unraveling Covid's genesis could have yielded more than valuable lessons in how to ensure new infectious diseases don't trigger catastrophic outbreaks; it could have averted a raging political debate that's already caused a trade war between China and Australia, as nations demand to know how SARS-CoV-2 emerged.

The evidence that scientists needed to solve the mystery of Covid's origins may have been in the hands of Xiao Xiao, a scientist whose roles straddled epidemiology and animal research at the Hubei University of Traditional Chinese Medicine and the government-funded Key Laboratory of Southwest China Wildlife Resources Conservation. Xiao routinely surveyed 17 shops selling live wild animals across four wholesale and retail centers from May 2017 through November 2019 -- finishing just weeks before the discovery of mysterious pneumonia cases at the Huanan market heralded the start of the pandemic.

Seven of the shops Xiao surveyed were in the Huanan market, which was linked two of the three earliest documented Covid-19 cases.

On each of his monthly visits, Xiao asked vendors what species they had sold over the preceding month and in what numbers and at what price. It wasn't the novel coronavirus that Xiao was hunting, but the source of a tick-borne disease that had spread in Hubei province years earlier.

Xiao checked the animals for injuries and disease, noting that almost a third bore trapping and shooting wounds, and that none of the shops displayed an origin or quarantine certificate, making the trade "fundamentally illegal." Of the 38 animal species Xiao documented, 31 were protected. Traders caught violating China's wild animal conservation law face fines and up to three years imprisonment.

As an objective observer unconnected to law enforcement, Xiao was granted "unique and complete access to trading practices," he and his colleagues noted. Xiao's list of animals included masked palm civets and raccoon dogs -- both involved in the 2003 SARS outbreak -- and other species susceptible to coronavirus infections, including bamboo rats, minks, hog badgers and hedgehogs.

The shop owners gave written consent for the research, but for the most part, their animal-wares were displayed openly, "caged, stacked and in poor condition," Xiao observed. Over the 30-month survey period, he estimated 47,381 wild animals were sold in Wuhan -- one of the 10 most-surveilled cities in the world, according to Comparitech Ltd., a U.K.-based security researcher which estimates there are 339 CCTV cameras per square mile in Wuhan.

The live animals weren't a cheap form of bushmeat, akin to the remains of animals killed in the jungles and savannas of Africa, Xiao said. These were luxury food items priced at up to \$25 a kilogram (\$11/pound) -- or more than four times costlier than pork, China's main meat staple. Most of the shops offered custom, onsite butchering services.

Remarkably Xiao's findings -- and broad awareness of Wuhan's flourishing wildlife trade -- didn't surface until June 2021 -- 18 months after Covid

surfaced and four months after a 17-person international team of experts convened by the World Health Organization completed a four-week mission in Wuhan in February to study Covid's origins.

It wasn't like Xiao and his colleagues -- Zhou Zhaomin, a researcher from a wildlife resources laboratory affiliated with China's Ministry of Education, and three seasoned scientists from the University of Oxford's Wildlife Conservation Research Unit -- held onto their research. A manuscript was submitted to a journal in February 2020. The authors anticipated "support and swift publication," enabling the data to be widely shared, co-author Chris Newman, a zoologist with some 177 publications to his credit, recalled in an email.

Instead, an independent expert assessing the paper as part of the peer-review process publications are typically subjected to "cast aspersions onto the veracity of our dataset, both in terms of Dr. Xiao's surveying and the extent to which these data might accurately reflect all species sold in the markets," Newman said. A revised version was met with a second round of questions that led to further delays. At the end of September 2020, the journal rejected the paper outright.

"They did not think it would have widespread appeal," Newman said. "It caused us, especially our Chinese co-authors, concern that these data would not be taken seriously."

The manuscript was revised a third time to include data on China's pangolin trade networks, and sent the following month to Scientific Reports. Springer Nature AG & Co., the journal's publisher submitted it directly to the WHO shortly after it was received as part of an agreement with the agency, said Ed Gerstner, Springer Nature's director of journals, policy and strategy. The paper, cryptically titled "Pangolin trading in China: Wuhan's alibi in the origin of Covid-19" went to a generic email address at WHO for receiving unpublished papers, with a copy sent to Maria van Kerkhove, the organization's technical lead for Covid-19. There, the paper languished amid the tens of thousands of manuscripts that have flooded the Geneva-based agency since January last year.

Newman said he was grateful Nature Scientific Reports ultimately published the paper after it was revised yet again, trimmed of the pangolin element, and recast to focus once more on the wildlife trade in Wuhan. Still, the process took eight months, held up by a common struggle journals faced finding scientists to review other researchers' manuscripts amid intense demands from the pandemic, he said.

Van Kerkhove found the process "very frustrating," she said, adding that she regretted there was no direct follow up from the journal during the eight-month review process or by the authors themselves to inform the WHO-convened global study of the origins of SARS-CoV-2 that began in mid-January 2021. "It's a shame this important information was not shared directly with the mission team while the team was in Wuhan and visited the markets," she said in an email. "This paper would certainly have added great value to the mission team."

Zhaomin Zhou, a scientist working across two government-affiliated labs in Nanchong, Sichuan province who was nominated to act as spokesman on the publication, said the paper had been rejected by several journals by the time it was submitted to Scientific Reports. "We were unwilling to disclose it to any other parties, unless the peer reviewers think the paper is almost ready," he said in an email in June.

Newman said the data weren't his to share, but belonged to Xiao, a recent collaborator in China. "These were his data and his contacts in the markets," Newman said. "Plus we were sensitive to not wanting to compromise our Chinese authors."

Xiao didn't respond to emails requesting comment. Newman said he "has essentially disappeared off of our radar, although we remain in close contact with my good friend Zhaomin."

The China-based authors had to be cautious. On Feb. 25, the China CDC issued supplementary regulations prohibiting scientists working on Covid-related research from sharing their data and requiring them to receive permission before conducting any studies or publishing the results. Days later, a State Council panel with oversight of coronavirus research took control of all publication work related to the pandemic for "coordinated deployment."

Newman's Chinese co-authors never told him why they didn't take their data directly to the WHO, he said, adding that it's possible they were more comfortable writing a report on market surveys for publishing in a journal. "But to take their data to the WHO directly would have required them to go through line management channels that would not be typical to their normal roles in their universities," Newman said.

"It was unfortunate that this paper had a chequered publication history," he said.

In the first months of the epidemic, researchers in China asserted that the new coronavirus resembled a spill-over from animals, reminiscent of the emergence of the SARS virus in wet markets in the nation's southern province of Guangdong almost 20 years ago.

Hedgehogs, badgers, snakes and birds were among "a variety of live wild animals" as well as animal carcasses and animal meat available for sale in Wuhan's Huanan market before the outbreak began, scientists from national and municipal health authorities and Chinese universities wrote in a study in the journal Nature in early February 2020.

Many of the earliest known Covid-19 cases were exposed to wild animals at the market, scientist from four Chinese universities wrote in a paper in the Journal of Medical Virology on Jan. 22, the day before Wuhan was placed under a 76-day lockdown (later extended later to the whole of Hubei province, stranding 35 million residents during the heavy-travel Chinese Spring Festival holidays.)

"Wild animals carry the risk of exposing people to new viruses," Xu Jianguo, head of an evaluation committee advising the Chinese government, told the journal Science a month earlier. "We should have more strict regulations and inspections of markets that sell wild animals."

In mid-January CNN broadcast unverified footage reportedly recorded inside the market in early December showing caged deer, marmots and raccoon dogs. Photographs of a menu board advertising the price and availability of exotic animals circulated online.



Yikai Luo
[@YikaiLuo](#)

A SARS-like #coronavirus is rapidly spreading in China and potentially abroad because some people in Wuhan were obsessed with eating wild animals. (If you read in Chinese you'll see the menu has a whole ZOO.) Not a teleologist but it does seem nature is taking its revenge.



Sent via Twitter for Android.
View original tweet.

The market was shuttered and its 678 stalls emptied and sanitized in the early hours of Jan. 1 to stem the spread. Authorities, though, had sprayed

disinfectant around the market on at least two nights before it closed, Beijing News reported.

China CDC disease detectives arriving from Beijing on the first day of 2020 ordered environmental samples to be collected from the market. Some 585 specimens were tested, including extra samples gathered on Jan. 12, two days after scientists published the first genetic sequence of SARS-CoV-2. Thirty-three of the samples were positive for SARS-CoV-2, and all were from 22 stalls and a garbage truck, state news broadcaster CCTV reported on Jan. 26. All but two of the positive specimens were concentrated in a dark, cavernous, poorly ventilated section of the market's western wing, where many shops sold animals -- a feature that the Beijing-based Caixin news organization said added to suspicions that "the epidemic is related to the wildlife trade." "We have found out which stalls on the seafood market in Wuhan had the virus," Tan Wenjie, a researcher at China CDC's viral disease control and prevention institute, was quoted telling state-owned China Daily newspaper also on Jan. 26. "It is an important discovery, and we will investigate which animal was the source."

China responded decisively the same day, temporarily banning the wildlife trade -- a market worth an estimated 520 billion yuan (\$80 billion) in 2016. Then a month later, trading and consumption of terrestrial, or land-dwelling, wild animals for food was banned permanently.

A WHO-China Joint Mission to Wuhan in February reported that an effort was underway to collect detailed records on the source and type of wildlife species sold at the Huanan market and the destination of those animals after the market was closed.

But there is no record of that happening.

Health officials and emergency and security services personnel dressed in protective clothing conducted an additional deep clean and purge of the market in early March 2020, Beijing News reported. Wild animals had already been removed by China CDC staff, it said.

References to wildlife in publications by Chinese scientists also began to disappear.

After describing the Huanan complex as a wholesale seafood and "animal" market in publications in the New England Journal of Medicine on Jan. 24 and Feb. 20, by March, when Covid was declared a pandemic, China CDC Director George Gao was seeding doubt about the role of the market and the existence of its live animals.

Wild animals were "purportedly available," the Oxford-educated virologist and colleagues wrote in the New England Journal of Medicine on March 26. "From the very beginning, everybody thought the origin was the market," Gao said in an interview with Science published the next day. "Now, I think the market could be the initial place, or it could be a place where the virus was amplified."

Data on what animals were present in the market, let alone tested weren't publicly released.

"Unfortunately, the apparent lack of direct animal sampling in the market may mean that it will be difficult, perhaps even impossible, to accurately identify any animal reservoir at this location," Zhang Yongzhen and Edward C. Holmes, the scientists who published the first genetic sequence of SARS-CoV-2, wrote in a commentary piece published in the journal Cell on March 26. One explanation was that there was no live wildlife on sale in the Huanan market -- or anywhere in China -- to begin with.

On April 23, then U.S. Secretary of State Mike Pompeo used part of his Earth Day message to call on China to close its wildlife wet markets to "reduce risks to human health inside and outside of China and discourage the consumption of trafficked wildlife and wildlife products." Days earlier,

Australia called for a global inquiry into the origins of the pandemic, including China's handling of the initial outbreak in Wuhan.

In response to Pompeo, Geng Shuang, a spokesman for China's Foreign Ministry denied such activity occurred in China or that "wildlife wet markets" even existed there. "The sale of wildlife at farmers' markets and seafood markets is illegal in China," Xinhua, the nation's official state-run press agency, quoted Geng as saying in an article titled "There are no so-called 'wildlife wet markets' in China."

Chinese government researchers now dismiss the market hypothesis completely: "SARS-CoV-2 could not have possibly evolved in an animal market in a big city and even less likely in a laboratory," they wrote in a paper released last month ahead of publication. A more recent one by Gao and colleagues contends that the virus may have been imported to the market from multiple locations worldwide, including parts of Europe where mink are raised in areas in inhabited also by horseshoe bats.

"The official narrative changed not because the evidence changed," said Tulane's Garry. "A spillover from a wet market was what caused SARS and embarrassingly for China, those wet markets were never shut down."

Members of the WHO-convened research team that visited Wuhan from Jan. 14 to Feb. 10 suspected so too, according to three scientists familiar with the mission.

But by the time the WHO-led team visited the Huanan market in the afternoon of Jan. 31 -- more than a year after its closure -- little remained to assist the kind of epidemiological detective work that led SARS investigators to Himalayan palm civets, raccoon dogs and Chinese ferret-badgers sold in live-animal markets in Guangdong almost two decades ago.

The researchers noted a mixed smell of animals and disinfectant in some areas of the market, but were told by the market's manager what they were probably smelling was the lingering stench of rotten meat and sewage, according to a joint WHO-China report.

Ten shops had been found to be selling frozen "domesticated" wild animals, including bamboo rats -- some sourced from Yunnan province, where scientists found a coronavirus that most closely matches SARS-CoV-2 from horseshoe bats. But no live animals had been seen before the market was closed, the official said. It was further stated that no live animals were sold and no animals were butchered on the premises.

The researchers saw nothing in the market to dispute that, including any sign of the cages used to house mammals like the raccoon dogs that University of Sydney researcher Edward Holmes photographed in the market in October 2014. Unpublished information and unverified photographs and videos in media reports weren't included in the research.

Instead, scientists were invited to quiz two Wuhan residents who had responded to an invitation to participate in a meeting. According to the report, both had shopped regularly in the market for 20 to 30 years and provided similar accounts: "Nothing out of the ordinary noticeable, all vendors had certificates and inspection certificates displayed in their stalls, they had never witnessed any live animals being sold, the market was kept clean and tidy and they had not noticed any stray cats or dogs, and there had been no confirmed cases in their residential block."

Earlier the same day, the international research team visited the larger Baishazhou Market in Wuhan where Xiao had been regularly surveying two shops selling live wild animals for 2 1/2 years. Yet, the group was told no live animals were sold there either; only frozen food, ingredients and kitchenware.

Liang Wannian, an epidemiologist who headed the Chinese experts collaborating with the WHO-convened team, said Xiao's data weren't known to his group either. "In January-February, when the team was working in Wuhan, we were not

aware of that information," he told reporters last month in response to questions about the June study in Scientific Reports. "Scientists should always communicate with each other in a common pursuit of truth," he said. Among the earliest clusters of infections recorded in Wuhan, one involved three Covid cases among staff working at a stall in the Huanan market that sold "frozen products such as pastry, and soy products." One of the employees, a 32-year-old who fell ill with Covid on Dec. 19, "purchased goods from the Baishazhou market and Huanan Market back and forth."

A confirmed case linking two markets known to sell live wild animals permissive to SARS-CoV-2 is "very intriguing," said Stephen Goldstein, a research associate in evolutionary virology at the University of Utah in Salt Lake City. But tracing any contact the employee might have had with infected animals is impossible now. The animals are long gone, along with any evidence.

"It seems to me, at a minimum, that local or regional authorities kept that information quiet deliberately," Goldstein said. "It's incredible to me that people theorize about one type of coverup, but an obvious coverup is staring them right in the face."