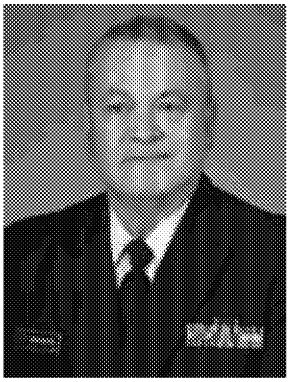
From: Morens, David (NIH/NIAID) [E] [b6]
(b6)
Sent: 12/3/2021 8:44:17 PM
To: 'Kevin Olival' [b6]
Subject: RE: Branswell 2021 reference from my EndNote library -- Some experts suggest Omicron variant may have evolved in an animal host

Agreed, but all of this is difficult because there are so many different micropopulations oif humans and animals. GFor example, here in the States do we have adequate and representational sampling and sequencing of white tailed deer populations? Hopefully yes, but I haven't heard about it. There are wild deer populations in SA as well. Given that ACE2 receptors on all mammals are pretty similar, which is generally not the case for receptors for other viruses, one could speculate that reverse transmission could be happening in multiple species, and we won't know unless we look for it.

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

☎ b6 (assistant: Whitney Robinson)
📠 301 496 4409
💻 b6



From: Kevin Olival b6
Sent: Thursday, December 2, 2021 4:47 PM
To: Morens, David (NIH/NIAID) [E] b6
Subject: Re: Branswell 2021 reference from my EndNote library -- Some experts suggest Omicron variant may have evolved in an animal host

Interesting, thanks David. Reverse zoonotic event is certainly a possibility here, but also possible for undiagnosed circulation in a subset of the human population. I guess this could be teased out by looking at coverage for SARS2 genomic surveillance in S. Africa human pops over the last year in areas where this evolution likely happened, archival sample testing to see if evolution could be teased out over time from this region, and perhaps paired w some animal sampling to see what variants may be circulating in spillback animal popn's. ??

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

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

> On Dec 2, 2021, at 1:46 PM, Morens, David (NIH/NIAID) [E] b6 wrote:
>
> <Branswell-2021-Some experts suggest Omicron va.pdf>

From: Morens, David (NIH/NIAID) [E] [b6
b6]
Sent: 11/22/2021 12:23:43 PM
To: William B. Karesh [b6]
CC: Catherine Machalaba [b6]; Daniel Mira-Salama [b6]
Subject: Re: figure for World Bank report
Attachments: PastedGraphic-1.tiff

PS, you might be able to get Cell to let you use it for free, as it is for a good cause, a non profit entity, and is good advertising for Cell. d

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

> On Nov 22, 2021, at 07:21, Morens, David (NIH/NIAID) [E] b6 wrote:
>
> Billy, this map was reconstructed from our original by the graphics department at the journal Cell. They did this purely so they could copyright it.
>
> You could contact Cell, abd they will charge you. Or else we can give you the original with you can have for free. The original has all the same info and the same color code, but is less spread out vertically and differs in other minor ways
>
> Let me know. My best to Peter and the gang. David
>
> Sent from my iPhone
> David M Morens
> OD, NIAID, NIH
>
>> On Nov 22, 2021, at 06:46, William B. Karesh b6 wrote:
>>
>> Dear David,
>>
>> Hope this finds you well.
>>
>> We are in the final stages of printer's proofs of a report on EID’s in Asia we did for the World Bank. We want to include your EID map from 2020 (attached), but the printer’s tell us that our version is not high enough resolution. Would you happen to have high resolution version that could be used?
>>
>> Hope you have a great Thanksgiving, all the best,
>>
>> Billy

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

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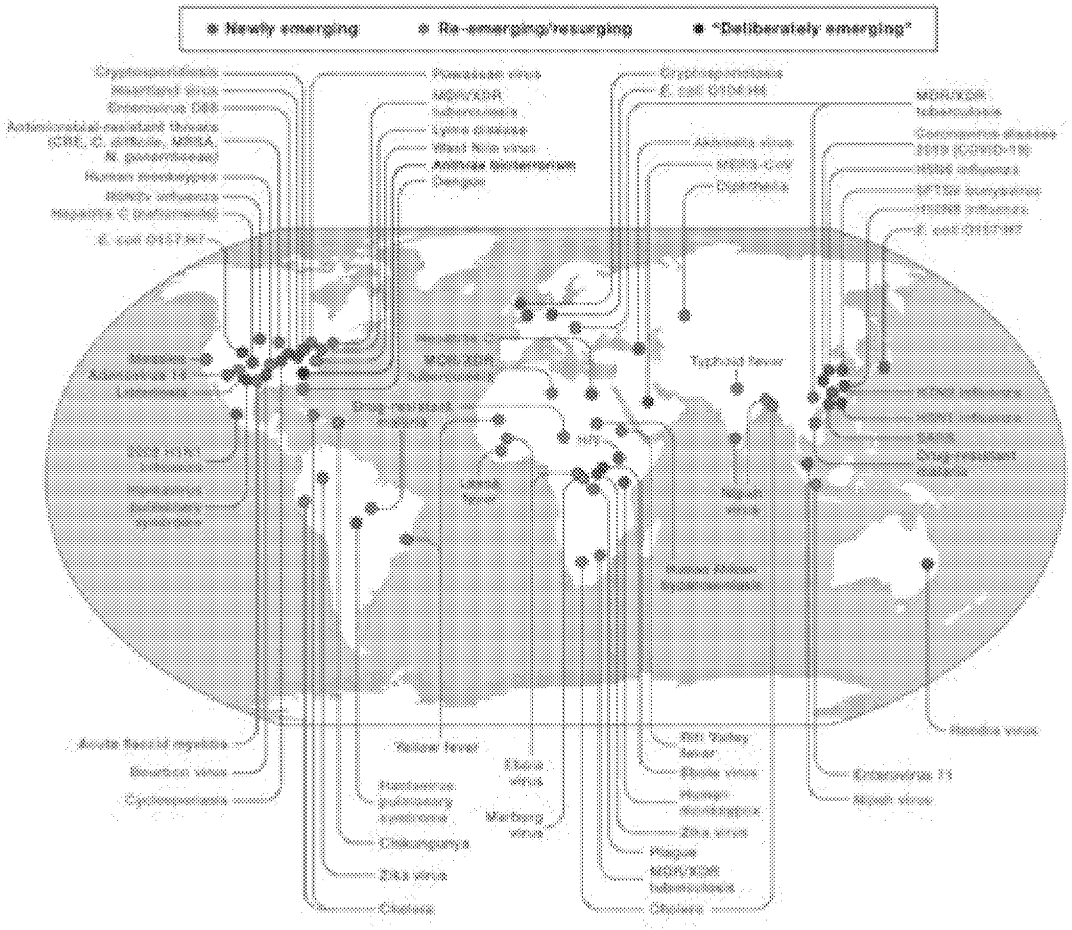
President, OIE Working Group on Wildlife

Co-chair, IUCN Species Survival Commission - Wildlife Health Specialist Group

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


Newly emerging
Re-emerging/resurging
"Deliberately emerging"
Cryptosporidiosis
Heartland virus
Enterovirus D68
Antimicrobial-resistant threats (CRE, C. difficile, MRSA, N. gonorrhoeae)
Human monkeypox
H3N2v influenza
Hepatitis C (behavioral)
E. coli O157:H7
Powassan virus
MDR/XDR tuberculosis
Lyme disease
West Nile virus
Anthrax bioterrorism
Dengue
Cryptosporidiosis
E. coli O104:H4
Alkhurma virus
MERS-CoV
Diphtheria
MDR/XDR tuberculosis
Coronavirus disease 2019 (COVID-19)
H5N6 influenza
SFTSV bunyavirus
H10N8 influenza
E. coli O157:H7
Measles
Adenovirus 14
Listeriosis
2009 H1N1 influenza
Hantavirus pulmonary syndrome
Hepatitis C
MDR/XDR tuberculosis
Drug-resistant malaria
HIV
Lassa fever
Typhoid fever
Nipah virus
Human African trypanosomiasis
H7N9 influenza
H5N1 influenza
SARS
Drug-resistant malaria
Acute flaccid myelitis
Bourbon virus
Cyclosporiasis
Yellow fever
Hantavirus pulmonary syndrome
Chikungunya
Zika virus
Cholera
Ebola virus
Marburg virus
Rift Valley fever
Ebola virus
Human monkeypox
Zika virus
Plague
MDR/XDR tuberculosis
Cholera
Enterovirus 71
Nipah virus
Hendra virus

From: Jon Epstein [b6]
Sent: 6/8/2020 9:18:12 PM
To: Sholts, Sabrina [b6]
CC: Daniel Lucey [b6]; Daniel Lucey [b6]; Dennis Carroll [b6]; Larry Madoff [b6]; Larry Madoff [b6]; Morens, David (NIH/NIAID) [E] [b6 b6]; Murray, Suzan [b6]; Rivers, Meg [b6]
Subject: Re: Outbreak extension and COVID-19 updates

Sabrina and team,
Congratulations! It's terrific news that you've been able to update the exhibit with COVID-19 material and extend through 2022! This is a huge win for the public who are looking for help understanding how this all happened. My not-so-secret belief is that this should become a permanent exhibit, given the extreme relevance it has now (!) and that it will continue to have long into the future. Failing that, I'm grateful for the extra year :)

Also, congrats to everyone there working hard to maximize the exhibit's reach through the DIY and virtual tours. Keep up the good work! I look forward to seeing the new additions and helping in any way you need.

Cheers,
Jon

On Fri, Jun 5, 2020 at 3:53 PM Sholts, Sabrina b6 wrote:

> Dear *Outbreak* friends,
>
> I hope you're all doing well in these incredibly challenging times. The *Outbreak* team at NMNH wanted to share some good news about exhibit, as we slowly move towards reopening the museum (at a date to be determined).
>
> During the temporary closure of Smithsonian museums since March 14, we've been hard at work on COVID-19 updates to the exhibit. Our goal is that when visitors return to NMNH, they will be able to see and understand COVID-19 through the lens of One Health. We are delighted to tell you that exhibit's run has been extended again (!) until **August 2022**, which will allow many more people to experience the updated show.
>
> The COVID-19 updates will be physically integrated into the exhibit in at least two sections:
>
> 1. Section 3: In the "International Spread of Disease" section of the exhibit, we will install a graphic panel and reader rail between the SARS and MERS stories and a video in the style of the SARS timeline (AV-3) on the existing screen. The physical installation will replace the interactive wheel about the

causal factors of infectious disease transmission that is currently mounted on the wall in this spot. The video may loop alternately with the SARS video, rather than replacing it.

- The COVID-19 reader rail will be consistent with the format of the other rails and the theme of the section, focusing on the zoonotic origin of SARS-CoV-2, what was needed to stop its global community spread (with respect to coordination, communication, testing and tracing, and treatment), and its impacts on frontline health workers (with a personal perspective from an infectious disease doctor at Mount Sinai Brooklyn).
- The COVID-19 video will be graphically consistent with the SARS video, visualizing the cumulative cases of COVID-19 in different countries over time (using data from JHU's coronavirus resource center), with narration and soundbites that emphasize the importance of a global response in stopping the international spread of disease.

2. Section 9: In the "One Health mosaic" at the Constitution Ave exit of the exhibit, we will replace the existing graphics with large panels that reinforce what individuals can do to lower risks for the spread of infectious disease (hand washing, getting vaccinated, etc.). One of these action items will be "using Outbreak DIY", illustrated with a customized panel about COVID-19.

As these physical updates cannot be easily revised or expanded as COVID-19 continues into the unforeseen future, we will provide to most up-to-date information about COVID-19 outbreaks, scientific advances, and other developments through our volunteers, the ProMED/HealthMap kiosks (AV-9), and public programming.

It's impossible to express how much we appreciate your help and support in creating *Outbreak* and making it so successful. We realize that this journey is becoming longer than anyone anticipated at the start of it, and at this time you're all busier than ever before. Some of you have been involved directly with the development of these updates, and there's always more work to do. We thus hope that you're all willing to continue your involvement with *Outbreak* as possible, and your tremendous efforts in promoting *Outbreak* for public education and One Health. During the closure of NMNH, we've already offered two virtual *Outbreak* programs (https://naturalhistory.si.edu/education/after-hours/conversation-dennis-carroll-predicting-pandemics) and eight more are being planned for the summer. I've been delighted for these opportunities to stay connected while we're all apart, and I hope that we get to see you in one way or another soon. We'll always let you know about upcoming events via the regular stakeholder updates, and please feel free to keep us current on your activities as well!

Take care and stay well,

Sabrina (on behalf of the *Outbreak* team)

Sabrina Sholts, PhD

Curator of Biological Anthropology

Department of Anthropology

w b6

Twitter: @sabrinabsholts

SMITHSONIAN INSTITUTION

NATIONAL MUSEUM OF NATURAL HISTORY

Facebook | Twitter | Instagram

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

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New York, NY 10001

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web: ecohealthalliance.org

Twitter: @epsteinjon

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

From: Morens, David (NIH/NIAID) [E] [b6
(b6)]
Sent: 3/8/2018 10:16:23 PM
To: Ellen Carlin [b6]
Subject: RE: Global health gaps meeting at World Bank

Ellen, yes, schedule is open, looking forward to joining u

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

☎ b6 (assistants: Meaghan Vance; Logan Salmon)
📠 301 496 4409
💻 b6

From: Ellen Carlin [mailto:b6]
Sent: Thursday, March 08, 2018 4:23 PM
To: Morens, David (NIH/NIAID) [E] b6
Subject: Re: Global health gaps meeting at World Bank

Hi David, I hope roughing it with cervezas in b6 was good to you! I have not been to that part of the world and wouldn't mind a trip to Patagonia.

I wanted to let you know that our roundtable guest list has come together but there is still room for you! We now have two CDC reps coming (Hamid Jafari from Center for Global Health and Casey Barton-Behrevesh from NCZEID), as well as two DOD folks (b6). The rest are non-government. I think it will be a nice discussion.

Let us know if your schedule is still open, and hope to see you soon either way!

Ellen

Ellen P. Carlin, DVM
Senior Health and Policy Specialist

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Adjunct Research Scientist, Columbia University National Center for Disaster Preparedness
Courtesy Lecturer, Cornell University College of Veterinary Medicine

EcoHealth Alliance leads cutting-edge scientific research into the critical connections between human and wildlife health and delicate ecosystems. With this science, we develop solutions that prevent pandemics and promote conservation.

On Fri, Mar 2, 2018 at 11:47 AM, Morens, David (NIH/NIAID) [E] b6 wrote:

> Yeah, i saw the nih shutdown alert, really bizarre. Here the weather is stunning as usual and the cerveza is perfect! one of these days I'll get back and go down to rough it in Patagonia! david
>
> David M Morens MD
> NIAID, NIH
> Sent from my iPhone
>
> On Mar 2, 2018, at 13:31, Ellen Carlin b6 wrote:
>
> Hi David, terrific! Understand you have to check on your schedule. Looking forward to hearing from you when you get back. We have a really nice group assembled.
>
> Enjoy b6—you are missing the federal closures in DC today due to high winds!
>
> Thank you so much,
> Ellen
>
>> On Mar 2, 2018, at 11:28 AM, Morens, David (NIH/NIAID) [E] b6 wrote:
>>
>> Hi Ellen, yes i think i can join you, thanks for thinking of me. I am in b6 at the moment until next Tue and will need to verify that my office hasn't filled in my schedule, but it should be ok. I will let you know
>>
>> david

David M Morens MD
NIAID, NIH
Sent from my iPhone

On Feb 28, 2018, at 21:02, Ellen Carlin b6 wrote:

Dear David,

It was great to see you at the One Health Academy in December. Thank you for attending my talk! I hope to see you at another one in the near future.

As you may know, I work at EcoHealth Alliance with Billy Karesh, and we are developing a global health security gaps analysis. We would like to invite you to participate in a roundtable discussion next month in DC at the World Bank. Please see the attached invitation for more details.

Thanks very much for your consideration. I look forward to hopefully seeing you on March 19!

Best regards,
Ellen

Ellen P. Carlin, DVM
Senior Health and Policy Specialist

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<Roundtable Invitation_Morens.pdf>

From: Morens, David (NIH/NIAID) [E] [b6
(b6]
Sent: 3/19/2018 11:22:55 AM
To: Ellen Carlin [b6]
Subject: RE: Reminder: Global Health Security Roundtable, Monday, March 19

C U soon

David

David M. Morens, M.D.
CAPT, United States Public Health Service
Senior Advisor to the Director
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National Institutes of Health
Building 31, Room 7A-03
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Bethesda, MD 20892-2520

☎ b6 (assistants: Meaghan Vance; Logan Salmon)
📠 301 496 4409
💻 b6

From: Ellen Carlin b6
Sent: Monday, March 19, 2018 7:16 AM
To: Morens, David (NIH/NIAID) [E] b6
Subject: Re: Reminder: Global Health Security Roundtable, Monday, March 19

Great, thank you! See you in just a bit.
Ellen

On Mar 18, 2018, at 8:23 PM, Morens, David (NIH/NIAID) [E] b6 wrote:

Hi Ellen, look forward to tomorrow. Yes i have read it carefully and it provoked some thoughts. All good. Se you soon! david

David M Morens MD
NIAID, NIH
Sent from my iPhone

On Mar 18, 2018, at 18:53, Ellen Carlin b6 wrote:

Dear Colleagues,

We look forward to seeing you Monday morning at the Roundtable on Core Capacities for Global Health Security **at the IFC (the World Bank 'F' building at 2121 Pennsylvania Avenue NW)**, Room F L-109. Please bring an ID to collect your building pass at the IFC.

Please find attached the final agenda and briefing materials. We greatly appreciate you taking 15 minutes to review these materials in advance as they will form the basis for the discussion. We will have hard copies available for everyone once they arrive.

Thank you again, and we look forward to seeing you tomorrow!

Kind regards,
Ellen and Catherine

Ellen P. Carlin, DVM
Senior Health and Policy Specialist

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Adjunct Research Scientist, Columbia University National Center for Disaster Preparedness
Courtesy Lecturer, Cornell University College of Veterinary Medicine

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<Roundtable on Global Health Security Capacities - Briefing Materials 3.19.18.pdf>

From: Ellen Carlin [b6]
Sent: 3/1/2018 12:01:20 AM
To: Morens, David (NIH/NIAID) [E] b6
(b6)
Subject: Global health gaps meeting at World Bank
Attachments: Roundtable Invitation_Morens.pdf

Dear David,

It was great to see you at the One Health Academy in December. Thank you for attending my talk! I hope to see you at another one in the near future.

As you may know, I work at EcoHealth Alliance with Billy Karesh, and we are developing a global health security gaps analysis. We would like to invite you to participate in a roundtable discussion next month in DC at the World Bank. Please see the attached invitation for more details.

Thanks very much for your consideration. I look forward to hopefully seeing you on March 19!

Best regards,
Ellen

Ellen P. Carlin, DVM
Senior Health and Policy Specialist

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Courtesy Lecturer, Cornell University College of Veterinary Medicine

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EcoHealth Alliance

February 28, 2018

Dr. David Morens
National Institute of Allergy and Infectious Diseases
National Institutes of Health

Dear Dr. Morens,

We invite you to participate in a closed-door, invitation-only roundtable discussion on global health implementation gaps on March 19, 2018 hosted at the World Bank headquarters in Washington, D.C. Please find attached a draft agenda.

EcoHealth Alliance and the World Bank are analyzing lingering gaps in global initiatives to improve health security capacity. We are examining not the country level but rather the global stage of actors and their initiatives to address the core capacities outlined in prominent global health security frameworks. We suspect that behind the many and productive policy and programmatic efforts, there remain capacities that are insufficiently addressed, or not addressed at all. We also suspect that the core capacity frameworks themselves might be drawn too narrowly to account for the full triad of outbreak sources – natural, intentional, or accidental – and the distinct but complementary capacities needed to address them.

To evaluate these areas, we are undertaking an end-to-end identification of the core capacities needed for effective prevention through recovery from pandemics regardless of origin, and an assessment of which of these capacities are receiving insufficient attention. The purpose of this closed-door, invitation-only roundtable is to hear from global health security experts on these two topics. In advance of the meeting, we will share brief materials outlining our preliminary findings on both questions. These will form the basis of the discussion.

Please let us know if you are able to attend by way of RSVP by March 1st to Ellen Carlin at b6 or Catherine Machalaba at b6.

Thank you very much in advance,

b6

Ellen P. Carlin, DVM EcoHealth Alliance	William B. Karesh, DVM EcoHealth Alliance	Catherine Machalaba, MPH EcoHealth Alliance

From: Morens, David (NIH/NIAID) [E] [b6]
Sent: 7/5/2016 8:27:29 PM
To: Love, Sally [b6]; Dennis Carroll [b6]; Jonathan Epstein [b6]; Helgen, Kristofer M. [b6]; Murray, Suzan [b6]; Phillips, Anna J. [b6]; Larry Madoff [b6]
CC: 'Daniel Lucey (b6)' [b6]; Lawrence, Michael [b6]; Roberts, Angela [b6]; Sholts, Sabrina [b6]; Rivers, Meg [b6]; b6 [b6]; Louie, Julia [b6]
Subject: RE: Outbreak 35% package Advisory Review

Sally, thanks, this looks great from a quick scan of it. I am off to the airport in a few but will have chance to look it over while in b6

I had a bit of trouble printing out Appendix A b/c it didn't want to zoom in, but finally got it to work.

Pretty exciting, don't you think?

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
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☎ b6 (assistants: Kelley, Meaghan)
📠 301 496 4409
💻 b6

From: Love, Sally [mailto b6]
Sent: Tuesday, July 05, 2016 4:15 PM
To: Dennis Carroll b6 ; Jonathan Epstein b6 ; Helgen, Kristofer M. b6 ; Murray, Suzan b6 ; Phillips, Anna J. b6 ; Morens, David (NIH/NIAID) [E] b6 ; Larry Madoff b6
Cc: 'Daniel Lucey (b6)' b6 ; Lawrence, Michael b6 ; Roberts, Angela b6 ; Sholts, Sabrina b6 ; Rivers, Meg b6 ; b6 ; Louie, Julia b6
Subject: Outbreak 35% package Advisory Review

Good afternoon,

Attached for your consideration and review is the 35% draft script for the ***Outbreak!*** exhibit. The exhibit team has been working diligently to take the project from the Statement of Purpose phase to this draft stage.

The draft design can be accessed via Dropbox at: b6 b6 There are 2 versions in the folder: full resolution and reduced res. Also in the Dropbox folder is the **Education Outreach Programming** document.

As you read the script, you will see that the text is in both gray and black: black text is what visitors will read, i.e., the "text on the wall." This text is to be reviewed for accuracy as well as voice and tone. Gray text indicates ideas, concepts, graphics, and general placeholders. Review this text for appropriateness for the exhibit and accuracy. Gray text is not concerned with voice, tone, grammar, or style. Angela has provided a useful guide on how to review this script at the beginning.

This exhibit and related programming explores emerging diseases at the animal-human and environmental interface, examine the mysteries of how infectious disease pathogens grow and propagate, and explore the stories and science of zoonotic outbreaks. We are drawing upon the combined expertise of Smithsonian biologists and anthropologists, NZP veterinarians, physician Dr. Daniel Lucey, who has worked overseas in Ebola, MERS, influenza, and SARS outbreaks, and from outside experts from various public health agencies. The exhibit will open to the public in March, 2018.

Please review the documents and send me your comments and questions by COB July 19. If this is a problem, let me know if you need more time.

Thank you!
Sally

Sally Love Connell
Exhibit Developer, Office of Exhibits

National Museum of Natural History
10th Street & Constitution Avenue NW Rm 79
Washington, DC 20560
Mail: MRC 101 PO Box 37012
Washington, DC 20013-7012
b6

Smithsonian
National Museum of Natural History

From: Morens, David (NIH/NIAID) [E] [b6]
Sent: 1/19/2017 5:08:32 PM
To: Love, Sally [b6]; 'Dennis Carroll' [b6]; 'Jonathan Epstein' [b6]; Murray, Suzan [b6]; Phillips, Anna J. [b6]; 'Larry Madoff' [b6]
CC: 'Daniel Lucey (b6)' [b6]; Roberts, Angela [b6]; Sholts, Sabrina [b6]; Rivers, Meg [b6]; b6 [b6]; Louie, Julia [b6]; Blond, Kara [b6]; Chinen, Junko [CHINENJ@si.edu]
Subject: RE: Outbreak 65% package Advisory Review

Thanks, Sally. Lots to go over! But from a quick scan it looks really impressive.

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
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Bethesda, MD 20892-2520

☎ b6 (assistants: Kelley, Meaghan)
📠 301 496 4409
💻 b6

From: Love, Sally [mailto:b6]
Sent: Wednesday, January 18, 2017 4:14 PM
To: 'Dennis Carroll' b6; 'Jonathan Epstein' b6; Murray, Suzan

b6; Phillips, Anna J. b6; Morens, David (NIH/NIAID) [E] b6; 'Larry Madoff' b6
Cc: 'Daniel Lucey (b6)' b6; Roberts, Angela b6; Sholts, Sabrina b6; Rivers, Meg b6; 'b6; Louie, Julia b6; Blond, Kara b6; Chinen, Junko b6
Subject: Outbreak 65% package Advisory Review

Good afternoon,

Attached for your consideration and review is the 65% draft script for the ***Outbreak!*** exhibit. The exhibit team has been working diligently to take the project from the 35% to the 65% stage.

Via Dropbox, you can access these files:

- The 65% Script:
  b6

The 65% Design (design and look of the exhibit) and Graphics (panel and rail layouts) packages:

- Exhibit Design:
  b6
- Graphics:
  b6

The 65% Education and Outreach Public Programming Plan:

- b6

How to Read the Script (from page 4)
As you read the script, you will see that the text is in both gray and black:
Black text is what visitors will read, i.e., the "text on the wall." **This text is to be reviewed for accuracy as well as voice and tone**. Each block of text has an associated word count. Suggested revisions should be in tracked changes or added as a comment.
Gray text in brackets indicates graphics, such as photos, graphs, and illustrations. If you have any suggestions for images, please add them as a comment.
Gray text without brackets indicates text rough text, notes about the content to be written, and general placeholders as the section is developed. Review this text for appropriateness for the exhibit and accuracy. Gray text is not concerned with voice, tone, grammar, or style.

This exhibit and related programming explores emerging diseases at the animal-human and environmental interface, examine the mysteries of how infectious disease pathogens grow and propagate, and explore the stories and science of zoonotic outbreaks. We are drawing upon the combined expertise of Smithsonian biologists and anthropologists, NZP veterinarians, physician Dr. Daniel Lucey, who has worked overseas in Ebola, MERS, influenza, and SARS outbreaks, and from outside experts from various public health agencies. The exhibit will open to the public in May, 2018.

Please review the documents and send me your comments and questions by **COB February 2**. If this is a problem, let me know if you need more time.

Thank you, and happy reading!
Sally

Sally Love Connell
Exhibit Developer, Office of Exhibits

National Museum of Natural History
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Mail: MRC 101 PO Box 37012

Washington, DC 20013-7012
b6

Smithsonian
National Museum of Natural History

From: Morens, David (NIH/NIAID) [E] [b6] ([b6])
Sent: 8/5/2021 10:39:21 PM
To: Roberts, Rich [b6]
CC: Edward Holmes [b6]; Peter Daszak (b6) [b6]; Keusch, Jerry (b6) [b6]; Kessler, Robert (b6) [b6]
BCC: Morens, David (NIH/NIAID) [E] [b6] ([b6])
Subject: Re: CNN: Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt https://protect-au.mimecast.com/s/xCyoCvl1rKi7NAywGIQWvWo?domain=cnn.it

I think Shakespeare needs to be updated. "Killed all the lawyers" should perhaps be changed to "Kill all the politicians". But i repeat myself..... d

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

> On Aug 5, 2021, at 18:28, Roberts, Rich b6 wrote:
>
> Me too, but until we get rid of the politicians that may not happen.
> Rich
> Richard J. Roberts
> New England Biolabs
> 240 County Road
> Ipswich, MA 01938-2723
> USA
> Tel: b6
> Fax: (978) 412 9910
> email: b6
>
> **From:** Morens, David (NIH/NIAID) [E] b6
> **Sent:** Thursday, August 5, 2021 5:42 PM
> **To:** Edward Holmes b6
> **Cc:** Peter Daszak (b6) b6; Keusch, Jerry (b6) b6; Kessler, Robert (b6) b6; Roberts, Rich b6
> **Subject:** Re: CNN: Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt https://protect-au.mimecast.com/s/xCyoCvl1rKi7NAywGIQWvWo?domain=cnn.it
>
> **EXTERNAL SENDER**
>
> I take some pleasure in knowing that in the end they will all kick themselves for having wasted their time.
>
> Sent from my iPhone
> David M Morens
> OD, NIAID, NIH

On Aug 5, 2021, at 17:29, Edward Holmes b6 wrote:

Yes, I hope that means we can put that particular issue to bed.
Professor Edward C. Holmes FAA FRS
The University of Sydney

On 6 Aug 2021, at 7:26 am, Morens, David (NIH/NIAID) [E] b6 wrote:

<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

☎ b6 (assistant: Whitney Robinson)
📠 301 496 4409
💻 b6

<image002.jpg>

From: Folkers, Greg (NIH/NIAID) [E] b6
Sent: Thursday, August 5, 2021 4:18 PM
Subject: CNN: Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt https://cnn.it/3fzBbsp

Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt

By Katie Bo Williams, Zachary Cohen and Natasha Bertrand, CNN

Updated 9:02 AM ET, Thu August 5, 2021

*Washington (CNN)*US intelligence agencies are digging through a treasure trove of genetic data that could be key to uncovering the origins of the coronavirus -- as soon as they can decipher it.

This giant catalog of information contains genetic blueprints drawn from virus samples studied at the lab in Wuhan, China which some officials believe may have been the source of the Covid-19 outbreak, multiple people familiar with the matter tell CNN.

It's unclear exactly how or when US intelligence agencies gained access to the information, but the machines involved in creating and processing this kind of genetic data from viruses are typically connected to external cloud-based servers -- leaving open the possibility they were hacked, sources said.

Still, translating this mountain of raw data into usable information -- which is only one part of the intelligence community's 90-day push to uncover the pandemic's origins -- presents a range of challenges, including harnessing enough computing power to process it all. To do that, intelligence agencies are relying on supercomputers at the Department of Energy's National Labs, a collection of 17 elite government research institutions.

There's also a manpower issue. Not only do intelligence agencies need government scientists skilled enough to interpret complex genetic sequencing data and who have the proper security clearance, they also need to speak Mandarin, since the information is written in Chinese with a specialized vocabulary.

"Obviously there are scientists who are (security) cleared," one source familiar with the intelligence told CNN. "But Mandarin-speaking ones who are cleared? That's a very small pool. And not just any scientists, but ones who specialize in bio? So you can see how this quickly becomes difficult."

Officials conducting the 90-day review hope this information will help answer the question of how the virus jumped from animals to humans. Unlocking that mystery is essential to ultimately determining whether Covid-19 leaked from the lab or was transmitted to humans from animals in the wild, multiple sources told CNN.

Investigators both inside and outside the government have long sought genetic data from 22,000 virus samples that were being studied at the Wuhan Institute of Virology. That data was removed from the internet by Chinese officials in September 2019, and China has since refused to turn over this and other raw data on early coronavirus cases to the World Health Organization and the US.

The question for investigators is whether the WIV or other labs in China possessed virus samples or other contextual information that could help them trace the coronavirus' evolutionary history.

Two scientists who study coronaviruses told CNN they are skeptical that there is any genetic data either in the tranche of 22,000 samples or any other database from the WIV that scientists don't already know about.

"Basically in [a 2020 research paper published in Nature], the WIV talked about all the sequences they had up until a certain point in time -- it's what most scientists virologists believe, that's pretty much what they had," said Dr. Robert Garry, a virologist at the Tulane University School of Medicine.

A source familiar with the US investigation would neither confirm nor deny that any of the data pertaining to those 22,000 samples is among what US intelligence agencies are currently analyzing.

No 'smoking gun'

Sources familiar with the effort say filling in that missing genetic link won't be enough to definitively prove whether the virus originated in the lab at Wuhan or first emerged naturally. Officials will still need to piece together other contextual clues to determine the true origins of the pandemic.

But it is a critical puzzle piece that the Biden administration has been prioritizing.

"The most prized technical data in this context are genetic sequences, database entries and contextual information about the provenance of the samples and the time and context in which they were acquired -- information people would use to place them in a narrative of the origins of SARS, Covid," one source familiar with the investigation told CNN.

For now, senior intelligence officials still say that they are genuinely split between the two prevailing theories on the pandemic's origins, or some combination of both scenarios. CNN reported last month that senior Biden administration officials overseeing the 90-day review now believe the theory that the virus accidentally escaped from a lab in Wuhan is at least as credible as the possibility that it emerged naturally in the wild -- a dramatic shift from a year ago, when Democrats publicly downplayed the so-called lab leak theory.

Multiple sources told CNN that absent an unexpected windfall of new information, officials don't expect to uncover a "smoking gun" -- like intercepted communications, for example -- that would offer definitive proof for either theory. The Biden administration's 90-day push is predicated on the expectation that science, not intelligence will be the key.

Intelligence officials are tasked with addressing several "scientific knowledge gaps" about the virus' evolution, according to the collection guidance governing the 90-day push, distributed to more than a dozen agencies on June 11 by the Office of the Director of National Intelligence and obtained by CNN.

The memo instructs the intelligence community to "expand its collection" and consider data already in its possession to identify both the initial host of the coronavirus and any species that it may have passed through as it adapted to humans -- or to find as "any progenitor virus and/or virus that could serve as backbone for genetic engineering purposes."

But former Director of National Intelligence John Ratcliffe told CNN that the US intelligence community already had sufficient collection on the topic of Covid origins.

"Obviously the more, the better. But we've had extraordinary insight into this topic for many months, much more than has been declassified. Pretending we didn't is political theater and a classic example of a politician trying to buy time by using the IC as a scapegoat," he told CNN in a statement.

Digging into the science

That's where the genomic data from the Wuhan lab could come in.

The genetic code of a given virus is the signature that allows scientists to tell the difference between the Delta and Beta variants of the coronavirus, for example. It can also offer clues as to how the virus has adapted or mutated over time, including whether it shows signs of human manipulation -- a kind of genetic history.

Many scientists continue to believe that the most likely scenario is that the virus jumped from animals to humans naturally. But despite testing thousands of animals, researchers still haven't identified the intermediate host through which the virus passed as it adapted to humans.

But some researchers, intelligence officials and Republican lawmakers believe that researchers at the WIV might have genetically altered a virus in the lab, using a controversial kind of research known as "gain of function" that could have infected researchers who then spread it in their community.

It's also plausible that the initial infection took place naturally outside of the lab, perhaps while a scientist was collecting a sample from an animal in the wild, and that scientist then spread the virus unknowingly when he returned to the lab with the samples, multiple sources familiar with the intelligence explained.

"If it was the latter, it was likely brought into a lab to study because someone got sick ... which means there were an unknowable number of other people who were already sick," the source familiar with the probe said.

Understanding exactly which viruses researchers at the WIV were working on could provide important evidence for any one of these theories. It's one of the reasons that investigators on Capitol Hill and elsewhere have been keenly focused on the database that was taken offline in 2019.

But it might not prove anything definitively, sources familiar with the intelligence say. Even if scientists in the intelligence community are able to use the data from the lab to stitch together a complete genetic history that shows how the virus mutated, they might not have enough information about how it was handled by the Chinese lab to determine with a high level of confidence that it leaked.

"Despite having that complete history of variants, [officials might] lack the contextual information to make sense of it in a narrative way," the source familiar with the investigation explained.

"Even a complete sequence history is difficult to obtain. And doesn't really tell us anything about the origins of the pandemic itself without the context," this person added.

Some Republicans on Capitol Hill have jumped into the uncertainty with their own report claiming that "the preponderance of evidence suggests" the coronavirus was "accidentally" released from a lab in Wuhan in 2019 -- an assertion that goes far beyond the intelligence community's current view of the matter.

90 days -- and then what?

It's possible that at the end of Biden's 90-day push, the intelligence community won't have reached what's known as a "high-confidence" assessment as to the pandemic's origins. Administration officials have previously suggested to CNN that it's possible a second review could be ordered at the end of the 90 days.

A bipartisan group of lawmakers on the Senate Intelligence and Foreign Relations Committees earlier this week sent a letter urging the administration to continue to prioritize the hunt until such a judgment can be made in order to prevent future pandemics.

But the lawmakers also zeroed in on a related focus for intelligence officials probing the pandemic's origins: China's "efforts to conceal the severity and scope of the outbreak of the SARS-CoV-2 virus that caused the COVID-19 pandemic."

"We also believe that the investigation should address PRC efforts to prevent international inquiries into the origins of SARS-CoV-2, and other actions PRC authorities have taken to obscure the nature of the virus and its transmission," the lawmakers said.

Republican lawmakers in the House, meanwhile, have latched onto the theory that the virus escaped from a lab. GOP lawmakers in a report released Monday by Rep. Michael McCaul of Texas have claimed that "the preponderance of evidence suggests" the coronavirus was "accidentally" released from a lab in Wuhan in 2019.

Intelligence officials say it's still far too soon to say.

From: Morens, David (NIH/NIAID) [E] [b6
(b6)]
Sent: 11/23/2021 2:25:42 AM
To: Daniel Mira-Salama [b6]
CC: Karesh,William Bamberger [b6]; b6
BCC: Morens, David (NIH/NIAID) [E] [b6
(b6)]
Subject: Re: figure for World Bank report

Daniel, it is complicated……. The image is of the data in the Cell paper. We (Morens and Fauci) made the image and the Cell staff doctored it to look different enough that their doctoring would be enough to copyright their new version of it. What i sent you was what we submitted to Cell and was accepted by Cell.

If you want you could just cite it as unpublished, Morens and Fauci or something like that. d

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

> On Nov 22, 2021, at 21:13, Daniel Mira-Salama b6 wrote:
>
> Thank you so much David and Bill, this graph (18MB) should really work! Regarding the suggested citation "**Morens and Fauci, NIH, 2021**": is this coming from a publication, or does this reflect authorship? I could not find any paper on the internet with only those two authors.
> Most appreciated!
> Daniel
>
> **From:** Morens, David (NIH/NIAID) [E] b6
> **Sent:** Tuesday, November 23, 2021 12:24 AM
> **To:** Karesh,William Bamberger b6
> **Cc:** b6; Daniel Mira-Salama b6
> **Subject:** RE: figure for World Bank report
>
> [External]
>
> Billy, this is our updated version of what I just sent, made in June 2021. Let me know if this big file gets through to all.
>
> 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

☎ b6 (assistant: Whitney Robinson)
📠 301 496 4409
💻 b6

From: William B. Karesh b6
Sent: Monday, November 22, 2021 7:27 AM
To: Morens, David (NIH/NIAID) [E] b6
Cc: Catherine Machalaba b6; Daniel Mira-Salama b6
Subject: Re: figure for World Bank report

Thanks David !!!

If you could share the original with the three of us, Daniel can check to see if it will serve the purpose.

Thanks again,

Billy

On Nov 22, 2021, at 7:21 AM, Morens, David (NIH/NIAID) [E] b6 wrote:

Billy, this map was reconstructed from our original by the graphics department at the journal Cell. They did this purely so they could copyright it.

You could contact Cell, abd they will charge you. Or else we can give you the original with you can have for free. The original has all the same info and the same color code, but is less spread out vertically and differs in other minor ways

Let me know. My best to Peter and the gang. David

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

> On Nov 22, 2021, at 06:46, William B. Karesh b6 wrote:
>
> Dear David,
>
> Hope this finds you well.
>
> We are in the final stages of printer's proofs of a report on EID's in Asia we did for the World Bank. We want to include your EID map from 2020 (attached), but the printer's tell us that our version is not high enough resolution. Would you happen to have high resolution version that could be used?
>
> Hope you have a great Thanksgiving, all the best,
>
> Billy
>
> William B. Karesh, D.V.M
> Executive Vice President for Health and Policy
>
> EcoHealth Alliance
> 520 Eighth Avenue, Suite 1200
> New York, NY 10018 USA
>
> b6 (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

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

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From: Morens, David (NIH/NIAID) [E] [b6
(b6)]
Sent: 11/22/2021 12:23:43 PM
To: William B. Karesh [b6]
CC: Catherine Machalaba [b6]; Daniel Mira-Salama [b6]
BCC: Morens, David (NIH/NIAID) [E] [b6
(b6)]
Subject: Re: figure for World Bank report
Attachments: PastedGraphic-1.tiff

PS, you might be able to get Cell to let you use it for free, as it is for a good cause, a non profit entity, and is good advertising for Cell. d

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

> On Nov 22, 2021, at 07:21, Morens, David (NIH/NIAID) [E] b6 wrote:
>
> Billy, this map was reconstructed from our original by the graphics department at the journal Cell. They did this purely so they could copyright it.
>
> You could contact Cell, abd they will charge you. Or else we can give you the original with you can have for free. The original has all the same info and the same color code, but is less spread out vertically and differs in other minor ways
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> David M Morens
> OD, NIAID, NIH
>
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>> Hope you have a great Thanksgiving, all the best,
>>
>> Billy

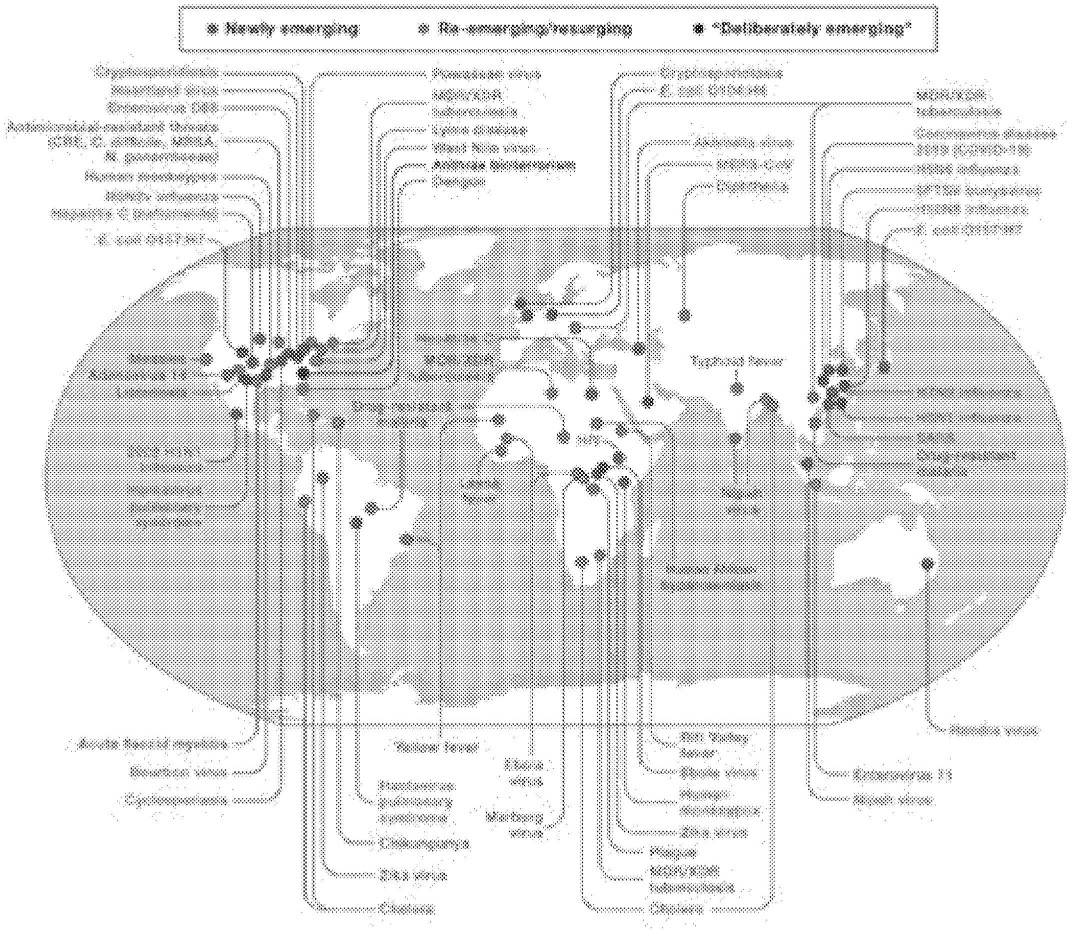
William B. Karesh, D.V.M
Executive Vice President for Health and Policy

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018 USA
b6 (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

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


Newly emerging
Re-emerging/resurging
"Deliberately emerging"
Cryptosporidiosis
Heartland virus
Enterovirus D68
Antimicrobial-resistant threats (CRE, C. difficile, MRSA, N. gonorrhoeae)
Human monkeypox
H3N2v influenza
Hepatitis C (heterosexual)
E. coli O157:H7
Powassan virus
MDR/XDR tuberculosis
Lyme disease
West Nile virus
Anthrax bioterrorism
Dengue
Cryptosporidiosis
E. coli O104:H4
Alkhurma virus
MERS-CoV
Diphtheria
MDR/XDR tuberculosis
Coronavirus disease 2019 (COVID-19)
H5N6 influenza
SFTSV bunyavirus
H10N8 influenza
E. coli O157:H7
Measles
Adenovirus 14
Listeriosis
2009 H1N1 influenza
Hantavirus pulmonary syndrome
Hepatitis C
MDR/XDR tuberculosis
Drug-resistant malaria
Lassa fever
HIV
Typhoid fever
Nipah virus
Human African trypanosomiasis
H7N9 influenza
H5N1 influenza
SARS
Drug-resistant malaria
Acute flaccid myelitis
Bourbon virus
Cyclosporiasis
Yellow fever
Hantavirus pulmonary syndrome
Chikungunya
Zika virus
Cholera
Ebola virus
Marburg virus
Rift Valley fever
Ebola virus
Human monkeypox
Zika virus
Plague
MDR/XDR tuberculosis
Cholera
Hendra virus
Enterovirus 71
Nipah virus

From: Morens, David (NIH/NIAID) [E] [b6
b6]
Sent: 1/31/2020 9:36:14 PM
To: Ellen Carlin [b6]
Subject: FW:
Attachments: [Untitled].pdf

Ellen, it wouldn't sign electronically, so I signed the old way, scanned and send as an attachment. Hope this works

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

☎ b6 (assistants: Kimberly Barasch; Whitney Robinson)
📠 301 496 4409
💻 b6

From: HP 3E05B-LJM775 Scanner <HP3E05B-LJM775-Sanner@nih.gov>
Sent: Friday, January 31, 2020 4:05 PM
To: Morens, David (NIH/NIAID) [E] b6
Subject:

THE LANCET
Global Health

Author statements

Please insert the relevant text under the subheadings below. A completed form must be signed by all authors. Please note that we will accept hand-signed and electronic (typewritten) signatures. Please complete multiple forms if necessary, and upload the signed copy with your submission, scan and email to: globalhealth@lancet.com, or fax to: +44 1865 853021.

Manuscript title:

Corresponding author:

Article type:

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Does your manuscript have a reference number? No ☑ Yes ☐ If yes, enter number here:

Does your manuscript have a handling editor? No ☑ Yes ☐ If yes, enter name here:

Authors' contributions

Please insert here the contribution each author made to the manuscript—eg, literature search, figures, study design, data collection, data analysis, data interpretation, writing etc. If all authors contributed equally, please state this. The information provided here must match the contributors' statement in the manuscript.

All authors contributed equally to this text.

THE LANCET
Global Health

Role of the funding source

Please disclose any funding sources and their role, if any, in the writing of the manuscript or the decision to submit it for publication. Examples of involvement include: data collection, analysis, or interpretation; trial design; patient recruitment; or any aspect pertinent to the study. Please also comment whether you have been paid to write this article by a pharmaceutical company or other agency. If you are the corresponding author, please indicate if you had full access to all the data in the study and had final responsibility for the decision to submit for publication. The information provided here must match the role of the funding source statement in the manuscript.

The Smith Richardson Foundation funded the study on which this Comment is based (SRF Grant #2017-1534). The Foundation was not involved in the execution of the study nor in the drafting of this manuscript. Neither the Foundation nor any other agency has paid the authors to write this piece.

I (Ellen P. Carlin) am the corresponding author and had full access to all data in the study and final responsibility to submit this manuscript for publication.

Conflicts of interest

Please complete the ICMJE conflict of interest form, which is available at http://download.thelancet.com/flatcontentassets/authors/icjme-coi-form.pdf. Please ensure that a conflict of interest statement is included at the end of the manuscript, which matches what is declared on the ICMJE conflict of interest form.

Patient consent (if applicable) - completion of this section is mandatory for Case Reports, Clinical Pictures, and Adverse Drug Reactions. Please sign below to confirm that all necessary consents required by applicable law from any relevant patient, research participant, and/or other individual whose information is included in the article have been obtained in writing. **The signed consent form(s) should be retained by the corresponding author and NOT sent to *The Lancet Global Health*.**

I agree with: the plan to submit to *The Lancet Global Health*; the contents of the manuscript; to being listed as an author; and to the conflicts of interest statement as summarised. I have had access to all the data in the study (for original research articles) and accept responsibility for its validity.

Title and name: Ellen P. Carlin	Highest degree: DVM	Signature: b6	Date: 1/31/20
Title and name: Catherine Machalaba	Highest degree: MPH	Signature:	Date:
Title and name: Kanya C. Long	Highest degree: PhD	Signature:	Date:
Title and name: Franck C. J. Berthe	Highest degree: DVM	Signature:	Date:
Title and name: David Morens	Highest degree: MD	Signature: b6	Date: 1/31/2020
Title and name: William B. Karesh	Highest degree: DVM	Signature:	Date:
Title and name:	Highest degree:	Signature:	Date:
Title and name:	Highest degree:	Signature:	Date:
Title and name:	Highest degree:	Signature:	Date:
Title and name:	Highest degree:	Signature:	Date:

Corresponding author declaration

I ....[Signature].........., the corresponding author of this manuscript, certify that the contributors' and conflicts of interest statements included in this paper are correct and have been approved by all co-authors.

From: Morens, David (NIH/NIAID) [E] [b6
(b6]

Sent: 12/23/2019 7:48:56 PM

To: Ellen Carlin [b6]

BCC: Morens, David (NIH/NIAID) [E] [b6
(b6]

Subject: Re: Journal contact?

Thanks, sounds good! Yes i am in b6 scaling down too. It's almost spring weather here, thank you global warming. I will be checking emails periodically

Please do feel free to remind b6 to send contact info, if you do connect with her. She may have the same email but i haven't tried yet.

d

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

> On Dec 23, 2019, at 13:27, Ellen Carlin b6 wrote:
>
> Thanks so much, David.... Not ignoring you, I'm just scaling down activity now for the holidays. I think we will go ahead and try submitting to Lancet as you suggest—I'll pull together a cover letter after the new year and make sure I've got everything formatted correctly. We will see where that gets us.
>
> I actually don't have b6 new address either! I'll mention it to her that we both would like it!!
>
> Have a great holiday in the meantime... have a wonderful time in b6!
>
> **Ellen P. Carlin, DVM**
> *Senior Health and Policy Specialist*
>
> EcoHealth Alliance
> b6 (direct)
> (mobile)
> b6
> www.ecohealthalliance.org
>
> *Research Associate*, Smithsonian Conservation Biology Institute
> *Adjunct Research Scientist*, Columbia University National Center for Disaster Preparedness
> *Courtesy Lecturer*, Cornell University College of Veterinary Medicine
>
> *EcoHealth Alliance leads cutting-edge scientific research into the critical connections between human and wildlife health and delicate ecosystems. With this science, we develop solutions that prevent pandemics and promote conservation.*

From: "Morens, David (NIH/NIAID) [E]" b6
Date: Wednesday, December 18, 2019 at 12:15 PM
To: Ellen Carlin b6
Subject: RE: Journal contact?

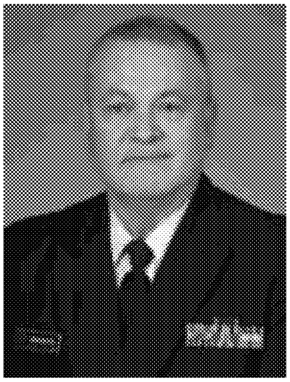
Ellen, I can certainly do as you suggest but it might be worth rethinking with Billy and others to rethink what journals might be the best. A number of journals have recently been publishing on pandemic preparedness, so some of those might be considered too. Just thinking broadly.

I have written a number of NEJM Perspective articles over the years, one just a month or so ago (see attached), and my sense is this may be of less interest to them, but maybe not, it can't hurt to try. If we do, then I might suggest reorienting the text a bit since the primary readership of NEJM is practicing physicians, so there has to be something in it for them. JID is perhaps more likely to be interested, and there must be a lot of alternatives. Also, just because Lancet GH didn't respond to Billy may not mean much: editors are always busy and way behind on answering emails, it's a chronic problem.

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

☎ b6 (assistants: Kimberly Barasch; Whitney Robinson)
301 496 4409
b6



From: Ellen Carlin b6
Sent: Tuesday, December 17, 2019 2:12 PM
To: Morens, David (NIH/NIAID) [E] b6
Subject: Re: Journal contact?

Oh yes! Billy did—he reached out to his Lancet contact twice, but got no response… ☹

I would be happy to reach out to either NEJM or JID and mention that you suggested it! That's no problem. NEJM has a nice category called "Perspective" with 1,200 word limit (we're at 765 of core text), 5 reference limit (we have 5), and usually include one figure or table (we have 1). So that is helpful! They recommend a "presubmission inquiry" when authors are unsure of the suitability of their manuscript for publication; they have an online system for that but perhaps they would be open to direct email contact? I don't want to use up any capital you might have with the journals unless you feel it's worthwhile!

Ellen

From: "Morens, David (NIH/NIAID) [E]" b6
Date: Tuesday, December 17, 2019 at 11:03 AM
To: Ellen Carlin b6
Subject: RE: Journal contact?

Hi Ellen, first I need to catch up as I had thought Billy was going to first run it by Lancet Global Health. Did he do that? If so, I may have missed that.

If not, I could certainly run it by NEJM or JID (one at a time). However, we should probably first put it in a format that fits one of theirs.

Although either way might work, I think the best would be for YOU as the first author to run it by them, perhaps mentioning that I had suggested it. That avoids putting them in the position of saying no to a friend if it doesn't fit their needs.

Once I hear from you about these several things, I can check the 2 journals to get up to date on their ms. categories, lengths and etc.

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

☎ b6 (assistants: Kimberly Barasch; Whitney Robinson)
📠 301 496 4409
💻 b6

From: Ellen Carlin b6
Sent: Monday, December 16, 2019 10:53 AM
To: Morens, David (NIH/NIAID) [E] b6
Subject: Re: Journal contact?

Hi David! That's great! Would you be interested in sharing the paper informally with NEJM or JID to see if they'd be interested? Or I can do it and cc you—whatever is easiest and most sensible. My contacts are at the vet journals and that won't be helpful!

I hear from our friend b6 that they've already had a fair amount of snow in b6, that b6 b6, and that she's b6 (b6, I guess to retain some sanity ☺).

Ellen

From: "Morens, David (NIH/NIAID) [E]" b6
Date: Wednesday, December 11, 2019 at 5:30 PM
To: Ellen Carlin b6
Subject: Re: Journal contact?

Ellen, i have contacts at nejm, jid, and several other journals but not lancet. b6 left and although i knew b6 slightly, i don't think i can do any good there.

I agree: go big. Sometimes you hit a bulls eye, other times not

But your work is good, and it will be published, read, and considered. I mean, after all, this is important stuff

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

> On Dec 11, 2019, at 15:03, Ellen Carlin b6 wrote:
>
> Hi David! I hope all is well.
>
> I wanted to ask if you know any editors at The Lancet who might be receptive to an email from you about our paper (attached)? Billy tried an editor he knows there but has received no response. We thought a pre-submission inquiry would be better than a cold submission.
>
> I also thought if The Lancet is a no-go, perhaps you might have a contact at NEJM or another high-impact journal? NEJM has a Commentary article type. I figure we should go big if we can!
>
> Thanks!!
> Ellen
>
> **Ellen P. Carlin, DVM**
> *Senior Health and Policy Specialist*
>
> EcoHealth Alliance
> b6 (direct)
> (mobile)
> b6
> www.ecohealthalliance.org
>
> *Research Associate*, Smithsonian Conservation Biology Institute
> *Adjunct Research Scientist*, Columbia University National Center for Disaster Preparedness
> *Courtesy Lecturer*, Cornell University College of Veterinary Medicine

EcoHealth Alliance leads cutting-edge scientific research into the critical connections between human and wildlife health and delicate ecosystems. With this science, we develop solutions that prevent pandemics and promote conservation.

From: Ellen Carlin [b6]
Sent: 2/26/2020 3:27:55 PM
To: Morens, David (NIH/NIAID) [E] [b6]
(b6)
Subject: Re: BMJ-2020-055182 Manuscript Decision Editorials

Hmm. Yes that could be.

"All exhibits must be editable; that is, they must not be simply graphic renditions of your exhibits."

Circular language indeed! But I do think that they want to restyle your figures so they have a certain look. What I might do is go ahead and create a longer-form piece with more of our data and analysis (I already got it going). We can then pull the trigger on Health Affairs, or decide to go elsewhere.

I'm excited for your NEJM piece, well done!

On Feb 26, 2020, at 10:18 AM, Morens, David (NIH/NIAID) [E] b6 wrote:

E, not sure what the "figures being editable" means, but my suspicion is that they, like some journals, want to tweak your figure so they can copyright it.

<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
☎ b6 (assistants: Kimberly Barasch; Whitney Robinson)
📠 301 496 4409
💻 b6

<image002.jpg>

From: Ellen Carlin b6
Sent: Wednesday, February 26, 2020 10:15 AM
To: Morens, David (NIH/NIAID) [E] b6
Cc: Franck Berthe b6; Kanya Long b6; Catherine Machalaba b6; Billy Karesh b6
Subject: Re: BMJ-2020-055182 Manuscript Decision Editorials

David, that's great news! Thanks for that shout-out in your great article. Nice to see my name in NEJM:)

I don't know Health Affairs' reputation for fast turn-around but will see what I can find out online. I'm reading through their instructions and they require all figures to be editable, which is not going to work. Our figures were designed and baked over a year ago. I'm' not sure if I can get around that, let me keep researching their requirements. We may need a Plan B (or C, D, E...)

On Feb 26, 2020, at 9:46 AM, Morens, David (NIH/NIAID) [E] b6 wrote:

Ellen, FYI, we have just cited your original report in a paper coming out today (still embargoed), co-authored with Peter D, see the reference section (ref. 4) in the attached. Thus your work is now being cited as important for pandemic planning vis a vis the coronavirus epidemic. Good work for sure, Let's get it into print. Health Affairs is good, will they potentially publish quickly?

<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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☎ b6 (assistants: Kimberly Barasch; Whitney Robinson)
📠 301 496 4409
💻 b6

<image002.jpg>

From: Ellen Carlin b6
Sent: Wednesday, February 26, 2020 9:37 AM
To: Franck Berthe b6
Cc: Kanya Long b6; Morens, David (NIH/NIAID) [E] b6; Catherine Machalaba b6; Billy Karesh b6
Subject: Re: BMJ-2020-055182 Manuscript Decision Editorials

Hi everyone, thanks for weighing in and for all your encouragement! I agree we have a unique product here, and that makes it hard to nail the right platform. We are inherently swimming against the tide given that our study finding is that no one cares about our finding (prevention and recovery)!

I am leaning toward Health Affairs and, since you can have up to 2000 words for Data Watch, I will spend an hour or so today to add a little more meat on the bones, giving us a chance to present a little more detail about our findings. We will still have the 750 word piece to fall back on if we need to submit again elsewhere. If you would like to see the updated piece before I submit let me know; otherwise I will proceed as planned and try to submit by tomorrow.

Ellen

On Feb 26, 2020, at 5:10 AM, Franck Cesar Jean Berthe b6 wrote:

Same on my side
I will support your decision
It is the time now
:-)

From: Kanya Long b6
Sent: Tuesday, February 25, 2020 5:33:42 PM
To: Morens, David (NIH/NIAID) [E] b6
Cc: Ellen Carlin b6; Catherine Machalaba b6; Franck Cesar Jean Berthe b6; Billy Karesh b6
Subject: Re: BMJ-2020-055182 Manuscript Decision Editorials

[External]
Ellen,

Supportive of whatever direction you think is best and can contribute if you choose to expand the piece.

I agree that the time is right.

Kanya

On Tue, Feb 25, 2020 at 2:26 PM Morens, David (NIH/NIAID) [E] b6 wrote:

> Just saw this and i think all options are viable. Whichever, this is/should be the perfect time (at the beginning of corona chaos) to think ahead. The whole world is focusing myopically on case and death counts. We need big picture voices and a perspective that sees the universe of things. d
>
> Sent from my iPhone
> David M Morens
> OD, NIAID, NIH
>
> > On Feb 25, 2020, at 16:38, Ellen Carlin b6 wrote:
> >
> > Hi everyone,
> >
> > This was nice of the editor to give us this kind of feedback. We took a chance on submitting our piece as an Editorial to BMJ because the Analysis is a longer piece at 1800-2000 words, and Original Research more involved still. Our paper is about 750 words. We did this as a short-form piece to begin with so it would be done quickly, alas...!
> >
> > Let me propose a few options, in no particular order, and get your feedback:

1. **Expand the paper** into a longer form analysis, suitable for submitting to BMJ or another journal as a more involved research/analysis piece.

2. **Keep the paper as is**, and submit elsewhere. I would suggest Health Affairs as a good next option; their “DataWatch” article type is 2000 words or less, up to 6 exhibits; these are short papers that highlight data that "speak for themselves" relative to important policy issues or topics. They should shed light on some important question and be "worth knowing." They do not typically test hypotheses, rely on sophisticated statistical methods, or include lengthy policy discussions. We aim to present new data or new analyses of existing data that are reliable and credible and that promote understanding among nonexperts on important, policy-relevant topics. We encourage work based on underused or new data sources.

If you want to submit as it but not to Health Affairs, please suggest a journal and article type.

3. **Take BMJ’s suggestion to redraft into a rapid response** to their coronavirus coverage.

All comments welcome.
Thank you,
Ellen

On Feb 24, 2020, at 10:48 AM, BMJ <onbehalfof@manuscriptcentral.com> wrote:

24-Feb-2020
BMJ-2020-055182 entitled "Global health security: targeting investments toward unmet needs"

Dear Dr. Carlin,

Thank you for sending us your editorial. We read it with interest but decided against publication and I'm sorry to disappoint you.

The piece falls somewhere between research (you report methods) and Analysis (a long form article type that includes some data), but doesn't in its current form fit either. BMJ editorials don't report original findings.

Your bottom line message is clear however, and you might consider writing a rapid response to any recent content about covid - 19, discussing the lack of preventive initiatives globally. On line rapid responses are well read and a selection are published in full as letters. I'm sure you appreciate that I can't prejudge that selection

You'll find all our coverage of the covid - 19 outbreak here: https://www.bmj.com/coronavirus

Sorry once again that I can't offer you an editorial, and thank you for your interest in the BMJ.

Yours sincerely,

Alison Tonks
Clinical Editor, BMJ
atonks@bmj.com

> If you elected during submission to send your article on to another journal the article will be transferred in 5 working days. If you intend to appeal against this decision please notify us before then.
> The journal(s) (if any) you have selected at submission are: BMJ Global Health
> If you want to speed up or stop this onward transmission please email the editorial office: papersadmin@bmj.com

<NEJM Pandora 02 26 2020.pdf>

From: Ellen Carlin [b6]
Sent: 2/25/2020 9:27:24 PM
To: b6
CC: Catherine Machalaba [b6]; b6; Franck Berthe [b6]; Morens, David (NIH/NIAID) [E] [b6 b6]; Billy Karesh [b6]
Subject: Re: BMJ-2020-055182 Manuscript Decision Editorials

Dr. Tonks,

Thank you so much for your prompt and very helpful reply. We realized that our piece wasn't a perfect fit for any of your categories, and we appreciate your feedback on that point.

I will speak with my co-authors about redirecting our work into a rapid response that would be appropriate for COVID-19. Thanks very much for that suggestion.

Sincerely,
Ellen

Ellen P. Carlin, DVM
Research Fellow

EcoHealth Alliance
b6 (mobile)
www.ecoheathalliance.org
b6

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Sorry once again that I can't offer you an editorial, and thank you for your interest in the BMJ.

Yours sincerely,

Alison Tonks
Clinical Editor, BMJ
atonks@bmj.com

If you elected during submission to send your article on to another journal the article will be transferred in 5 working days. If you intend to appeal against this decision please notify us before then.
The journal(s) (if any) you have selected at submission are: BMJ Global Health
If you want to speed up or stop this onward transmission please email the editorial office:
papersadmin@bmj.com

From: Ellen Carlin [b6]
Sent: 1/31/2020 8:44:18 PM
To: Billy Karesh [b6]; Catherine Machalaba [b6]; Kanya Long [b6]; Franck Berthe [b6]; Morens, David (NIH/NIAID) [E] [b6] ([b6])
CC: Amanda Andre [b6]
Subject: Action required: global health security manuscript
Attachments: Carlin et al Building resilience Draft 1.31.19 v2.docx

Dear Team,

I hope your 2020 is off to a great start!

I'm writing to give an update on our global health security paper. b6 which delayed things a bit, but we are ready to submit now. Attached is the version of the manuscript we will submit. Billy and I have updated the lead to reflect current events.

We're going to give *The Lancet Global Health* a try. **Please find attached an author contribution form that Kenya, Franck, and David need to sign electronically. Amanda is helping get signatures from Billy and Catherine. If you can please turn this around by Monday Feb 3, I can submit that day.** I have indicated that all authors contributed equally; if you prefer to word your contribution differently, please do so.

Some of you may not be aware that December 31 was my last day at EcoHealth Alliance. I am running my own consulting gig now and have a lot of exciting projects in store that I look forward to sharing with you as they develop. I am still affiliated with EHA as a Research Fellow.

Thanks again for all of your efforts!

Best wishes,
Ellen

Title
Global health security: targeting investments toward unmet needs

Authors

Ellen P. Carlin, DVM
EcoHealth Alliance, 460 West 34th Street, New York, NY 10001

Catherine Machalaba, MPH
EcoHealth Alliance, 460 West 34th Street, New York, NY 10001

Kanya C. Long, PhD
University of California San Diego, 6304 Atkinson Hall, La Jolla, CA 92093
Dr. Long was a fellow at the World Bank at the time of the study.

Franck C. J. Berthe, DVM
World Bank, 1818 H Street, NW, Washington, DC 20433

David Morens, MD
National Institutes of Allergy and Infectious Diseases, 5601 Fishers Lane, Bethesda, MD 20892

William B. Karesh, DVM
EcoHealth Alliance, 460 West 34th Street, New York, NY 10001
b6

As another novel coronavirus has predictably emerged in humans and spread quickly into a pandemic and the second largest Ebola outbreak in history continues to simmer in the Democratic Republic of the Congo, a global reckoning is due. Understanding why especially dangerous pathogens are emerging with increasing frequency continues to take a back seat to response and response preparedness. This crisis-centered approach is bound to keep us trapped in a perpetual cycle of panic and neglect.[1]

To document this dynamic and reveal its extent, we collated the functions needed for effective defenses against major biological incidents and assessed which areas are receiving insufficient attention.[2] Our organizing construct included four "pillars"—prevent, detect, respond, and recover. Through extensive review of the scientific and gray literature, and with expert input via roundtable discussions, interviews, and peer review, we identified 60 functions that undergird these four pillars and to which countries must have sufficient access to optimize their health security. We also identified 22 major initiatives global in architecture or oversight and designed to support the development of local, country, or regional capacities. We then mapped the initiatives to the pillars to reveal areas of global neglect (Figure 1).

[Insert Figure 1 here]

Activities directed at prevention are minimal in number. We defined prevention as a multi-dimensional concept that captures prevention of 1) epidemics at pre-initiation (*before* pathogens emerge into people); 2) bioweapons development and deployment; and 3) accidental releases of pathogens, such as from laboratories. The majority of funded efforts do not address prevention at all, and even fewer deal with the underlying risk factors that lead to epidemic emergence. Most programs view epidemic prevention narrowly (i.e., preventing small outbreaks from growing) rather than addressing what drives outbreaks to occur in the first place. The latter entails politically challenging decisions about societal priorities ranging from land use and agricultural practices to urbanization and climate change.

Few efforts address recovery, and the very inclusion of recovery as a core pillar in our construct is novel among frameworks. (A recent World Bank publication designed to strengthen human, animal, and environmental public health systems at their interface is one of the only examples, and has not yet been adopted into global efforts.[3]) Since strong recovery from one epidemic event can pre-empt future outbreaks, systematic and sustained attention to this pillar is badly needed.

We also found two strategic points of concern. One is that, by current design, global health security implementation efforts and their attached financing tackle particular objectives—vaccine development, regional surveillance, training—while no governance effort or strategic inter-institutional guiding framework aligns them toward a commonly defined set of goals. The other is that there seems to be a tendency to view biothreats in terms of the single end consequence that worries people the most: our own health. The problem with this approach is that it drives reverse engineering of structures and decisions to deal with only human health consequences, and forward engineering of response activity tailored to human health needs. Defense, environment, and animal health are often treated as needs outside of human health security frameworks, even though their full inclusion would restore the breadth of the health *security* concept. Ebola in DRC exists at this nexus: viral circulation in an ecological environment that supports spillover and a fragile, violent, and conflict-ridden setting that hampers both prevention and response.

The international community's approaches diverge from what may be fundamentally needed to grapple with the new epidemic threat reality and ultimately stave off its worst consequences. Some of the functions we identified require less investment than others to achieve great benefit—addressing drivers of epidemics is a case in point. The World Bank estimates that an annual expenditure of ~\$3·4 billion to prevent one in every eight severe pandemics will save \$30 billion.[4] Assessing cost-benefits and returns on investment of particular activities is precisely what a unifying strategic framework could do. The release of the 2019 Global Health Security Index, which finds among 195 countries assessed an average preparedness score of 40·2 out of a possible 100, may provide new impetus to act.[5] A substantial but feasible rethinking of the orientation of global and national investment is achievable within the major guiding frameworks and efforts that are already underway. As the Global Health Security Agenda embarks on its second five years, this is a timely opportunity to strengthen neglected lines of effort and support a holistic approach to dealing with the global health challenge of epidemic disease.

Acknowledgements

This work was funded by the Smith Richardson Foundation.

Author Contributions

All authors contributed equally to this text.

References

1. World Bank. *From panic and neglect to investing in health security: Financing pandemic preparedness at a national level.* Washington, DC: World Bank;2017.
2. Carlin EP, Machalaba C, Berthe FCJ, Long KC, Karesh WB. *Building resilience to biothreats: An assessment of unmet core global health security needs.* New York, NY: EcoHealth Alliance;2019.
3. World Bank. *Operational framework for strengthening human, animal and environmental public health systems at their interface.* Washington, DC: World Bank Group;2018.
4. World Bank. *People, pathogens, and our planet: The economics of one health, volume 2.* Washington, DC: World Bank;June 2012.
5. Nuclear Threat Initiative. *Global health security index: Building collective action and accountability.* Washington, DC: Nuclear Threat Initiative;2019.

Figure 1: Mapping of global health security initiatives to core needs

Initiative	[redacted]
Australia Group	[redacted]
CEPI*	[redacted]
CP3	[redacted]
Gavi†	[redacted]
GLASS	[redacted]
GLEWS‡	[redacted]
Global Financing Facility	[redacted]
Global Fund	[redacted]
GHSA§	[redacted]
GHSI	[redacted]
Global Partnership	[redacted]
International Reagent Resource	[redacted]
OIE WAHIS	[redacted]
Proliferation Security Initiative	[redacted]
World Bank PEF‖	[redacted]
World Bank Pandemic Preparedness Plan	[redacted]
WEF Epidemics Readiness Accelerator	[redacted]
WHO CFE	[redacted]
WHO Global Influenza Programme	[redacted]
WHO GOARN	[redacted]
WHO Health Emergencies Program	[redacted]
WHO R&D Blueprint	[redacted]

Major global health security initiatives were mapped to four pillars of global health security activity: prevent, detect, respond, and recover, revealing a predominance of focus on detection and response. Figure reprinted from Carlin EP, Machalaba C, Berthe FCJ, et al. *Building Resilience to Biothreats: An assessment of unmet core global health security needs*. EcoHealth Alliance. 2019.

*Committed to funding through Phase 2 investigational stockpiles; not funded for Phase 3 or linked to a system for procurement, distribution, or dispensing. †To the extent that Gavi covers Prevent it is for the specific prevention of yellow fever spillover through vaccination in high-risk areas; does not address drivers. ‡Predominantly focused on risk monitoring and information alerts for Rift Valley fever in livestock. §Addresses prevention in the sense of containing outbreaks; attention to and capacity for spillover risk management is extremely limited. ‖Disbursement of funds only applies to select viruses.

From: Ellen Carlin [b6]
Sent: 2/4/2020 6:17:27 PM
To: Morens, David (NIH/NIAID) [E] [b6
(b6]
Subject: Re: Action required: global health security manuscript

Yeah, it was kind of big news for me, too! We can catch up when I see you next. I'm actually quite happy with the way things are shaking out, though. Despite some drawbacks, there are benefits to being self-employed! b6 b6

I had NO idea about b6. Thats terrifying! b6 and I have been playing phone tag. I do know she's coming in February and plan to see her when she's here. I think between b6 b6, she will be back pretty regularly.

On Jan 31, 2020, at 4:26 PM, Morens, David (NIH/NIAID) [E] b6 wrote:

Ellen, WOW, that's shocking news. All the best in this new venture. No, I didn't know that. Keep in touch as things go forward. Assume you will b6?

You may have heard that b6 b6. Hope we can all get together. b6.

Also, I didn't find any form to sign as an attachment.

<image001.gif>

David M. Morens, M.D.
CAPT, United States Public Health Service
Senior Advisor to the Director
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📠 301 496 4409
💻 b6

<image002.jpg>

From: Ellen Carlin b6
Sent: Friday, January 31, 2020 3:44 PM
To: Billy Karesh b6; Catherine Machalaba b6; Kanya Long b6; Franck Berthe b6; Morens, David (NIH/NIAID) [E] b6
Cc: Amanda Andre b6
Subject: Action required: global health security manuscript

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Thanks again for all of your efforts!

Best wishes,
Ellen

From: Morens, David (NIH/NIAID) [E] [b6
b6]
Sent: 12/18/2019 6:32:04 PM
To: Ellen Carlin [b6]
Subject: RE: Journal contact?

Ellen, I forgot to mention that around the time they were moving I DID email b6 but said no need to reply now, I know this is a chaotic time, but when you have time later on let me know your contact info. No word so far, so I won't bug her. Will be in b6 next week to see b6 b6!, also b6 and b6, and then off to b6 to be with b6 b6

David

David M. Morens, M.D.
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☎ b6 (assistants: Kimberly Barasch; Whitney Robinson)
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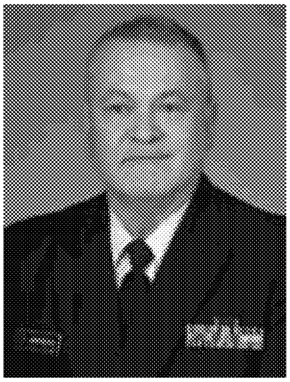
💻 b6



From: Ellen Carlin b6
Sent: Tuesday, December 17, 2019 2:12 PM
To: Morens, David (NIH/NIAID) [E] b6
Subject: Re: Journal contact?

Oh yes! Billy did—he reached out to his Lancet contact twice, but got no response… ☹

I would be happy to reach out to either NEJM or JID and mention that you suggested it! That's no problem. NEJM has a nice category called "Perspective" with 1,200 word limit (we're at 765 of core text), 5 reference limit (we have 5), and usually include one figure or table (we have 1). So that is helpful! They recommend a "presubmission inquiry" when authors are unsure of the suitability of their manuscript for publication; they have an online system for that but perhaps they would be open to direct email contact? I don't want to use up any capital you might have with the journals unless you feel it's worthwhile!

Ellen

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OD, NIAID, NIH

On Dec 11, 2019, at 15:03, Ellen Carlin b6 wrote:

Hi David! I hope all is well.

I wanted to ask if you know any editors at The Lancet who might be receptive to an email from you about our paper (attached)? Billy tried an editor he knows there but has received no response. We thought a pre-submission inquiry would be better than a cold submission.

I also thought if The Lancet is a no-go, perhaps you might have a contact at NEJM or another high-impact journal? NEJM has a Commentary article type. I figure we should go big if we can!

Thanks!!
Ellen

Ellen P. Carlin, DVM
Senior Health and Policy Specialist

EcoHealth Alliance
b6 (direct)
(mobile)
b6
www.ecohealthalliance.org

Research Associate, Smithsonian Conservation Biology Institute
Adjunct Research Scientist, Columbia University National Center for Disaster Preparedness
Courtesy Lecturer, Cornell University College of Veterinary Medicine

EcoHealth Alliance leads cutting-edge scientific research into the critical connections between human and wildlife health and delicate ecosystems. With this science, we develop solutions that prevent pandemics and promote conservation.

From: Morens, David (NIH/NIAID) [E] [b6 b6]
Sent: 2/26/2020 2:46:49 PM
To: Ellen Carlin [b6]; Franck Berthe [b6]
CC: Kanya Long [b6]; Catherine Machalaba [b6]; Billy Karesh [b6]
Subject: RE: BMJ-2020-055182 Manuscript Decision Editorials
Attachments: NEJM Pandora 02 26 2020.pdf

Ellen, FYI, we have just cited your original report in a paper coming out today (still embargoed), co-authored with Peter D, see the reference section (ref. 4) in the attached. Thus your work is now being cited as important for pandemic planning vis a vis the coronavirus epidemic. Good work for sure, Let's get it into print. Health Affairs is good, will they potentially publish quickly?

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
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☎ b6 (assistants: Kimberly Barasch; Whitney Robinson)
📠 301 496 4409
💻 b6

From: Ellen Carlin b6
Sent: Wednesday, February 26, 2020 9:37 AM
To: Franck Berthe b6
Cc: Kanya Long b6; Morens, David (NIH/NIAID) [E] b6; Catherine Machalaba b6; Billy Karesh b6
Subject: Re: BMJ-2020-055182 Manuscript Decision Editorials

Hi everyone, thanks for weighing in and for all your encouragement! I agree we have a unique product here, and that makes it hard to nail the right platform. We are inherently swimming against the tide given that our study finding is that no one cares about our finding (prevention and recovery)!

I am leaning toward Health Affairs and, since you can have up to 2000 words for Data Watch, I will spend an hour or so today to add a little more meat on the bones, giving us a chance to present a little more detail about our findings. We will still have the 750 word piece to fall back on if we need to submit again elsewhere. If you would like to see the updated piece before I submit let me know; otherwise I will proceed as planned and try to submit by tomorrow.

Ellen

On Feb 26, 2020, at 5:10 AM, Franck Cesar Jean Berthe b6 wrote:

Same on my side
I will support your decision
It is the time now
:-)

From: Kanya Long b6
Sent: Tuesday, February 25, 2020 5:33:42 PM
To: Morens, David (NIH/NIAID) [E] b6
Cc: Ellen Carlin b6; Catherine Machalaba b6; Franck Cesar Jean Berthe b6; Billy Karesh b6
Subject: Re: BMJ-2020-055182 Manuscript Decision Editorials

[External]
Ellen,

Supportive of whatever direction you think is best and can contribute if you choose to expand the piece.

I agree that the time is right.

Kanya

On Tue, Feb 25, 2020 at 2:26 PM Morens, David (NIH/NIAID) [E] b6 wrote:

> Just saw this and i think all options are viable. Whichever, this is/should be the perfect time (at the beginning of corona chaos) to think ahead. The whole world is focusing myopically on case and death counts. We need big picture voices and a perspective that sees the universe of things. d
>
> Sent from my iPhone
> David M Morens

OD, NIAID, NIH

On Feb 25, 2020, at 16:38, Ellen Carlin b6 wrote:

Hi everyone,

This was nice of the editor to give us this kind of feedback. We took a chance on submitting our piece as an Editorial to BMJ because the Analysis is a longer piece at 1800-2000 words, and Original Research more involved still. Our paper is about 750 words. We did this as a short-form piece to begin with so it would be done quickly, alas...!

Let me propose a few options, in no particular order, and get your feedback:

1. **Expand the paper** into a longer form analysis, suitable for submitting to BMJ or another journal as a more involved research/analysis piece.

2. **Keep the paper as is**, and submit elsewhere. I would suggest Health Affairs as a good next option; their "DataWatch" article type is 2000 words or less, up to 6 exhibits; these are short papers that highlight data that "speak for themselves" relative to important policy issues or topics. They should shed light on some important question and be "worth knowing." They do not typically test hypotheses, rely on sophisticated statistical methods, or include lengthy policy discussions. We aim to present new data or new analyses of existing data that are reliable and credible and that promote understanding among nonexperts on important, policy-relevant topics. We encourage work based on underused or new data sources.

If you want to submit as it but not to Health Affairs, please suggest a journal and article type.

3. **Take BMJ's suggestion to redraft into a rapid response** to their coronavirus coverage.

All comments welcome.
Thank you,
Ellen

On Feb 24, 2020, at 10:48 AM, BMJ <onbehalfof@manuscriptcentral.com> wrote:

24-Feb-2020
BMJ-2020-055182 entitled "Global health security: targeting investments toward unmet needs"

Dear Dr. Carlin,

Thank you for sending us your editorial. We read it with interest but decided against publication and I'm sorry to disappoint you.

The piece falls somewhere between research (you report methods) and Analysis (a long form article type that includes some data), but doesn't in its current form fit either. BMJ editorials don't report original findings.

Your bottom line message is clear however, and you might consider writing a rapid response to any recent content about covid - 19, discussing the lack of preventive initiatives globally. On line rapid responses are well read and a selection are published in full as letters. I'm sure you appreciate that I can't prejudge that selection

You'll find all our coverage of the covid - 19 outbreak here: https://www.bmj.com/coronavirus

Sorry once again that I can't offer you an editorial, and thank you for your interest in the BMJ.

Yours sincerely,

Alison Tonks
Clinical Editor, BMJ
atonks@bmj.com

If you elected during submission to send your article on to another journal the article will be transferred in 5 working days. If you intend to appeal against this decision please notify us before then.
The journal(s) (if any) you have selected at submission are: BMJ Global Health
If you want to speed up or stop this onward transmission please email the editorial office: papersadmin@bmj.com

The NEW ENGLAND JOURNAL of MEDICINE

Perspective

Escaping Pandora's Box — Another Novel Coronavirus

David M. Morens, M.D., Peter Daszak, Ph.D., and Jeffery K. Taubenberger, M.D., Ph.D.

The 1918 influenza pandemic was the deadliest event in human history (50 million or more deaths, equivalent in proportion to 200 million in today's global population). For more than a century, it has stood as a benchmark against which all other pandemics and disease emergences have been measured. We should remember the 1918 pandemic as we deal with yet another infectious-disease emergency: the growing epidemic of novel coronavirus infectious disease (Covid-19), which is caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). This virus has been spreading throughout China for at least 2 months, has been exported to at least 36 other countries, and has been seeding more than two secondary cases for every primary case. The World Health Organization has declared the epidemic a Public Health Emergency of International Concern. If public health efforts cannot control viral spread, we will soon be witnessing the birth of a fatal global pandemic.

The Greek myth of Pandora's box (actually a *pithos*, or jar) comes to mind: the gods had given Pandora a locked jar she was never to open. Driven by human weaknesses, she nevertheless opened it, releasing the world's misfortunes and plagues.

Of course, scientists tell us that SARS-CoV-2 did not escape from a jar: RNA sequences closely resemble those of viruses that silently circulate in bats, and epidemiologic information implicates a bat-origin virus infecting unidentified animal species sold in China's live-animal markets. We have recently seen many such emerging zoonoses, including the 2003 bat-coronavirus–derived SARS (an earlier severe acute respiratory syndrome, caused by a closely related coronavirus), which came terrifyingly close to causing a deadly global pandemic that was prevented only by swift global public health actions and luck.[1] Now, 17 years later, we stand at a similar precipice. How did we get to this point, and what happens next?

We must realize that in our crowded world of 7.8 billion people, a combination of altered human behaviors, environmental changes, and inadequate global public health mechanisms now easily turn obscure animal viruses into existential human threats.[1-3] We have created a global, human-dominated ecosystem that serves as a playground for the emergence and host-switching of animal viruses, especially genetically error-prone RNA viruses, whose high mutation rates have, for millions of years, provided opportunities to switch to new hosts in new ecosystems. It took the genome of the human species 8 million years to evolve by 1%. Many animal RNA viruses can evolve by more than 1% in a matter of days. It is not difficult to understand why we increasingly see the emergence of zoonotic viruses.

We have actually been watching such dramas play out in slow motion for more than a millennium in the case of pandemic influenza, which begins with viruses of wild waterfowl that host-switch to humans and then cause human-to-human transmission. A bird virus thereby becomes a human virus. Coronavirus emergence takes a different trajectory, but the principles are similar: SARS, the Middle Eastern respiratory syndrome (MERS), and Covid-19 all apparently have their origins in enzootic bat viruses. The parallels between the two SARS viruses are striking, including emergence from bats to infect animals sold in live-animal markets, allowing direct viral access to crowds of humans, which exponentially increases opportunities for host-switching. Such live markets have also led to avian epizootics with fatal human "spillover" cases caused by nonpandemic, poultry-adapted influenza viruses such as H5N1 and H7N9. One human cultural practice in one populous country has thus recently led to two coronavirus near-pandemics and thousands of severe and fatal international cases of "bird flu."

But these are not the only examples of deadly viral emergences associated with human behaviors.[2] HIV emerged from primates and was spread across Africa by truck routes and sexual practices. The origin of Ebola remains uncertain, but in 2014–2016 the virus spread explosively in West Africa in association with fear and secrecy, inadequate infrastructure and information systems, and unsafe nursing and burial practices. Emergences of arenaviruses causing Argentine and Bolivian hemorrhagic fever are associated with agricultural practices, and Bolivian hemorrhagic fever was spread across Bolivia by road building that fostered migration of reservoir rodents. In Southeast Asia, Nipah virus emerged from bats because of the intensification of pig farming in a bat-rich biodiversity hot spot. Human monkeypox emerged in the United States because of a booming international wildlife trade. In the 1980s, *Aedes albopictus* mosquitoes were being spread globally by humans; in 2014 and 2015, we had pandemics of aedes-borne chikungunya and Zika viruses.

Major epidemics associated with human crowding, movement, and sanitary inadequacy once occurred without spreading globally — for example, interregional plague pandemics of the 6th, 14th, and later centuries; influenza pandemics beginning in the 9th century; and cholera pandemics in the late 18th and early 19th centuries. When truly global pandemics did become common — for instance, influenza in 1889, 1918, and 1957 — they were spread internationally by rail and ship. Then, in 1968, influenza became the first pandemic spread by air travel, and it was soon followed by the emergence of acute enteroviral hemorrhagic conjunctivitis spread between international airports. These events ushered in our modern epidemic era, in which any disease occurring anywhere in the world can appear the next day in our neighbor's backyard. We have reached this point because of continuing increases in the human population, crowding, human movement, environmental alteration, and ecosystemic complexity related to human activities and creations. Cartoonist Walt Kelly had it right decades ago: "We have met the enemy, and he is us."

Preventing and controlling future pandemic occurrences remains a global priority.[4] With Covid-19, are we seeing a replay of 1918? Although we did not "witness" the beginning of the 1918 pandemic, evidence suggests that wherever it began, it silently spread around the world, causing mostly mild cases but also mortality of 0.5 to 1% or higher — a rate that was initially too low to be detected against a high background rate of death from unrelated respiratory illnesses. Then it suddenly exploded in urban centers almost everywhere at once, making a dramatic entrance after a long, stealthy approach. We are now recognizing early stages of Covid-19 emergence in the form of growing and geographically expanding case totals, and there are alarming similarities between the two respiratory disease emergences. Like pandemic influenza in 1918, Covid-19 is associated with respiratory spread, an undetermined percentage of infected people with presymptomatic or asymptomatic cases transmitting infection to others, and a high fatality rate.[5]

We are taking swift public health actions to prevent an emergence from becoming a pandemic, including isolation of patients and contacts to prevent secondary spread. But will these actions be adequate? Most experts agree that such measures could not have prevented the 1918 influenza pandemic. In fact, in the past century we have never been able to completely prevent influenza spread at the community level, even with vaccination and antiviral drugs. The problem is that most influenza cases are either asymptomatic, subsymptomatic, undiagnosed, or transmitted before the onset of symptoms. Can we do better with SARS-CoV-2, a virus with a presumably longer incubation period and serial generation time, but with an as-yet-undetermined ratio of inapparent cases to apparent cases and an unknown rate of asymptomatic spread? The answer to this question is critical, because without the ability to prevent such spread, we will cross a threshold where pandemic prevention becomes impossible. And we won't know that we have arrived there until it is too late.

With luck, public health control measures may be able to put the demons back in the jar. If they do not, we face a daunting challenge equal to or perhaps greater than that posed by the influenza pandemic of a century ago. As the late Nobel laureate Joshua Lederberg famously lamented about emerging infectious diseases, "It's our wits versus their genes." Right now, their genes are outwitting us by adapting to infectivity in humans and to sometimes silent spread, without — so far — revealing all their secrets. But we are catching up. As we push ahead, we should take heart in the Hesiod version of the Pandora myth, in which Pandora managed to prevent a single escape: "Only Hope was left . . ., she remained under the lip of the jar, and did not fly away."

Disclosure forms provided by the authors are available at NEJM.org.

From the Office of the Director (D.M.M.) and the Viral Pathogenesis and Evolution Section, Laboratory of Infectious Diseases (J.K.T.), National Institute of Allergy and Infectious Diseases, Bethesda, MD; and EcoHealth Alliance, New York, New York (P.D.).

This article was published on February 26, 2020, at NEJM.org.

1. Allen T, Murray KA, Zambrana-Torrelio C, et al. Global hotspots and correlates of emerging zoonotic diseases. Nat Commun 2017;8:1124.
2. Morens DM, Folkers GK, Fauci AS. The challenge of emerging and re-emerging infectious diseases. Nature 2004;430:242-9.
3. Parrish CR, Holmes EC, Morens DM, et al. Cross-species virus transmission and the emergence of new epidemic diseases. Microbiol Mol Biol Rev 2008;72:457-70.
4. Carlin EP, Machalaba C, Berthe FCJ, Long KC, Karesh WB. Building resilience to biothreats: an assessment of unmet core global health security needs. New York: Ecohealth Alliance, 2019.
5. Morens DM, Taubenberger JK. Influenza cataclysm, 1918. N Engl J Med 2018;379:2285-7.

DOI: 10.1056/NEJMp2002106

From: Ellen Carlin [b6]
Sent: 1/31/2020 10:50:12 PM
To: Morens, David (NIH/NIAID) [E] [b6
b6]
Subject: Re:

Many thanks, David! It's a quirky form. This should be fine. Will let you know if I need anything else.

On Jan 31, 2020, at 4:36 PM, Morens, David (NIH/NIAID) [E] b6 wrote:

Ellen, it wouldn't sign electronically, so I signed the old way, scanned and send as an attachment. Hope this works

<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
☎ b6 (assistants: Kimberly Barasch; Whitney Robinson)
📠 301 496 4409
💻 b6

<image002.jpg>

From: HP 3E05B-LJM775 Scanner <HP3E05B-LJM775-Sanner@nih.gov>
Sent: Friday, January 31, 2020 4:05 PM
To: Morens, David (NIH/NIAID) [E] b6
Subject:

<[Untitled].pdf>

From: Morens, David (NIH/NIAID) [E] [b6
b6]
Sent: 12/18/2019 5:15:06 PM
To: Ellen Carlin [b6]
Subject: RE: Journal contact?
Attachments: EEE 2019 NEJM.pdf

Ellen, I can certainly do as you suggest but it might be worth rethinking with Billy and others to rethink what journals might be the best. A number of journals have recently been publishing on pandemic preparedness, so some of those might be considered too. Just thinking broadly.

I have written a number of NEJM Perspective articles over the years, one just a month or so ago (see attached), and my sense is this may be of less interest to them, but maybe not, it can't hurt to try. If we do, then I might suggest reorienting the text a bit since the primary readership of NEJM is practicing physicians, so there has to be something in it for them. JID is perhaps more likely to be interested, and there must be a lot of alternatives. Also, just because Lancet GH didn't respond to Billy may not mean much: editors are always busy and way behind on answering emails, it's a chronic problem.

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
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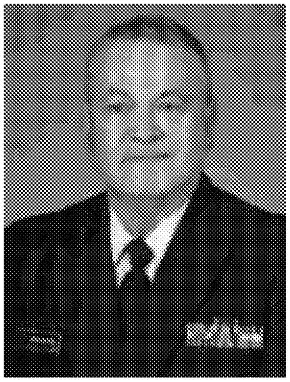

From: Ellen Carlin b6
Sent: Tuesday, December 17, 2019 2:12 PM
To: Morens, David (NIH/NIAID) [E] b6
Subject: Re: Journal contact?

Oh yes! Billy did—he reached out to his Lancet contact twice, but got no response… ☹

I would be happy to reach out to either NEJM or JID and mention that you suggested it! That's no problem. NEJM has a nice category called "Perspective" with 1,200 word limit (we're at 765 of core text), 5 reference limit (we have 5), and usually include one figure or table (we have 1). So that is helpful! They recommend a "presubmission inquiry" when authors are unsure of the suitability of their manuscript for publication; they have an online system for that but perhaps they would be open to direct email contact? I don't want to use up any capital you might have with the journals unless you feel it's worthwhile!

Ellen

From: "Morens, David (NIH/NIAID) [E]" b6
Date: Tuesday, December 17, 2019 at 11:03 AM
To: Ellen Carlin b6
Subject: RE: Journal contact?

Hi Ellen, first I need to catch up as I had thought Billy was going to first run it by Lancet Global Health. Did he do that? If so, I may have missed that.

If not, I could certainly run it by NEJM or JID (one at a time). However, we should probably first put it in a format that fits one of theirs.

Although either way might work, I think the best would be for YOU as the first author to run it by them, perhaps mentioning that I had suggested it. That avoids putting them in the position of saying no to a friend if it doesn't fit their needs.

Once I hear from you about these several things, I can check the 2 journals to get up to date on their ms. categories, lengths and etc.

David

David M. Morens, M.D.
CAPT, United States Public Health Service
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☎ b6 (assistants: Kimberly Barasch; Whitney Robinson)
📠 301 496 4409
💻 b6

From: Ellen Carlin b6
Sent: Monday, December 16, 2019 10:53 AM
To: Morens, David (NIH/NIAID) [E] b6
Subject: Re: Journal contact?

Hi David! That's great! Would you be interested in sharing the paper informally with NEJM or JID to see if they'd be interested? Or I can do it and cc you—whatever is easiest and most sensible. My contacts are at the vet journals and that won't be helpful!

I hear from our friend b6 that they've already had a fair amount of b6 in b6 b6 (on different days, I guess to retain some sanity 😵).

Ellen

From: "Morens, David (NIH/NIAID) [E]" b6
Date: Wednesday, December 11, 2019 at 5:30 PM

To: Ellen Carlin b6
Subject: Re: Journal contact?

Ellen, i have contacts at nejm, jid, and several other journals but not lancet. b6 left and although i knew b6 slightly, i don't think i can do any good there.

I agree: go big. Sometimes you hit a bulls eye, other times not

But your work is good, and it will be published, read, and considered. I mean, after all, this is important stuff

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

> On Dec 11, 2019, at 15:03, Ellen Carlin b6 wrote:
>
> Hi David! I hope all is well.
>
> I wanted to ask if you know any editors at The Lancet who might be receptive to an email from you about our paper (attached)? Billy tried an editor he knows there but has received no response. We thought a pre-submission inquiry would be better than a cold submission.
>
> I also thought if The Lancet is a no-go, perhaps you might have a contact at NEJM or another high-impact journal? NEJM has a Commentary article type. I figure we should go big if we can!
>
> Thanks!!
> Ellen
>
> **Ellen P. Carlin, DVM**
> *Senior Health and Policy Specialist*
>
> EcoHealth Alliance
> b6 (direct)
> (mobile)
> b6
> www.ecohealthalliance.org
>
> *Research Associate*, Smithsonian Conservation Biology Institute
> *Adjunct Research Scientist*, Columbia University National Center for Disaster Preparedness
> *Courtesy Lecturer*, Cornell University College of Veterinary Medicine
>
> *EcoHealth Alliance leads cutting-edge scientific research into the critical connections between human and wildlife health and delicate ecosystems. With this science, we develop solutions that prevent pandemics and promote conservation.*

Case Follow-up

Rather than follow Mr. P.'s suggestion to increase his medication doses and emphasize how poorly he was doing, his psychiatrist highlighted the ways in which his psychiatric illness interfered with his ability to seek and sustain competitive employment. He wrote a letter for Mr. P. to submit with his next SSI application. Mr. P.'s case manager worked with him on his reapplication and accompanied him to his interview, and Mr. P. ultimately received SSI.

An audio interview with Dr. Kalofonos is available at NEJM.org

From the Center for Social Medicine, Department of Psychiatry, and the International Institute, University of California, Los Angeles, and the Greater Los Angeles Veterans Affairs Medical Center — all in Los Angeles.

1. Petryna A. Life exposed: biological citizens after Chernobyl. Rev. ed. Princeton, NJ: Princeton University Press, 2013.
2. Hansen H, Bourgois P, Drucker E. Pathologizing poverty: new forms of diagnosis, disability, and structural stigma under welfare reform. Soc Sci Med 2014;103:76-83.
3. Nguyen V-K. The republic of therapy: triage and sovereignty in West Africa's time of AIDS. Durham, NC: Duke University Press, 2010.
4. Braslow JT. The manufacture of recovery. Annu Rev Clin Psychol 2013;9:781-809.
5. Ferguson J. Give a man a fish: reflections on the new politics of distribution. Durham, NC: Duke University Press, 2015.

DOI: 10.1056/NEJMp1811661

Eastern Equine Encephalitis Virus — Another Emergent Arbovirus in the United States

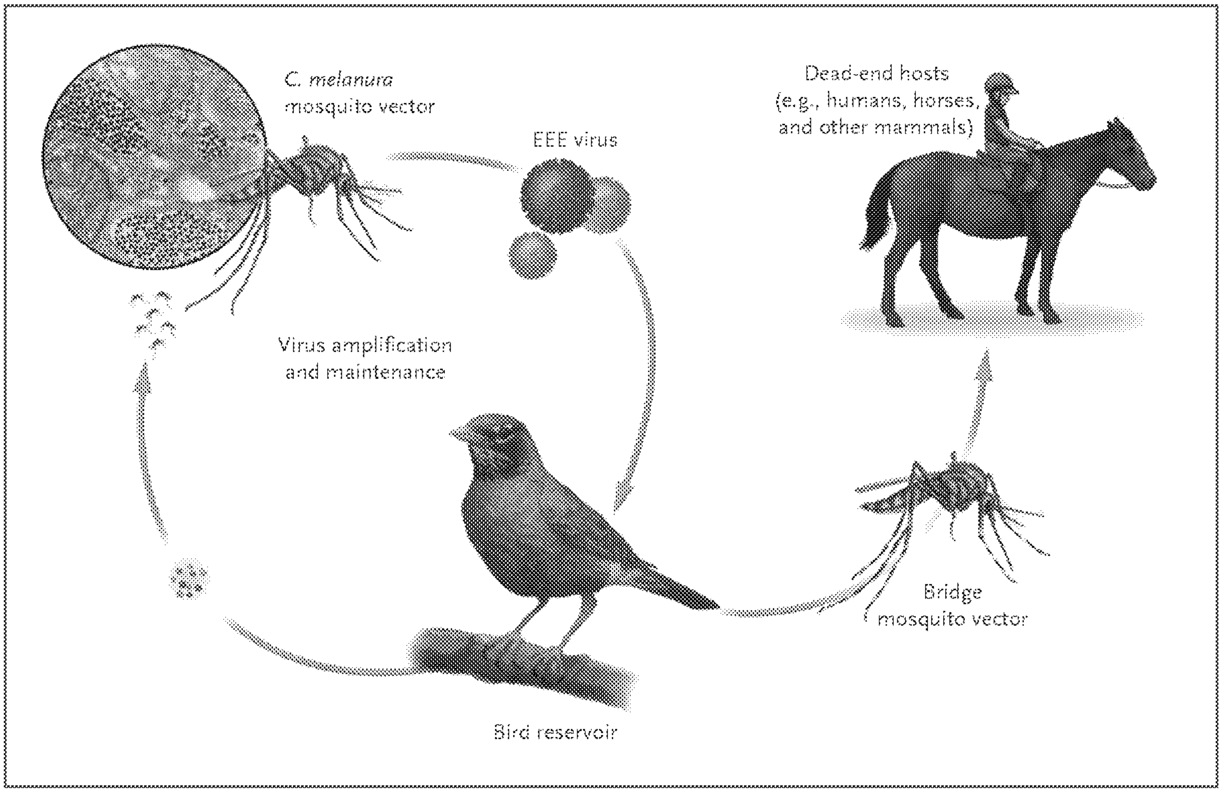
David M. Morens, M.D., Gregory K. Folkers, M.S., M.P.H., and Anthony S. Fauci, M.D.

Humans have always lived in intimate association with arthropods that transmit pathogens between humans or from animals to humans. About 700,000 deaths due to vectorborne diseases occur globally each year, according to World Health Organization estimates. In the summer and fall of 2019, nine U.S. states have reported 36 human cases (14 of them fatal) of one of the deadliest of these diseases: eastern equine encephalitis (EEE), an arthropod-borne viral (arboviral) disease transmitted by mosquitoes. In recent years, the Americas have witnessed a steady stream of other emerging or reemerging arboviruses, such as dengue, West Nile, chikungunya, Zika, and Powassan, as well as increasing numbers of travel-related cases of various other arboviral infections. This year's EEE outbreaks may thus be a harbinger of a new era of arboviral emergences.

EEE has probably prevailed for centuries, and 12 U.S. EEE epidemics or epizootics were documented between 1831 and 1959. Most known arboviruses that can infect humans, such as EEE virus (EEEV), circulate generally unnoticed in enzootic reservoirs of arthropods and vertebrate hosts such as birds and mammals.[1] EEEV spreads between *Culiseta melanura* mosquitoes and various passerine (tree-perching) birds found in forested wetlands (see figure). Small mammals, reptiles, or amphibians may also be involved in its environmental circulation.

The virus occasionally spills over from its usual reservoirs to infect dead-end hosts such as humans, equids, swine, pheasants, various game and exotic birds, and gallinaceous poultry. These spillovers occur at unpredictable intervals and are usually mediated by "bridging vectors" (nonenzootic mosquitoes that feed on both birds and mammals) (see figure). EEEV is not transmitted between dead-end hosts such as horses and humans. Determinants of spillover most likely include complex interactions among human behaviors, weather, environmental perturbation, movement of birds, and other variables. EEEV is also a potential bioweapon, since it is transmissible by aerosol. Although it has been found in most of the eastern United States, major persistent enzootic sites are relatively few and geographically focal; they can, however, be the source of seeding of additional EEEV foci.

Many other mosquito-borne or tickborne diseases of mammals and humans occur throughout the United States and globally.



Transmission Cycle of Eastern Equine Encephalitis Virus (EEEV).

Multiple bird and mosquito species and environmental variables are associated with human EEEV infection. There are numerous other arboviruses in the continental United States, including the mosquito-borne alphavirus disease western equine encephalitis, the California group bunyavirus diseases such as La Crosse encephalitis, and the flavivirus diseases St. Louis encephalitis and West Nile, the latter two prevailing over most of the continental United States. Tickborne encephalitis viruses include Powassan (a flavivirus) and Colorado tick fever (an orbivirus). These six viruses also extend northward into Canada, and some are found in Central and South America. In addition, the four *Aedes aegypti*–borne viruses (yellow fever, dengue, chikungunya, and Zika) circulate globally and present ongoing threats, from endemic circulation or importation, to the continental United States and especially to U.S. tropical jurisdictions. Adapted from the U.S. Centers for Disease Control and Prevention.

The types of arthropods and other vectors vary geographically, and complex interactions between humans and the environment may be unique in each situation and location. Variables influencing disease emergence in one Massachusetts EEE focus exemplify the ecologic complexity of arboviruses.[2] After Atlantic white cedar trees were harvested for use in houses and carpentry products and the resulting swamps were drained in the early 1800s, wetland forests were reestablished over the next century; these forests included red maple trees, whose roots — lying just below bird-roosting sites — provide excellent oviposition (egg-laying) sites for *C. melanura* mosquitoes. As passerine birds such as American robins foraged from these trees in burgeoning suburbs, growth and movement of the human population facilitated spillovers of EEEV to humans, leading to cases of encephalitis.

More than 130 human and 50 animal arboviral diseases occur around the world. Most are transmitted by mosquitoes or ticks. Symptomatic human arboviral disease falls into three distinct syndromes: febrile systemic illness (e.g., uncomplicated dengue), hemorrhagic fever (e.g., dengue hemorrhagic fever and yellow fever), and encephalitis (e.g., EEE, Venezuelan equine encephalitis, Japanese encephalitis, and La Crosse encephalitis). Each of these syndromes may be caused by multiple arboviruses from multiple unrelated taxonomic groups. Four of the human-infecting arboviruses — the flaviviruses dengue, yellow fever, and Zika, and the alphavirus chikungunya — have evolved to infect a mosquito that is uniquely anthropophilic (feeding almost exclusively on humans): *Aedes aegypti*. Humans serve not only as the reservoir for these four viruses, but also as an amplification host that up-regulates viral cycling. Any virus that can efficiently infect *A. aegypti* also has potential access to billions of humans, which explains why the four viruses that have done so have spread pandemically. We cannot discount the possibility that other arboviruses will adapt to *A. aegypti* in the future — a sobering thought, given the high case-fatality rate of diseases such as EEE.

After inoculation of virus-infected mosquito saliva into perivascular dermal tissue, EEEV infects Langerhans and dendritic cells, which migrate to regional lymphoid tissue, where virus replication leads to systemic viremic seeding. After an incubation period of approximately a week (range, 3 to 10 days), EEEV infection presents nonspecifically with fever, malaise, intense headache, muscle aches, and nausea and vomiting — a sign and symptom complex not easily distinguishable from those of most other arboviral infections or from influenza and a host of other diseases.

At the onset of symptoms, specific diagnostic tests may be unrevealing: viral isolation and polymerase-chain-reaction analysis from blood and spinal fluid, as well as testing for EEEV-specific IgM, may be negative. Neurologic signs appearing soon (0 to 5 days) after onset are initially nonspecific and are indistinguishable from those associated with enteroviral meningoencephalitis, which is also prevalent in late summer. However, rapid clinical progression ensues. By the time definitive serologic diagnosis is possible, within a week after infection, neurologic damage may already have occurred. Neuroimaging typically shows involvement of the basal ganglia and thalami.

An estimated 96% of people infected with EEEV remain asymptomatic; however, of those who have symptoms, 33% or more die and most of the rest sustain permanent, often severe, neurologic damage.

Point-of-care differential diagnostics for the many arboviral and nonarboviral causes of encephalitis are currently lacking and would be of limited value without effective treatments. Although antiviral drug screening efforts have been undertaken in vitro and in vivo, no antiviral drug has thus far been demonstrated to have efficacy against EEEV. An important requirement of such a drug, were it available, would be the ability to cross the blood–brain barrier. EEE-specific monoclonal antibodies have been effective in an experimental animal model only when given before infection, and data from experiments with Venezuelan equine encephalitis virus (a related alphavirus) suggest that immunopathogenic mechanisms could be involved. Supportive care, often including admission to an intensive care unit with ventilatory support, is the mainstay of treatment. Patients need not be isolated, since they are not infectious. Given the seriousness of the disease, social support and counseling of the patient and family are critically important.

Several EEEV vaccines are in development; however, there may not be strong incentives to proceed to advanced development and licensure because of the nature of the disease: outbreaks are rare, brief, and focal, and they occur sporadically in unpredictable locations, making it difficult to identify an appropriate target population for vaccination. Such vaccines, however, might have utility for persons at high occupational risk — laboratory workers, for instance — as is the case for an early-generation experimental EEEV vaccine now available under a U.S. Army Investigational New Drug program. Efforts to develop mosquito saliva vaccines that would be effective against multiple mosquito-borne diseases are in early stages.[3] A theoretical advantage of such vaccines is the inclusion of various salivary proteins from selected mosquitoes that transmit multiple arboviruses that infect humans.

In the absence of vaccines or specific treatments, state and local health departments can provide early warning of imminent human infections by surveilling equids, birds, and mosquitoes; however, even these blunt prevention tools are continuously threatened by underfunding of public health efforts. Sadly, the United States' ability to control arboviral diseases is little better in 2019 than it was more than a century ago, when William Crawford Gorgas eliminated *A. aegypti* from Havana and the Panama Canal Zone. Recently, several American public health experts have called for a national defense strategy for arboviruses and other vectorborne diseases,[4] an idea also supported by international experts.[5] We strongly agree. Arbovirus threats are not easily thwarted by piecemeal efforts. Multiple potentially deadly viruses are constantly present in virologically occult enzootic foci throughout the United States and globally. Effects of climate and weather, such as changes in heat and rainfall and their impact on variables associated with viruses, vectors, and vertebrates, are cause for additional concern, since they may affect the life cycles and geographic distribution of arthropod vectors and viral transmission patterns. Given the near certainty of future emergences, arboviruses constitute a real and present danger. Although EEE is not yet a disease of major national importance, this year's spike in cases exposed our inadequate preparation for emergent disease threats. Though the best way to respond to these threats is not entirely clear, to ignore them completely and do nothing would be irresponsible.

Disclosure forms provided by the authors are available at NEJM.org.

From the Office of the Director, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD.

1. Weaver SC, Winegar R, Manger ID, Forrester NL. Alphaviruses: population genetics and determinants of emergence. Antiviral Res 2012;94:242-57.
2. Komar N, Spielman A. Emergence of eastern encephalitis in Massachusetts. Ann N Y Acad Sci 1994;740:157-68.
3. Manning JE, Morens DM, Kamhawi S, Valenzuela JG, Memoli M. Mosquito saliva: the hope for a universal arbovirus vaccine? J Infect Dis 2018;218:7-15.
4. Petersen LR, Beard CB, Visser SN. Combatting the increasing threat of vector-borne disease in the United States with a national vector-borne disease prevention and control system. Am J Trop Med Hyg 2019;100:242-5.
5. Espinal MA, Andrus JK, Jauregui B, et al. Emerging and re-emerging *Aedes*-transmitted arbovirus infections in the region of the Americas: implications for health policy. Am J Public Health 2019;109:387-92.

DOI: 10.1056/NEJMp1914328

The Den

Sauarbh Jha, M.B., B.S.

When I recall my house job (internship), I remember fatigue and camaraderie. I also remember the hospital pub. Nestled in the hospital complex, a stone's throw from the main entrance, the pub was unassuming, unmarked, and innominate. I called it "the den."

On first approach, the den could have been mistaken for the ICU, with white coats hung at its entrance as if they were prohibited from entering. Indistinguishable from one another, the coats all held a folded stethoscope in one pocket and the yellow *Oxford Handbook of Clinical Medicine* in the other. If you took someone else's coat by mistake, it scarcely mattered; we were all cut from the same cloth. In a sense, the den *was* an ICU — a site of intensive care for the hospital staff, a place to unload after another intense day of work. It was also a place where ranks were temporarily forgotten and gradients were abolished — it was egalitarianism in practice. We knew each other by name and by our preferred drinks. Mine was vodka and Red Bull.

The den was empty at 5 p.m., but by 7, it was buzzing with doctors, nurses, pharmacists, porters, administrative assistants, technologists, and even hospital managers. In the small, stuffy, utterly undecorated room, clusters of people formed for no particular reason. The den wasn't divided into doctors and nurses or residents and attendings or surgeons and internists. Everyone spoke with everyone. When you joined a group, it was good manners to buy everyone a round of drinks, though this etiquette was waived for radiologists, who, as the most important people in the hospital, never bought drinks.

By all objective indicators, I should have been unhappy in those grueling months I spent as a medical house officer. The town was dreary, even by British standards, and had a limited range of restaurants. I was distant from my friends in London, where I went to medical school, and I found myself suddenly laden with responsibility, working hours I'd never imagined I was capable of working. Like most junior doctors, I lived on the hospital campus in free housing that pushed minimalism to its limits. One of our many hardships was the difficulty of maintaining a comfortable room temperature during the winter nights. The rooms were warmed by centrally controlled radiators that emitted far too much heat; I had to keep my room window open precisely 6 inches — at 8 inches I'd shiver, at 4 I'd sweat.

The den was an escape, a redoubt where we reflected and planned and spoke about our patients — what else, after all, was there to talk about? Education was delivered informally over banter and beer. I learned more medicine in the den than in all the grand rounds I've ever attended.

From: Morens, David (NIH/NIAID) [E] [b6
b6]
Sent: 2/4/2020 5:30:23 PM
To: Ellen Carlin [b6]; Billy Karesh [b6]; Catherine Machalaba [b6]; Kanya Long [b6]; Franck Berthe [b6]
CC: Amanda Andre [b6]
Subject: RE: Action required: global health security manuscript

Super-exciting Ellen, fingers are tightly crossed!

David

David M. Morens, M.D.
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National Institutes of Health
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Bethesda, MD 20892-2520

☎ b6 (assistants: Kimberly Barasch; Whitney Robinson)
📠 301 496 4409
💻 b6

From: Ellen Carlin b6
Sent: Tuesday, February 4, 2020 11:19 AM
To: Billy Karesh b6; Catherine Machalaba b6; Kanya Long b6; Franck Berthe b6; Morens, David (NIH/NIAID) [E]
b6

Cc: Amanda Andre b6
Subject: Re: Action required: global health security manuscript

Hi everyone, you should by now have received an email confirming your co-authorship in the article just submitted to Lancet Global Health by Billy (as corresponding author). Please think good thoughts! We should know their decision fairly quickly, and will take next steps from there.

Thanks for everyone for getting signatures to me so quickly and For being such enthusiastic co-authors.

Elle

Sent from my iPhone

> On Jan 31, 2020, at 3:44 PM, Ellen Carlin b6 wrote:
>
> Dear Team,
>
> I hope your 2020 is off to a great start!
>
> I'm writing to give an update on our global health security paper. [redacted] which delayed things a bit, but we are ready to submit now.   Attached is the version of the manuscript we will submit. Billy and I have updated the lead to reflect current events.
>
> We're going to give *The Lancet Global Health* a try. **Please find attached an author contribution form that Kenya, Franck, and David need to sign electronically. Amanda is helping get signatures from Billy and Catherine. If you can please turn this around by Monday Feb 3, I can submit that day.** I have indicated that all authors contributed equally; if you prefer to word your contribution differently, please do so.
>
> Some of you may not be aware that December 31 was my last day at EcoHealth Alliance. I am running my own consulting gig now and have a lot of exciting projects in store that I look forward to sharing with you as they develop. I am still affiliated with EHA as a Research Fellow.
>
> Thanks again for all of your efforts!
>
> Best wishes,
> Ellen
>
> <Carlin et al Building resilience Draft 1.31.19 v2.docx>

From: Jon Epstein [b6]
Sent: 10/19/2020 5:21:26 PM
To: Morens, David (NIH/NIAID) [E] [b6
b6]
Subject: Re: Bennett et al Nature s41586-020-2812-9.pdf

Working on it....

On Mon, Oct 19, 2020 at 1:07 PM Morens, David (NIH/NIAID) [E] b6 wrote:

> Congrats on the U01, and Vincent is a great guy to work with. Do you guys have an experimental bat colony?
>
> I don't sell tickets, but I really wish you would join if you haven't and come to ASTMH. Yes, it is a diffuse 5,000 person meeting with most things not very interesting to the rest, but we also have subgroups with lots of people interested in EcoHealth type stuff. Peter just joined ASTMH as well as our ACAV subgroup, that's Am Committee on Arthropod Borne viruses, which also covers hemorrhagic fevers and high consequence viruses. Started in 1959 by among others Albert Sabin, Bill Reeves, and the father of One Health Karl Meyer.
>
> b6 and b6 are ACAV members and b6 an ASTMH but not ACAV member. Over the years ACASV members have been involved in the discovery and or characterization of Ebola (eg, Karl Johnson), various arena viruses, hantaviruses including Korean hemorrhagic fever and hantavirus pulmonary syndrome, Crimean Congo hemorrhagic fever, etc.
>
> b6 and b6 are running a corona symposium this year, and b6 is doing a special ASTMH TWiV show.
>
> Lots of good folks who are good to connect with professionally….
>
> Just sayin'… Not selling tickets… All the best,

David

David M. Morens, M.D.
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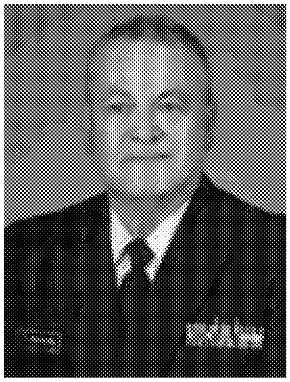

From: Jon Epstein b6
Sent: Saturday, October 17, 2020 9:43 PM
To: Morens, David (NIH/NIAID) [E] b6
Subject: Re: Bennett et al Nature s41586-020-2812-9.pdf

I had been going to Trop Med conferences for years - it's really great, though I missed the last two meetings. I'll try to pick it up again.

Sometimes I've felt that the emerging viruses area was fairly fringe at the meeting, with most of the sections devoted to the more classical diseases.

Maybe that's changing? In any case, it's always a great networking meeting, and I'll rejoin this year.

Work's been crazy on this end, too, but all good. I was just awarded my first U01 from NIAID, to continue my work on Nipah in Bangladesh. I'm really excited about it and will be partnering with Vincent Munster at RML to look at genotype/phenotype relationships in animal models - including bats! I'm also starting two new projects in India, which is always a challenge. We'll be looking at spillover of ebola-like and Nipah viruses from bats to livestock and people in rural India.

So surreal to be operating amidst a pandemic caused by a bat virus...

Would be nice to reconnect sometime soon. Stay safe.

-Jon

On Sat, Oct 17, 2020 at 11:06 AM Morens, David (NIH/NIAID) [E] < b6 > wrote:

> Yes, this is pretty interesting. Mumps has been described in humans for almost 2,500 years. We don't know how long for rubella but certainly over 200 years and probably much longer. How many other related viruses are bout there that could at some point jump into humans? If we had a rubella part 2 or a mumps part 2, it would probably cause a global pandemic with countless deaths, at least in the case of a rubella-like virus.

We absolutely need more work in this area!

I'm doing OK, goinmg crazy with work and running ASTMH stuff. Are you an ASTMH member? I think I saw you at at least one of the recent annual meetings. If not, please join and you will be connected with a lot of folks interested in these things. Peter just joined this year.

David

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From: Jon Epstein b6
Sent: Wednesday, October 14, 2020 2:51 PM
To: Morens, David (NIH/NIAID) [E] b6
Subject: Re: Bennett et al Nature s41586-020-2812-9.pdf

I know, it's incredible. We've found loads of new rubulaviruses in bats over the years - particularly Pteropus species. I'm actually not too surprised that mumps would have originated in bats.

I also wouldn't be surprised if we find evidence that people are getting exposed to other bat rubulaviruses.

I hope you're doing well!

-Jon

On Fri, Oct 9, 2020 at 12:17 PM Morens, David (NIH/NIAID) [E] b6 wrote:

> Wow!
>
> David

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CAPT, United States Public Health Service

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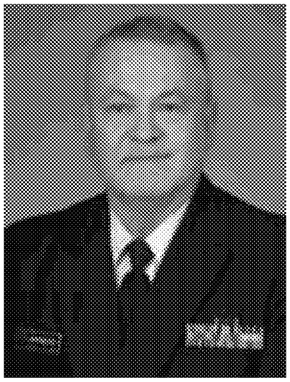

From: Robert Tesh b6
Sent: Friday, October 9, 2020 3:45 AM
To: Garcia-Blanco, Mariano A. b6; Murphy, Frederick A. b6; Charles H Calisher b6; Weaver, Scott b6; Morens, David (NIH/NIAID) [E] b6
Subject: Fwd: Bennett et al Nature s41586-020-2812-9.pdf

---------- Forwarded message ---------
From: **Ksiazek, Thomas G.** b6
Date: Fri, Oct 9, 2020, 12:15 AM
Subject: Bennett et al Nature s41586-020-2812-9.pdf
To: Amman Brian b6, Towner Jonathan (CDC/CCID/NCZVED) b6, Nichol Stuart b6, Rollin Pierre b6, Tesh Robert b6, Bob Swanepoel b6

One of the papers

--

Jonathan H. Epstein DVM, MPH, PhD

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

--

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

--

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Twitter: @epsteinjon

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

---

From: William B. Karesh b6
Sent: 8/11/2016 1:19:30 PM
To: Morens, David (NIH/NIAID) [E] b6 b6
Subject: Re: NEW YORK DAILY NEWS: Raising our biodefenses now

Thanks - LoL. No bar hopping with b6, but I have been enjoying talking with him from time to time.

BK

William B. Karesh, D.V.M
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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] b6 wrote:
>
> Billy, great article! Have you been bar-hopping with b6? 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

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📠 301 496 4409
💻 b6

<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] [b6 b6]

Sent: 3/2/2020 12:15:32 AM

To: Gonsalves, Gregg [b6]

CC: Art Reingold [b6]; Ko, Albert [b6]; Lee Riley [b6]; Eva Harris [b6 (b6 er]; Breman, Joel (NIH/FIC) [V] [b6 b6]; b6; Julie Jacobson [b6]; b6; Jamie Lloyd-Smith [b6]; Vasiliou, Vasilis [b6]; Friedland, Gerald [b6]; Shapiro, Eugene [b6]; b6; Akira Homma (b6) [b6]; Alan Rothman (b6) [b6]; Aubree Lynn Gordon [b6]; Emu, Brinda [b6]; Panter-Brick, Catherine [b6]; Dela Cruz, Charles [b6]; Plowe, Christopher (NIH) [b6 (b6]; b6; Hamer, David (NIH) [b6 b6]; b6; Derek Adam Cummings [b6]; Vlahov, David [b6]; Donald Burke [b6]; Eric J. M. D. M. S. C. Nilles (b6) [b6]; Velazquez, Eric [b6]; Krammer, Florian (b6) [b6]; Gary J. Weil M.D. (b6) [b6]; Koehler, Jane [b6]; Jason Andrews [b6]; Jason Corburn [b6]; Lim, Jean (b6) [b6]; Jeffrey Klausner (b6) [b6]; b6; John David [b6]; b6 [b6]; b6 [b6]; Joseph Eisenberg [b6]; Fauver, Joseph [b6]; Juan Salazar (b6) [b6]; b6; Mary Wilson [b6]; Milton L. Wainberg (b6) [b6]; b6; Peter Hotez [b6]; Peter F. Wright [b6]; b6; Melby, Peter C. [b6]; Professor Christian Brechot (b6) [b6]; b6; b6 [b6]; b6; Richard Guerrant [b6]; b6; Bucala, Richard [b6]; Dubrow, Robert [b6]; Hecht, Robert [b6]; Scott C. Weaver (b6) [b6]; W. Ian Lipkin [b6]; Yazdan Yazdanpanah (b6) [b6]; Yukari Manabe [b6 b6]; Kozal, Michael [b6]

Subject: Re: HOW TO SIGN ON: Next Steps on COVID: Letter from Public Health and Legal Experts

David M Morens MD, Bethesda, Maryland USA

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

> On Mar 1, 2020, at 19:06, Gonsalves, Gregg b6 wrote:

Just email your name, title and affiliation to b6 if you want to sign on. Feel free to send to colleagues as well. We can’t make changes unfortunately at this late date as we’re on such a tight deadline.

On 3/1/20, 6:50 PM, "Art Reingold" b6 wrote:

happy to have my name added

> On Mar 1, 2020, at 2:51 PM, Ko, Albert b6 wrote:
>
> Dear Friends and Colleagues
>
> I want to raise attention of a letter that a group at Yale, Temple and Northeastern have drafted on the next steps for the Covid19 response which is attached and at:
>
https://nam05.safelinks.protection.outlook.com/?url=https%3A%2F%2Fdocs.google.com%2Fdocument%2Fd%2F1NVOSECOEp8deYnmJfO0uKtRHcNcbmNrk7dW752dzMeE%2Fedit%3Fusp%3Dsharing&data=02%7C01%7Cgregg.gonsalves%40yale.edu%7C3f6deee28cf743a07aaf08d7be3b5600%7Cdd8cbebb21394df8b4114e3e87abeb5c%7C0%7C0%7C637187034378579611&sdata=ETC5VnkM6N8WJRxpOE0wn09THVLOa5eNvkbkHNqjYOw%3D&reserved=0.
>
> Gregg Gonsalves has provided instructions below (as well as a list of signees as of early today). If you want to sign please email your name, title and affiliation to Gregg Gonsalves at
b6
>
> Thank you for your consideration.
>
> Best albert
>
> Albert Icksang Ko, M.D.
> Professor of Epidemiology and Medicine
> Chair, Department of Epidemiology of Microbial Diseases
> Yale School of Public Health
> 60 College Street, LEPH Room 319B
> P.O. Box 208034
> New Haven, CT 06520-8034 USA
> Tel: b6; Fax: +1 203 785 6193
> email: b6
>
>
>
> From: Gregg Gonsalves b6
> Date: Sunday, March 1, 2020 at 2:48 PM
> Subject: FW: Next Steps on COVID Letter from Public Health and Legal Experts
>
> Hi, all. A bunch of Yale, Temple, Northeastern public health and legal experts drafted this sign-on letter:
>
https://nam05.safelinks.protection.outlook.com/?url=https%3A%2F%2Fdocs.google.com%2Fdocument

%2Fd%2F1NVOSECOEp8deYnmJfO0uKtRHcNcbmNrk7dW752dzMeE%2Fedit%3Fusp%3Dsharing&data=02%7C01%7Cgregg.gonsalves%40yale.edu%7C3f6deee28cf743a07aaf08d7be3b5600%7Cdd8cbebb21394df8b4114e3e87abeb5c%7C0%7C0%7C637187034378579611&sdata=ETC5VnkM6N8WJRxpOE0wn09THVLOa5eNvkbkHNqjYOw%3D&reserved=0.

>

> Just email your name, title and affiliation to b6 if you want to sign on. Feel free to send to colleagues as well. We can't make changes unfortunately at this late date as we're on such a tight deadline.

> If you do it today we can include on first blast out of letter, which we'll release via our collaborative comms people at law, public health and main communications offices on Monday. We will also send to White House and Congress then.

> Don't circulate on social media as we're embargoed until 2PM Monday.

> Gregg

>

> -----Original Message-----

> From: Gonsalves, Gregg

> Sent: Sunday, March 1, 2020 16:26

> To: Scott Burris; Jay Stanley

> Cc: Abdullah Hasan; Omer, Saad; Kapczynski, Amy; Greenwood, Michael; Chen, Xi; Ko, Albert; Esha Bhandari; Vermund, Sten; Wishnie, Michael; Omar Jadwat; Miller, Ali; Mary Petrone; Gilles, Marguerite; b6; Steven Galinat; Madhuri Grewal; Kroszner, Debra; Peart, Karen; Mamoun, Fred; Conroy, Janet

> Subject: Sign-Ons at of Now (4:24PM Sunday)

>

> Link to letter with sign-ons: https://nam05.safelinks.protection.outlook.com/?url=https%3A%2F%2Fdocs.google.com%2Fdocument%2Fd%2F1NVOSECOEp8deYnmJfO0uKtRHcNcbmNrk7dW752dzMeE%2Fedit%3Fusp%3Dsharing&data=02%7C01%7Cgregg.gonsalves%40yale.edu%7C3f6deee28cf743a07aaf08d7be3b5600%7Cdd8cbebb21394df8b4114e3e87abeb5c%7C0%7C0%7C637187034378579611&sdata=ETC5VnkM6N8WJRxpOE0wn09THVLOa5eNvkbkHNqjYOw%3D&reserved=0

>

> And sign-ons also below:

>

> Gregg S. Gonsalves, Assistant Professor, Department of Epidemiology of Microbial Diseases, Yale School of Public Health * Amy Kapczynski, Professor of Law, Yale Law School * Albert I. Ko, Professor and Chair, Department of Epidemiology of Microbial Diseases, Yale School of Public Health * Wendy E. Parmet, Professor of Law, Public Policy and Urban Affairs, Northeastern University * Scott Burris, Professor and Director, Center for Public Health Law Research, Policy Surveillance Program, Temple University Beasley School of Law * Xi Chen, Assistant Professor, Department of Health Policy and Management, Yale School of Public Health * Saad B. Omer, Director, Yale Institute for Global Health, Professor of Medicine (Infectious Diseases), Professor of Epidemiology of Microbial Diseases, Adjunct Professor (Nursing), Yale Medical School, Yale School of Public Health, Yale School of Nursing * Michael J. Wishnie, Clinical Professor of Law and Counselor to the Dean, Yale Law School * Kayoko Shioda, Ph.D. Candidate, Department of Epidemiology of Microbial Diseases, Yale School of Public Health * Mary Petrone, Ph.D. Candidate, Department of Epidemiology of Microbial Diseases, Yale School of Public Health * Hanna Ehrlich, Ph.D. Candidate, Department of Epidemiology of Microbial Diseases, Yale School of Public Health Rita Gilles, J.D. Candidate, Yale Law School * Ann Kurth, Dean and Professor, Yale School of Nursing Robert Heimer, Professor of Epidemiology and of Pharmacology, Yale School of Public Health Amy Bei, Department of Epidemiology of Microbial Diseases, Yale School of Public Health Glenn Cohen, Professor of Law and Director, Petrie-Flom Center for Health Law Policy, Biotechnology & Bioethics, Harvard Law School A. David Paltiel, Professor, Department of Health Policy and Management, Yale School of Public Health and Yale School of Management Forrest W. Crawford, Associate Professor, Department of Biostatistics, Yale School of Public Health Trace Kershaw, Professor and Chair,

Department of Social and Behavioral Sciences, Yale School of Public Health Carlos del Rio, Professor of Medicine and Global Health, Emory University Lynn E. Taylor, Research Professor, University of Rhode Island, Director of HIV and Viral Hepatitis Services, CODAC Behavioral Health, Director, RI Defeats Hep C Alexander Breskin, Senior Epidemiologist, NoviSci Lynn E. Fiellin, Associate Professor of Medicine and the Yale Child Study Center, Director, play2PREVENT Lab at the Yale Center for Health & Learning Games, Yale University School of Medicine Tracy L. Rabin, Assistant Professor of Medicine, Yale University School of Medicine Julia Marcus, Assistant Professor, Harvard Medical School Nathan D. Grubaugh, Assistant Professor, Department of Epidemiology of Microbial Diseases, Yale School of Public Health Lesley Meng, Assistant Professor of Operations Management, Yale School of Management Heather Edney, Director, Communications and Development, Homeless Health Care Los Angeles Nicolas Terry, Professor of Law, Indiana University Robert H. McKinney School of Law Richard Daynard, University Distinguished Professor of Law, Northeastern University, President, Public Health Advocacy Institute Peter D. Jacobson, Professor Emeritus of Health Law and Policy, Director, Center for Law, Ethics, and Health, University of Michigan School of Public Health Marcella Nunez-Smith, Associate Professor, Yale Schools of Medicine, Public Health, and Management Zhuo Chen, Associate Professor, University of Georgia, and Li Dak Sum Chair Professor in Health Economics, University of Nottingham Kasia J. Lipska, Assistant Professor of Medicine, Yale School of Medicine Ruochen Sun, Student, Yale School of Public Health Linda M. Niccolai, Professor, Epidemiology of Microbial Diseases, Yale School of Public Health, Director, Connecticut Emerging Infections Program at Yale Qi (Harry) Zhang, Associate Professor, School of Community and Environmental Health, Old Dominion University Huiwen Xu, Research Assistant Professor, University of Rochester.

> Gene W. Matthews, Retired Chief Legal Advisor to CDC Hongyun Fu, Associate Professor, Division of Community Health and Research, Pediatrics Department, Eastern Virginia Medical School Shutong Huo, Student,Yale School of Public Health Sheela Shenoi, Assistant Professor of Medicine, Yale School of Medicine Jing Ma, MD, PhD, Associate Professor of Population Medicine, Department of Population Medicine, Harvard Medical School Carmen Portillo, Executive Deputy Dean, Yale School of Nursing Joe Amon, Director of Global Health, Clinical Professor, Community Health and Prevention, Dornsife School of Public Health, Drexel University Lauren W. Kestner, Harm Reduction Program Manager, Prevention Specialist Alison Galvani, Director, Yale Center for Infectious Disease Modeling and Analysis (CIDMA), Burnett and Stender Families Professor of Epidemiology, Yale School of Public Health Harlan M. Krumholz, Harold H. Hines, Jr. Professor of Medicine, Department of Internal Medicine, Section of Cardiovascular Medicine, Director, Yale-New Haven Hospital Center for Outcomes Research and Evaluation Cary P. Gross, Director, National Clinician Scholars Program at Yale, Cancer Outcomes, Public Policy & Effectiveness Research Center, Yale School of Medicine Hanming Fang, Class of 1965 Term Professor of Economics, Department of Economics, University of Pennsylvania Reza Yaesoubi, Assistant Professor of Health Policy and Management, Yale Schools of Public Health David A. Fiellin, Professor of Medicine, Emergency Medicine and Public Health, Yale School of Medicine Kenneth A. Freedberg, Professor of Medicine, Massachusetts General Hospital, Harvard Medical School Miguel Hernan, Professor of Epidemiology, Harvard T.H. Chan School of Public Health Harold Pollack, Helen Ross Professor, School of Social Service Administration, University of Chicago Kathryn N. Shands, former Chief of the Toxic Shock Syndrome Task Force at CDC Alexandra L Phelan, Faculty, Georgetown University Center for Global Health Science & Security, Adjunct Professor, Georgetown University Law Center Ellen Isaacs, Retired Assistant Professor, New York Medical College Robin W. Simon, Professor of Sociology, Wake Forest University Jessica Athens, Policy and Research Officer, New York State Health Foundation Jean Grassman, Associate Professor, Environmental, Occupational and Geospatial Health Sciences, CUNY Graduate School of Public Health and Health Policy Jeffrey Bratberg, Clinical Professor of Pharmacy Practice, URI College of Pharmacy Carolyn Prouty, Faculty, Public Health and Health Sciences, The Evergreen State College, Olympia, WA Wendy B. Bostwick, Associate Professor, University of Illinois at Chicago, College of Nursing Kim M. Blankenship, Professor, Department of Sociology, Associate Dean of Research, College of Arts and Sciences, Co-Director, Social and Behavioral Sciences Core, DC CFAR, American University David R. Williams, Norman Professor of Public Health,Harvard T.H. Chan School of Public Health John Steen, Immediate Past President, American Health Planning Association Amanda S. Birnbaum, Professor and Chair, Department of Public Health, Montclair State University T. Stephen

Jones, Centers for Disease Control and Prevention (retired) Elizabeth A. Samuels, Assistant Professor of Emergency Medicine, Brown Emergency Medicine Leo Beletsky, Professor of Law and Health Sciences, Northeastern University, Adjunct Associate Professor, UC San Diego School of Medicine Mindy Fullilove, Professor of Urban policy and Health, The New School Ryan McNeil, Assistant Professor, Internal Medicine, Director of Harm Reduction Research, Program in Addiction Medicine, Yale School of Medicine Andrew Bäck, MPH Candidate, Department of Epidemiology and Biostatistics, University of Maryland School of Public Health Sunil Parikh, Associate Professor, Yale Schools of Public Health and Medicine Kaveh Khoshnood, Associate Professor, Yale School of Public Health Jennifer E. Miller, Assistant Professor, Yale Medical School, Founder, Bioethics International Jeanette M. Tetrault, Associate Professor of Medicine, Program Director, Addiction Medicine Fellowship, Associate Director for Education and Training, Program in Addiction Medicine, Yale School of Medicine J. Lucian Davis, Associate Professor, Department of Epidemiology of Microbial Diseases, Yale School of Public Health David Vlahov, Professor of Nursing, Professor of Epidemiology Microbial Diseases, Yale University Lindsay F. Wiley, Professor of Law and Director of the Health Law and Policy Program, American University Alice M. Miller, Co-Director, Global Health Justice Partnership of the Yale Law School and the School of Public Health, Yale University Judith Feinberg Professor of Medicine/Infectious Diseases, Professor of Behavioral Medicine & Psychiatry, West Virginia University School of Medicine Deborah Cotton, Professor of Medicine, Boston University School of Medicine, Professor of Epidemiology, Boston University School of Public Health Ross D. Silverman, Professor of Health Policy and Management, Indiana University Fairbanks School of Public Health, Professor of Public Health and Law, Indiana University McKinney School of Law Polly J. Price, Asa Griggs Candler Professor of Law and Professor of Global Health, Emory University Jonathan Kahn, Professor of Law and Biology, Northeastern University School of Law Xuerong Wen, Assistant Professor of Pharmacoepidemiology and Health Outcome, University of Rhode Island Paul D. Cleary, PhD, Anna M.R. Lauder Professor of Public Health, Yale School of Public Health Muneer I. Ahmad, Clinical Professor of Law and Deputy Dean for Experiential Education, Yale Law School Rev. Dr. Gary Gunderson, Vice President, FaithHealth, Professor, Division of Public Health Sciences, Wake Forest University Baptist Medical Center and Professor of Faith and the Health of the Public Mary Crossley, John E. Murray Faculty Scholar and Professor of Law, University of Pittsburgh School of Law Shelley Geballe, Assistant Clinical Professor of Public Health, Yale School of Public Health; Clinical Lecturer, Yale Law School Rev. Dr. Gary Gunderson, Vice President, FaithHealth, Professor, Division of Public Health Sciences, Wake Forest University Baptist Medical Center and Professor of Faith and the Health of the Public Allan M. Brandt, Amalie Moses Kass Professor of the History of Medicine, Professor of the History of Science, Department of the History of Science, Department of Global Health and Social Medicine, Harvard University Melissa M. Goldstein, Associate Professor, Milken Institute School of Public Health, George Washington University Kimford J. Meador, Professor, Department of Neurology & Neurological Sciences, Stanford University School of Medicine Megan Ranney, Attending Physician, Department of Emergency Medicine, Alpert Medical School, Brown University Aiden Shapiro, Resident Physician, NYU/Bellevue Department of Emergency Medicine Nancy Krieger, Professor of Social Epidemiology, American Cancer Society Clinical Research Professor, Department of Social and Behavioral Sciences, Harvard T.H. Chan School of Public Health Mary Anglin, Associate Professor of Anthropology, University of Kentucky

> Kata Chillag, Hamilton McKay Professor in Biosciences and Human Health, Davidson College Christina S. Ho, Professor of Law, Associate Dean of Faculty Research and Development and New Programs, Rutgers Law School, Newark Angela Jarman, Assistant Professor of Emergency Medicine, UC Davis Debra DeBruin, Interim Director, Associate Professor, Director of Graduate Studies, Center for Bioethics, University of Minnesota Sam Snodgrass, Board of Directors, Broken No More/GRASP Samuel R. Friedman, Research Professor, Dept of Population Health, New York University School of Medicine Matthew M. Kavanagh, Faculty Affiliate, Department of International Health & Law Center, Georgetown University Marianne Sullivan, Professor, Public Health, William Paterson University of New Jersey Kim D. Jaffee, Associate Professor, School of Social Work, Wayne State University Alicia Ely Yamin, Senior Fellow at the Petrie-Flom Center for Health Law Policy, Biotechnology and Bioethics at Harvard Law School Lundy Braun, Professor of Medical Science, Professor of Africana Studies. Departments of Africana Studies and Pathology and Laboratory Medicine, Brown University Jacky Jennings, Associate Professor,

Johns Hopkins School of Medicine & Bloomberg School of Public Health Don Mathis, Adjunct Faculty, Delaware Technical Community College Duana Fullwiley, Associate Professor of Anthropology, Stanford University Marian Moser Jones, Associate Professor & Graduate Director, Department of Family Science, University of Maryland School of Public Health Marc Lipsitch, Professor of Epidemiology, Department of Epidemiology, Department of Immunology and Infectious Diseases, Director of the Center for Communicable Disease Dynamics, Harvard T.H. Chan School of Public Health Nicole Blum, MD Candidate, University of Illinois College of Medicine Jing Li, Assistant Professor of Health Policy and Economics, Department of Population Health Sciences, Weill Cornell Medical College W. P. Hanage, Associate Professor, Center for Communicable Disease Dynamics, Department of Epidemiology, Harvard T. H. Chan School of Public Health Glorian Sorensen, Professor, Harvard T.H. Chan School of Public Health David Rosner, Ronald Lauterstein Professor of Public Health and History, Columbia University Kimberly Sue, Medical Director, Harm Reduction Coalition Valerie Horsley, Assoc. Professor of Molecular, Cellular & Developmental Biology, Yale University Jason A. Smith, Associate Professor of Health Sciences, California State University, East Bay James G Kahn, Professor in Residence, Department of Epidemiology and Biostatistics, School of Medicine, UCSF Simon Sang, Associate Professor in Animal and One Health, Department of Agricultural and Environmental Sciences, College of Agriculture, Environment and Human Science Robert Field, Professor of Law and Professor of Health Management and Policy, Drexel University Matthew Wynia, Professor of Medicine and Public Health, Director, Center for Bioethics and Humanities, University of Colorado Robin W. Simon, Professor of Sociology, Wake Forest University Catherine DeLorey, President, Women's Health Institute Erica Concors, Medical Student, Rutgers Robert Wood Johnson Medical School Atheendar S. Venkataramani, Assistant Professor of Health Policy and Medicine, Perelman School of Medicine, University of Pennsylvania Lillian Tom-Orme, AIANNH Caucus, APHA, Co-Chair, Native Research Network, INC Steven Seeche, Community Mediator, Cambridge Mass Katherine M. Keyes, Ph.D., Associate Professor of Epidemiology, Columbia University, Mailman School of Public Health Elana Silver, Principal Epidemiologist, Laurelton Research Carole S. Vance, Senior Fellow, Global Health Justice Partnership, Yale University Mary T Bassett, Professor of the Practice of Health and Human Rights, Director, François-Xavier Bagnoud Center for Health and Human Rights at Harvard University Donald K Milton, Professor, Environmental & Occupational Health, Institute for Applied Environmental Health, School of Public Health, University of Maryland Martha Livingston, Professor and Chair, Public Health, SUNY Old Westbury Gay Young, Professor & Chair, Department of Sociology, American University Suzanne M. Babich, Associate Dean of Global Health, Acting Chair, Dept of Global Health, Professor of Health Policy and Management, Indiana University Matthew Kohrman, Associate Professor of Anthropology, Stanford University & Faculty Fellow at Stanford Center for Innovation in Global Health Wendy K. Mariner, Edward R. Utley Professor of Health Law, Boston University School of Public Health, Professor of Law, Boston University School of Law, Professor of Medicine, Boston University School of Medicine Alan Goodman, Professor of Biological Anthropology, Hampshire College Steven B. Auerbach, CAPT (Retired) U.S. Public Health Service, Board of Directors & Executive Committee, PNHP-NY Metro, Active/Public Volunteer for the Elizabeth Warren for President Campaign T.M. Luhrmann, Medical Anthropologist, Howard H. and Jessie T. Watkins University Professor of Anthropology and Professor, by courtesy, of Psychology, Stanford University Jim Bloyd, PhD Student, University of Illinois at Chicago School of Public Health Michael Barthman, Resident Physician, Brown Emergency Medicine Anna Reisman, Professor of Medicine, Yale School of Medicine Crissaris Sarnelli, Physician, Ryan Health Center Alison Buttenheim, Associate Professor of Nursing and Health Policy, University of Pennsylvania Lara Stemple, Assistant Dean; Director, Health and Human Rights Law Project, UCLA School of Law

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> Organizational Signatures
>
> Broken No More
> The Public Health Advocacy Institute
> Big Cities Health Coalition

>
> <Final COVID-19 Letter from Public Health and Legal Experts.docx>

From: Morens, David (NIH/NIAID) [E] [b6
b6]
Sent: 6/8/2020 5:47:37 PM
To: Sholts, Sabrina [b6]; Jon Epstein [b6]; Daniel Lucey [b6]; Daniel Lucey [b6]; Dennis Carroll [b6]; Larry Madoff [b6]; Larry Madoff [b6]; Murray, Suzan [b6]
CC: Rivers, Meg [b6]
Subject: RE: Outbreak extension and COVID-19 updates

Sabrina, you guys are doing such a great job it's just hard to believe, and of course, the exhibit has become timely in a way that we all feared, which is exactly why it was so important in the first place, and should remain so.

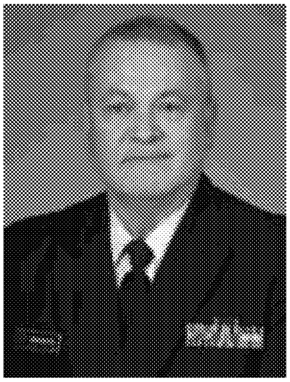
I am sure you must be giving thought to how the exhibit and what it represents will continue on, in some form, after it formally ends. Eventually we will know enough about COVID-19 to fill a whole exhibit on that subject alone. So, I'm hoping you won't let the subject fade away; it's a big subject, an existential one, and we'll be facing it again and again in coming years.

Kudo's to y'all

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

☎ b6 (assistants: Kimberly Barasch; Whitney Robinson)
📠 301 496 4409
💻 b6



From: Sholts, Sabrina b6
Sent: Friday, June 5, 2020 3:54 PM
To: Jon Epstein b6; Daniel Lucey b6; Daniel Lucey b6; Dennis Carroll b6; Larry Madoff b6; Larry Madoff b6; Morens, David (NIH/NIAID) [E] b6; Murray, Suzan b6
Cc: Rivers, Meg b6
Subject: Outbreak extension and COVID-19 updates

Dear *Outbreak* friends,

I hope you're all doing well in these incredibly challenging times. The *Outbreak* team at NMNH wanted to share some good news about exhibit, as we slowly move towards reopening the museum (at a date to be determined).

During the temporary closure of Smithsonian museums since March 14, we've been hard at work on COVID-19 updates to the exhibit. Our goal is that when visitors return to NMNH, they will be able to see and understand COVID-19 through the lens of One Health. We are delighted to tell you that exhibit's run has been extended again (!) until **August 2022**, which will allow many more people to experience the updated show.

The COVID-19 updates will be physically integrated into the exhibit in at least two sections:

1. Section 3: In the "International Spread of Disease" section of the exhibit, we will install a graphic panel and reader rail between the SARS and MERS stories and a video in the style of the SARS timeline (AV-3) on the existing screen. The physical installation will replace the interactive wheel about the causal factors of infectious disease transmission that is currently mounted on the wall in this spot. The video may loop alternately with the SARS video, rather than replacing it.
    - The COVID-19 reader rail will be consistent with the format of the other rails and the theme of the section, focusing on the zoonotic origin of SARS-CoV-2, what was needed to stop its global community spread (with respect to coordination, communication, testing and tracing, and treatment), and its impacts on frontline health workers (with a personal perspective from an infectious disease doctor at Mount Sinai Brooklyn).
    - The COVID-19 video will be graphically consistent with the SARS video, visualizing the cumulative cases of COVID-19 in different countries over time (using data from JHU's coronavirus resource center), with narration and soundbites that emphasize the importance of a global response in stopping the international spread of disease.
2. Section 9: In the "One Health mosaic" at the Constitution Ave exit of the exhibit, we will replace the existing graphics with large panels that reinforce what individuals can do to lower risks for the spread of infectious disease (hand washing, getting vaccinated, etc.). One of these action items will be "using Outbreak DIY", illustrated with a customized panel about COVID-19.

As these physical updates cannot be easily revised or expanded as COVID-19 continues into the unforeseen future, we will provide to most up-to-date information about COVID-19 outbreaks, scientific advances, and other developments through our volunteers, the ProMED/HealthMap kiosks (AV-9), and public programming.

It's impossible to express how much we appreciate your help and support in creating *Outbreak* and making it so successful. We realize that this journey is becoming longer than anyone anticipated at the start of it, and at this time you're all busier than ever before. Some of you have been involved directly with the development of these updates, and there's always more work to do. We thus hope that you're all willing to continue your involvement with *Outbreak* as possible, and your tremendous efforts in promoting *Outbreak* for public education and One Health. During the closure of NMNH, we've already offered two virtual *Outbreak* programs (https://naturalhistory.si.edu/education/after-hours/conversation-dennis-carroll-predicting-pandemics) and eight more are being planned for the summer. I've been delighted for these opportunities to stay connected while we're all apart, and I hope that we get to see you in one way or another soon. We'll always let you know about upcoming events via the regular stakeholder updates, and please feel free to keep us current on your activities as well!

Take care and stay well,
Sabrina (on behalf of the *Outbreak* team)

Sabrina Sholts, PhD
Curator of Biological Anthropology
Department of Anthropology
w b6
Twitter: @sabrinabsholts

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From: Morens, David (NIH/NIAID) [E] [b6
b6]
Sent: 2/25/2020 11:49:21 PM
To: William B. Karesh [b6]
BCC: Morens, David (NIH/NIAID) [E] [b6
(b6]
Subject: Re: BMJ-2020-055182 Manuscript Decision Editorials

OK, i need to go back and look at it. Not surprising because after all the truth is always the truth. Even in the Trump era. d

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

> On Feb 25, 2020, at 18:44, William B. Karesh b6 wrote:
>
> That would be great. And congrats.
>
> I looked at the Foreign Affairs website this afternoon and they have my article from 2005 posted under in Coronavirus section. It reads like it was written last week, not very much has changed.
>
> Sent from my iPhone
>
> **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
>
> b6 (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 develops science-based solutions to prevent pandemics and promote conservation.***
>
>> On Feb 25, 2020, at 6:32 PM, Morens, David (NIH/NIAID) [E]
>> b6 wrote:

And you probably know Peter and I and Jeff Taubenberger have a piece coming out tomorrow in the New England J Med

It might be a good tome for like minded colleagues to push harder, in concert, to wake up all those folks with their heads in the sands. Maybe the time has come? d

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

> On Feb 25, 2020, at 17:32, William B. Karesh b6 wrote:
>
> Along that "bigger picture" line David, stay tuned. Peter has on op-ed coming out in the next few day in the NYT International edition and Catherine has one coming out this week for Foreign Affairs
>
> **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
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> b6 (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 develops science-based solutions to prevent pandemics and promote conservation.*
>
>> On Feb 25, 2020, at 5:26 PM, Morens, David (NIH/NIAID) [E] b6 wrote:
>>
>> Just saw this and i think all options are viable. Whichever, this is/should be the perfect time (at the beginning of corona chaos) to think

ahead. The whole world is focusing myopically on case and death counts. We need big picture voices and a perspective that sees the universe of things. d

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

On Feb 25, 2020, at 16:38, Ellen Carlin b6 wrote:

Hi everyone,

This was nice of the editor to give us this kind of feedback. We took a chance on submitting our piece as an Editorial to BMJ because the Analysis is a longer piece at 1800-2000 words, and Original Research more involved still. Our paper is about 750 words. We did this as a short-form piece to begin with so it would be done quickly, alas…!

Let me propose a few options, in no particular order, and get your feedback:

1. **Expand the paper** into a longer form analysis, suitable for submitting to BMJ or another journal as a more involved research/analysis piece.

2. **Keep the paper as is**, and submit elsewhere. I would suggest Health Affairs as a good next option; their “DataWatch” article type is 2000 words or less, up to 6 exhibits; these are short papers that highlight data that "speak for themselves" relative to important policy issues or topics. They should shed light on some important question and be "worth knowing." They do not typically test hypotheses, rely on sophisticated statistical methods, or include lengthy policy discussions. We aim to present new data or new analyses of existing data that

are reliable and credible and that promote understanding among nonexperts on important, policy-relevant topics. We encourage work based on underused or new data sources.

If you want to submit as it but not to Health Affairs, please suggest a journal and article type.

3. **Take BMJ's suggestion to redraft into a rapid response** to their coronavirus coverage.

All comments welcome.
Thank you,
Ellen

On Feb 24, 2020, at 10:48 AM, BMJ <onbehalfof@manuscriptcentral.com> wrote:

24-Feb-2020
BMJ-2020-055182 entitled "Global health security: targeting investments toward unmet needs"

Dear Dr. Carlin,

Thank you for sending us your editorial. We read it with interest but decided against publication and I'm sorry to disappoint you.

The piece falls somewhere between research (you report methods) and Analysis (a long form article type that includes some data), but doesn't in its current form fit either. BMJ editorials don't report original findings.

Your bottom line message is clear however, and you might consider writing a rapid response to any recent content about covid - 19, discussing the lack of preventive initiatives globally. On line rapid responses are well read and a

selection are published in full as
letters. I'm sure you appreciate that I
can't prejudge that selection

You'll find all our coverage of the
covid - 19 outbreak here:
https://www.bmj.com/coronavirus

Sorry once again that I can't offer
you an editorial, and thank you for
your interest in the BMJ.

Yours sincerely,

Alison Tonks
Clinical Editor, BMJ
atonks@bmj.com

If you elected during submission to
send your article on to another
journal the article will be transferred
in 5 working days. If you intend to
appeal against this decision please
notify us before then.
The journal(s) (if any) you have
selected at submission are: BMJ
Global Health
If you want to speed up or stop this
onward transmission please email the
editorial office:
papersadmin@bmj.com

From: Morens, David (NIH/NIAID) [E] [b6
b6]

Sent: 10/9/2020 4:17:11 PM

To: 'Robert Tesh' [b6]; 'Garcia-Blanco, Mariano A.' [b6]; 'Murphy, Frederick A.' [b6]; 'Charles H Calisher' [b6]; 'Weaver, Scott' [b6]

CC: Peter Daszak (b6) [b6]; b6;
Taubenberger, Jeffery (NIH/NIAID) [E] [b6
b6]

Subject: RE: Bennett et al Nature s41586-020-2812-9.pdf

Wow!

David

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

☎ b6 (assistants: Kimberly Barasch; Whitney Robinson)
301 496 4409
b6

From: Robert Tesh b6
Sent: Friday, October 9, 2020 3:45 AM
To: Garcia-Blanco, Mariano A. b6; Murphy, Frederick A. b6; Charles H Calisher b6; Weaver, Scott b6; Morens, David (NIH/NIAID) [E] b6
Subject: Fwd: Bennett et al Nature s41586-020-2812-9.pdf

---------- Forwarded message ---------
From: **Ksiazek, Thomas G.** b6
Date: Fri, Oct 9, 2020, 12:15 AM
Subject: Bennett et al Nature s41586-020-2812-9.pdf
To: Amman Brian b6, Towner Jonathan (CDC/CCID/NCZVED) b6, Nichol Stuart b6, Rollin Pierre b6, Tesh Robert b6, Bob Swanepoel b6

One of the papers

From: Morens, David (NIH/NIAID) [E] [b6 b6]
Sent: 2/26/2020 3:18:37 PM
To: Ellen Carlin [b6]
Subject: RE: BMJ-2020-055182 Manuscript Decision Editorials

E, not sure what the “figures being editable” means, but my suspicion is that they, like some journals, want to tweak your figure so they can copyright it.

David

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

☎ b6 (assistants: Kimberly Barasch; Whitney Robinson)
📠 301 496 4409
💻 b6

From: Ellen Carlin b6
Sent: Wednesday, February 26, 2020 10:15 AM
To: Morens, David (NIH/NIAID) [E] b6
Cc: Franck Berthe b6; Kanya Long b6; Catherine Machalaba

b6; Billy Karesh b6
Subject: Re: BMJ-2020-055182 Manuscript Decision Editorials

David, that's great news! Thanks for that shout-out in your great article. Nice to see my name in NEJM:)

I don't know Health Affairs' reputation for fast turn-around but will see what I can find out online. I'm reading through their instructions and they require all figures to be editable, which is not going to work. Our figures were designed and baked over a year ago. I'm' not sure if I can get around that, let me keep researching their requirements. We may need a Plan B (or C, D, E…)

On Feb 26, 2020, at 9:46 AM, Morens, David (NIH/NIAID) [E] b6 wrote:

Ellen, FYI, we have just cited your original report in a paper coming out today (still embargoed), co-authored with Peter D, see the reference section (ref. 4) in the attached. Thus your work is now being cited as important for pandemic planning vis a vis the coronavirus epidemic. Good work for sure, Let's get it into print. Health Affairs is good, will they potentially publish quickly?

<image001.gif>

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<image002.jpg>

From: Ellen Carlin b6
Sent: Wednesday, February 26, 2020 9:37 AM
To: Franck Berthe b6
Cc: Kanya Long b6 Morens, David (NIH/NIAID) [E] b6; Catherine Machalaba b6; Billy Karesh b6
Subject: Re: BMJ-2020-055182 Manuscript Decision Editorials

Hi everyone, thanks for weighing in and for all your encouragement! I agree we have a unique product here, and that makes it hard to nail the right platform. We are inherently swimming against the tide given that our study finding is that no one cares about our finding (prevention and recovery)!

I am leaning toward Health Affairs and, since you can have up to 2000 words for Data Watch, I will spend an hour or so today to add a little more meat on the bones, giving us a chance to present a little more detail about our findings. We will still have the 750 word piece to fall back on if we need to submit again elsewhere. If you would like to see the updated piece before I submit let me know; otherwise I will proceed as planned and try to submit by tomorrow.

Ellen

On Feb 26, 2020, at 5:10 AM, Franck Cesar Jean Berthe b6 wrote:

Same on my side
I will support your decision
It is the time now
:-)

From: Kanya Long b6
Sent: Tuesday, February 25, 2020 5:33:42 PM
To: Morens, David (NIH/NIAID) [E] b6
Cc: Ellen Carlin b6; Catherine Machalaba b6; Franck Cesar Jean Berthe b6; Billy Karesh b6
Subject: Re: BMJ-2020-055182 Manuscript Decision Editorials

[External]
Ellen,

Supportive of whatever direction you think is best and can contribute if you choose to expand the piece.

I agree that the time is right.

Kanya

On Tue, Feb 25, 2020 at 2:26 PM Morens, David (NIH/NIAID) [E] b6 wrote:

> Just saw this and i think all options are viable. Whichever, this is/should be the perfect time (at the beginning of corona chaos) to think ahead. The whole world is focusing myopically on case and death counts. We need big picture voices and a perspective that sees the universe of things. d
>
> Sent from my iPhone
> David M Morens
> OD, NIAID, NIH
>
> > On Feb 25, 2020, at 16:38, Ellen Carlin b6 wrote:
> >
> > Hi everyone,
> >
> > This was nice of the editor to give us this kind of feedback. We took a chance on submitting our piece as an Editorial to BMJ because the Analysis is a longer piece at 1800-2000 words, and Original Research more involved still. Our paper is about 750 words. We did this as a short-form piece to begin with so it would be done quickly, alas…!

Let me propose a few options, in no particular order, and get your feedback:

1. **Expand the paper** into a longer form analysis, suitable for submitting to BMJ or another journal as a more involved research/analysis piece.

2. **Keep the paper as is**, and submit elsewhere. I would suggest Health Affairs as a good next option; their “DataWatch” article type is 2000 words or less, up to 6 exhibits; these are short papers that highlight data that "speak for themselves" relative to important policy issues or topics. They should shed light on some important question and be "worth knowing." They do not typically test hypotheses, rely on sophisticated statistical methods, or include lengthy policy discussions. We aim to present new data or new analyses of existing data that are reliable and credible and that promote understanding among nonexperts on important, policy-relevant topics. We encourage work based on underused or new data sources.

If you want to submit as it but not to Health Affairs, please suggest a journal and article type.

3. **Take BMJ’s suggestion to redraft into a rapid response** to their coronavirus coverage.

All comments welcome.
Thank you,
Ellen

On Feb 24, 2020, at 10:48 AM, BMJ <onbehalfof@manuscriptcentral.com> wrote:

24-Feb-2020
BMJ-2020-055182 entitled "Global health security: targeting investments toward unmet needs"

Dear Dr. Carlin,

Thank you for sending us your editorial. We read it with interest but decided against publication and I'm sorry to disappoint you.

The piece falls somewhere between research (you report methods) and Analysis (a long form article type that includes some data), but doesn't in its current form fit either. BMJ editorials don't report original findings.

Your bottom line message is clear however, and you might consider writing a rapid response to any recent content about covid - 19, discussing the lack of preventive initiatives globally. On line rapid responses are well read and a selection are published in full as letters. I'm sure you appreciate that I can't prejudge that selection

You'll find all our coverage of the covid - 19 outbreak here: https://www.bmj.com/coronavirus

Sorry once again that I can't offer you an editorial, and thank you for your interest in the BMJ.

Yours sincerely,

Alison Tonks
Clinical Editor, BMJ
b6

> If you elected during submission to send your article on to another journal the article will be transferred in 5 working days. If you intend to appeal against this decision please notify us before then.
> The journal(s) (if any) you have selected at submission are: BMJ Global Health
> If you want to speed up or stop this onward transmission please email the editorial office: papersadmin@bmj.com

<NEJM Pandora 02 26 2020.pdf>

From: Ellen Carlin [b6]
Sent: 2/18/2020 7:15:29 PM
To: Morens, David (NIH/NIAID) [E] [b6
b6]
CC: Sarah Babcock [b6]
Subject: Re:

Thanks, David! It was great to see you, too. EHA email is still good. I'm a fellow there.

And thanks for following up the papers—particularly looking forward to reading Meyer and Schultz.

On Feb 18, 2020, at 12:45 PM, Morens, David (NIH/NIAID) [E] b6 wrote:

Hi Sarah,
Thanks again for dinner and great to see you both! I just realized that the email I have for Ellen is an EcoHealth one, so if she has a new/better email can you forward to her and let me know the address?
b6 is a pretty cool place, I can see why you like it. And my first French 75!
I promised I'd send the paper on Eastern equine encephalitis we just did so here it is, attached. I also mentioned a couple anthrax history papers making the point tangentially that there was One Health thinking in the 1700s, also attached. Also, below, a blurb from a chapter I am writing on the history of arbovirology, giving thumbnail bios of the guys I mentioned, Meyer and May (sounds like a comedy duo), who were big One Health guys in the early to mid 1900s. Meyer was a big influenza on Jim Steele, DVM, who more than anyone else, pioneered the One Health concept, and who I knew well way back when... Jim in turn influenced my close friend b6), who carried on the One Health tradition at CDC. Also attached. Lots of history!
Don't forget next time you come back if you need a place to stay or car to drive, just let me know. Also, what your summer plans are up in b6. I hope to get up there, maybe in conjunction with hydroplane races?
David

Karl Friedrich Meyer (1884-1974) and *Jacques Meyer May* (1896-1975) were European-born/American-based scientists whose ideas about disease ecology, zoonotic diseases, and environmental determinants of disease [61], were highly influential on arbovirologists of the era, and were among the first modern conceptualizations of what is now referred to as "One Health". The Swiss-born Meyer received a veterinary degree, then studied with **Arnold Theiler** (1867-1936) in South Africa. At age 36 he came to the U.S., was appointed professor at UC Berkeley, and began working with Nobel laureate **George Hoyt Whipple** (1878-1976) at the Hooper Foundation. In the 1930s, Meyer and colleagues isolated and were among those who characterized Western equine encephalitis (WEE), greatly influencing Meyer's young protégé **Bill Reeves**. In an era in which few top research scientists published as many as 100 papers in a lifetime, Meyer published over 800 in virology, epidemiology, epizootiology, and a host of other biomedical disciplines. His intellect and productivity astounded all. He became among the most revered biomedical scientists of the 20th century. I never met Meyer, but mycobacteriologist Jim Douglas, who knew him in the 1960s, describes Meyer as tall and broad shouldered, making a striking contrast to his protégé Bill Reeves, also tall, who was at that one time extraordinarily thin. The Switzerland-born Meyer had a strong German accent, dressed expensively, belonged to an exclusive private club, and drank 'French 75s", a cocktail mixture of champagne and brandy named after a light field gun used by the French in WWI. Douglas also remembers a story Meyer told about isolating WEE, in which he stalled off a rancher with a dead horse in deep conversation after badgering Berkeley colleague **Stewart H. Madin** (of MDCK cell line fame [1918-2002]) to sneak behind the barn and decapitate the horse to sneak the tissue back to the lab. An audio recording of the same event survives, but features altered details, and is related by Meyer as a swashbuckling adventure.

May was a French-born physician and tropical medicine researcher who had worked in Thailand, Vietnam, Singapore, and Africa, before joining the medical staff of exiled General Charles De Gaulle during WWII. He came to the U.S. in 1948 as a medical geographer, a term that now roughly corresponds to global health expert. Thereafter his career focused on disease ecology and nutrition. May's 1959 book *The Ecology of Human Disease* was an instant classic and remains so today. Though working entirely independently, Meyer and May both promoted a "one health" focus, were leading members of tropical medicine societies, and were regarded as important thought leaders by arbovirologists of the era.

<image001.gif>

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<image002.jpg>

<EEE 2019 NEJM.pdf><picrender.pdf><Copy of ms148.pdf><Schultz memoriam publ 07 17 2019 19-0356 - Copy.pdf>

From: Morens, David (NIH/NIAID) [E] [b6
(b6]
Sent: 8/5/2021 11:03:18 PM
To: Peter Daszak [b6]
CC: Roberts, Rich [b6]; Edward Holmes [b6]; Keusch, Jerry
[b6]; Robert Kessler [b6]
BCC: Morens, David (NIH/NIAID) [E] [b6
(b6]
Subject: Re: CNN: Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt https://protect-au.mimecast.com/s/xCyoCvl1rKi7NAywGIQWvWo?domain=cnn.it

Don’t hold your effing breath!!!!!!!! d

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

> On Aug 5, 2021, at 19:02, Peter Daszak b6 wrote:
>
> Once the intel agencies have used their “elite institution’s supercomputers” to crank out a phylogeny, perhaps they’d like to publish it in a journal. As Editor-in-Chief of the Springer journal “EcoHealth”, we’d be interesting in looking at a manuscript…
>
> Cheers,
>
> Peter
>
> **Peter Daszak**
> *President*
>
> EcoHealth Alliance
> 520 Eighth Avenue, Suite 1200
> New York, NY 10018-6507
> USA
>
> Tel.: b6
> Website: www.ecohealthalliance.org
> Twitter: @PeterDaszak
>
> *EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation*
>
> **From:** Roberts, Rich b6
> **Sent:** Thursday, August 5, 2021 6:28 PM
> **To:** Morens, David (NIH/NIAID) [E] b6; Edward Holmes
> b6

Cc: Peter Daszak (b6) <b6>; Keusch, Jerry (b6) <b6>; Kessler, Robert (b6) b6
Subject: RE: CNN: Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt https://protect-au.mimecast.com/s/xCyoCvl1rKi7NAywGIQWvWo?domain=cnn.it

Me too, but until we get rid of the politicians that may not happen.

Rich

Richard J. Roberts
New England Biolabs
240 County Road
Ipswich, MA 01938-2723
USA
Tel: b6
Fax: (978) 412 9910
email: b6

From: Morens, David (NIH/NIAID) [E] b6
Sent: Thursday, August 5, 2021 5:42 PM
To: Edward Holmes b6
Cc: Peter Daszak (b6) <b6>; Keusch, Jerry (b6) <b6>; Kessler, Robert (b6) b6; Roberts, Rich b6
Subject: Re: CNN: Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt https://protect-au.mimecast.com/s/xCyoCvl1rKi7NAywGIQWvWo?domain=cnn.it

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> Yes, I hope that means we can put that particular issue to bed.
>
> Professor Edward C. Holmes FAA FRS
> The University of Sydney
>
>> On 6 Aug 2021, at 7:26 am, Morens, David (NIH/NIAID) [E] b6 wrote:

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From: Folkers, Greg (NIH/NIAID) [E] b6
Sent: Thursday, August 5, 2021 4:18 PM
Subject: CNN: Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt https://cnn.it/3fzBbsp

Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt

By Katie Bo Williams, Zachary Cohen and Natasha Bertrand, CNN

Updated 9:02 AM ET, Thu August 5, 2021

*Washington (CNN)*US intelligence agencies are digging through a treasure trove of genetic data that could be key to uncovering the origins of the coronavirus -- as soon as they can decipher it.

This giant catalog of information contains genetic blueprints drawn from virus samples studied at the lab in Wuhan, China which some officials believe may have been the source of the Covid-19 outbreak, multiple people familiar with the matter tell CNN.

It's unclear exactly how or when US intelligence agencies gained access to the information, but the machines involved in creating and processing this kind of genetic data from viruses are typically connected to external cloud-based servers -- leaving open the possibility they were hacked, sources said.

Still, translating this mountain of raw data into usable information -- which is only one part of the intelligence community's 90-day push to uncover the pandemic's origins -- presents a range of challenges, including harnessing enough computing power to process it all. To do that, intelligence agencies are relying on supercomputers at the Department of Energy's National Labs, a collection of 17 elite government research institutions.

There's also a manpower issue. Not only do intelligence agencies need government scientists skilled enough to interpret complex genetic sequencing data and who have the proper security clearance, they also need to speak Mandarin, since the information is written in Chinese with a specialized vocabulary.

"Obviously there are scientists who are (security) cleared," one source familiar with the intelligence told CNN. "But Mandarin-speaking ones who are cleared? That's a very small pool. And not just any scientists, but ones who specialize in bio? So you can see how this quickly becomes difficult."

Officials conducting the 90-day review hope this information will help answer the question of how the virus jumped from animals to humans. Unlocking that mystery is essential to ultimately determining whether Covid-19 leaked from the lab or was transmitted to humans from animals in the wild, multiple sources told CNN.

Investigators both inside and outside the government have long sought genetic data from 22,000 virus samples that were being studied at the Wuhan Institute of Virology. That data was removed from the internet by Chinese officials in September 2019, and China has since refused to turn over this and other raw data on early coronavirus cases to the World Health Organization and the US.

The question for investigators is whether the WIV or other labs in China possessed virus samples or other contextual information that could help them trace the coronavirus' evolutionary history.

Two scientists who study coronaviruses told CNN they are skeptical that there is any genetic data either in the tranche of 22,000 samples or any other database from the WIV that scientists don't already know about.

"Basically in [a 2020 research paper published in Nature], the WIV talked about all the sequences they had up until a certain point in time -- it's what most scientists virologists believe, that's pretty much what they had," said Dr. Robert Garry, a virologist at the Tulane University School of Medicine.

A source familiar with the US investigation would neither confirm nor deny that any of the data pertaining to those 22,000 samples is among what US intelligence agencies are currently analyzing.

No 'smoking gun'

Sources familiar with the effort say filling in that missing genetic link won't be enough to definitively prove whether the virus originated in the lab at Wuhan or first emerged naturally. Officials will still need to piece together other contextual clues to determine the true origins of the pandemic.

But it is a critical puzzle piece that the Biden administration has been prioritizing.
"The most prized technical data in this context are genetic sequences, database entries and contextual information about the provenance of the samples and the time and context in which they were acquired -- information people would use to place them in a narrative of the origins of SARS, Covid," one source familiar with the investigation told CNN.

For now, senior intelligence officials still say that they are genuinely split between the two prevailing theories on the pandemic's origins, or some combination of both scenarios. CNN reported last month that senior Biden administration officials overseeing the 90-day review now believe the theory that the virus accidentally escaped from a lab in Wuhan is at least as credible as the possibility that it emerged naturally in the wild -- a dramatic shift from a year ago, when Democrats publicly downplayed the so-called lab leak theory.

Multiple sources told CNN that absent an unexpected windfall of new information, officials don't expect to uncover a "smoking gun" -- like intercepted communications, for example -- that would offer definitive proof for either theory. The Biden administration's 90-day push is predicated on the expectation that science, not intelligence will be the key.

Intelligence officials are tasked with addressing several "scientific knowledge gaps" about the virus' evolution, according to the collection guidance governing the 90-day push, distributed to more than a dozen agencies on June 11 by the Office of the Director of National Intelligence and obtained by CNN.

The memo instructs the intelligence community to "expand its collection" and consider data already in its possession to identify both the initial host of the coronavirus and any species that it may have passed through as it adapted to humans -- or to find as "any progenitor virus and/or virus that could serve as backbone for genetic engineering purposes."

But former Director of National Intelligence John Ratcliffe told CNN that the US intelligence community already had sufficient collection on the topic of Covid origins.

"Obviously the more, the better. But we've had extraordinary insight into this topic for many months, much more than has been declassified. Pretending we didn't is political theater and a classic example of a politician trying to buy time by using the IC as a scapegoat," he told CNN in a statement.

Digging into the science

That's where the genomic data from the Wuhan lab could come in.

The genetic code of a given virus is the signature that allows scientists to tell the difference between the Delta and Beta variants of the coronavirus, for example. It can also offer clues as to how the virus has adapted or mutated over time, including whether it shows signs of human manipulation -- a kind of genetic history.

Many scientists continue to believe that the most likely scenario is that the virus jumped from animals to humans naturally. But despite testing thousands of animals, researchers still haven't identified the intermediate host through which the virus passed as it adapted to humans.

But some researchers, intelligence officials and Republican lawmakers believe that researchers at the WIV might have genetically altered a virus in the lab, using a controversial kind of research known as "gain of function" that could have infected researchers who then spread it in their community.

It's also plausible that the initial infection took place naturally outside of the lab, perhaps while a scientist was collecting a sample from an animal in the wild, and that scientist then spread the virus unknowingly when he returned to the lab with the samples, multiple sources familiar with the intelligence explained.

"If it was the latter, it was likely brought into a lab to study because someone got sick ... which means there were an unknowable number of other people who were already sick," the source familiar with the probe said.

Understanding exactly which viruses researchers at the WIV were working on could provide important evidence for any one of these theories. It's one of the reasons that investigators on Capitol Hill and elsewhere have been keenly focused on the database that was taken offline in 2019.

But it might not prove anything definitively, sources familiar with the intelligence say. Even if scientists in the intelligence community are able to use the data from the lab to stitch together a complete genetic history that shows how the virus mutated, they might not have enough information about how it was handled by the Chinese lab to determine with a high level of confidence that it leaked.

"Despite having that complete history of variants, [officials might] lack the contextual information to make sense of it in a narrative way," the source familiar with the investigation explained.
"Even a complete sequence history is difficult to obtain. And doesn't really tell us anything about the origins of the pandemic itself without the context," this person added.

Some Republicans on Capitol Hill have jumped into the uncertainty with their own report claiming that "the preponderance of evidence suggests" the coronavirus was "accidentally" released from a lab in Wuhan in 2019 -- an assertion that goes far beyond the intelligence community's current view of the matter.

90 days -- and then what?

It's possible that at the end of Biden's 90-day push, the intelligence community won't have reached what's known as a "high-confidence" assessment as to the pandemic's origins. Administration officials have previously suggested to CNN that it's possible a second review could be ordered at the end of the 90 days.

A bipartisan group of lawmakers on the Senate Intelligence and Foreign Relations Committees earlier this week sent a letter urging the administration to continue to prioritize the hunt until such a judgment can be made in order to prevent future pandemics.

But the lawmakers also zeroed in on a related focus for intelligence officials probing the pandemic's origins: China's "efforts to conceal the severity and scope of the outbreak of the SARS-CoV-2 virus that caused the COVID-19 pandemic."
"We also believe that the investigation should address PRC efforts to prevent international inquiries into the origins of SARS-CoV-2, and other actions PRC authorities have taken to obscure the nature of the virus and its transmission," the lawmakers said.

Republican lawmakers in the House, meanwhile, have latched onto the theory that the virus escaped from a lab. GOP lawmakers in a report released Monday by Rep. Michael McCaul of Texas have claimed that "the preponderance of evidence suggests" the coronavirus was "accidentally" released from a lab in Wuhan in 2019.

Intelligence officials say it's still far too soon to say.

From: b6 [b6]
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Subject: Re: CNN: Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt https://protect-au.mimecast.com/s/xCyoCvl1rKi7NAywGIQWvWo?domain=cnn.it

I think Shakespeare needs to be updated. "Killed all the lawyers" should perhaps be changed to "Kill all the politicians". But i repeat myself..... d

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Richard J. Roberts
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email: b6

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Sources familiar with the effort say filling in that missing genetic link won't be enough to definitively prove whether the virus originated in the lab at Wuhan or first emerged naturally. Officials will still need to piece together other contextual clues to determine the true origins of the pandemic.

But it is a critical puzzle piece that the Biden administration has been prioritizing.

"The most prized technical data in this context are genetic sequences, database entries and contextual information about the provenance of the samples and the time and context in which they were acquired -- information people would use to place them in a narrative of the origins of SARS, Covid," one source familiar with the investigation told CNN.

For now, senior intelligence officials still say that they are genuinely split between the two prevailing theories on the pandemic's origins, or some combination of both scenarios. CNN reported last month that senior Biden administration officials overseeing the 90-day review now believe the theory that the virus accidentally escaped from a lab in Wuhan is at least as credible as the possibility that it emerged naturally in the wild -- a dramatic shift from a year ago, when Democrats publicly downplayed the so-called lab leak theory.

Multiple sources told CNN that absent an unexpected windfall of new information, officials don't expect to uncover a "smoking gun" -- like intercepted communications, for example -- that would offer definitive proof for either theory. The Biden administration's 90-day push is predicated on the expectation that science, not intelligence will be the key.

Intelligence officials are tasked with addressing several "scientific knowledge gaps" about the virus' evolution, according to the collection guidance governing the 90-day push, distributed to more than a dozen agencies on June 11 by the Office of the Director of National Intelligence and obtained by CNN.

The memo instructs the intelligence community to "expand its collection" and consider data already in its possession to identify both the initial host of the coronavirus and any species that it may have passed through as it adapted to humans -- or to find as "any progenitor virus and/or virus that could serve as backbone for genetic engineering purposes."

But former Director of National Intelligence John Ratcliffe told CNN that the US intelligence community already had sufficient collection on the topic of Covid origins.

"Obviously the more, the better. But we've had extraordinary insight into this topic for many months, much more than has been declassified. Pretending we didn't is political theater and a classic example of a politician trying to buy time by using the IC as a scapegoat," he told CNN in a statement.

Digging into the science

That's where the genomic data from the Wuhan lab could come in.

The genetic code of a given virus is the signature that allows scientists to tell the difference between the Delta and Beta variants of the coronavirus, for example. It can also offer clues as to how the virus has adapted or mutated over time, including whether it shows signs of human manipulation -- a kind of genetic history.

Many scientists continue to believe that the most likely scenario is that the virus jumped from animals to humans naturally. But despite testing thousands of animals, researchers still haven't identified the intermediate host through which the virus passed as it adapted to humans.

But some researchers, intelligence officials and Republican lawmakers believe that researchers at the WIV might have genetically altered a virus in the lab, using a controversial kind of research known as "gain of function" that could have infected researchers who then spread it in their community.

It's also plausible that the initial infection took place naturally outside of the lab, perhaps while a scientist was collecting a sample from an animal in the wild, and that scientist then spread the virus unknowingly when he returned to the lab with the samples, multiple sources familiar with the intelligence explained.

"If it was the latter, it was likely brought into a lab to study because someone got sick ... which means there were an unknowable number of other people who were already sick," the source familiar with the probe said.
Understanding exactly which viruses researchers at the WIV were working on could provide important evidence for any one of these theories. It's one of the reasons that investigators on Capitol Hill and elsewhere have been keenly focused on the database that was taken offline in 2019.

But it might not prove anything definitively, sources familiar with the intelligence say. Even if scientists in the intelligence community are able to use the data from the lab to stitch together a complete genetic history that shows how the virus mutated, they might not have enough information about how it was handled by the Chinese lab to determine with a high level of confidence that it leaked.

"Despite having that complete history of variants, [officials might] lack the contextual information to make sense of it in a narrative way," the source familiar with the investigation explained.
"Even a complete sequence history is difficult to obtain. And doesn't really tell us anything about the origins of the pandemic itself without the context," this person added.

Some Republicans on Capitol Hill have jumped into the uncertainty with their own report claiming that "the preponderance of evidence suggests" the coronavirus was "accidentally" released from a lab in Wuhan in 2019 -- an assertion that goes far beyond the intelligence community's current view of the matter.

90 days -- and then what?

It's possible that at the end of Biden's 90-day push, the intelligence community won't have reached what's known as a "high-confidence" assessment as to the pandemic's origins. Administration officials have previously suggested to CNN that it's possible a second review could be ordered at the end of the 90 days.

A bipartisan group of lawmakers on the Senate Intelligence and Foreign Relations Committees earlier this week sent a letter urging the administration to continue to prioritize the hunt until such a judgment can be made in order to prevent future pandemics.

But the lawmakers also zeroed in on a related focus for intelligence officials probing the pandemic's origins: China's "efforts to conceal the severity and scope of the outbreak of the SARS-CoV-2 virus that caused the COVID-19 pandemic."

"We also believe that the investigation should address PRC efforts to prevent international inquiries into the origins of SARS-CoV-2, and other actions PRC authorities have taken to obscure the nature of the virus and its transmission," the lawmakers said.

Republican lawmakers in the House, meanwhile, have latched onto the theory that the virus escaped from a lab. GOP lawmakers in a report released Monday by Rep. Michael McCaul of Texas have claimed that "the preponderance of evidence suggests" the coronavirus was "accidentally" released from a lab in Wuhan in 2019.

Intelligence officials say it's still far too soon to say.

From: Peter Daszak [b6]
Sent: 9/18/2021 1:44:43 PM
To: Edward Holmes [b6]; Wang Linfa b6
CC: Jason Gale [j.gale@bloomberg.net]; Stephen Goldstein [b6]; b6; Garry, Robert F [b6];
b6; Morens, David (NIH/NIAID) [E]
[b6
[b6]; Robert Kessler
[b6]
Subject: RE: Study from 2007 shows SARS-infected civets on farms in Hubei

SARSr-CoV-2 related bat CoV (97-99% whole genome) w/ an FCS and ACE2 binding would be the smoking gun, but only in the last few weeks, we've found the shooter, the place where he bought the gun, the wide diversity of guns available, and boxes of ammo lying all over the place. How's that for a distorted, overextended metaphor…

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-6507
USA

Tel.: b6
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

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

---

From: Edward Holmes b6
Sent: Friday, September 17, 2021 11:05 PM
To: Wang Linfa b6
Cc: Jason Gale <j.gale@bloomberg.net>; Stephen Goldstein b6;
b6; Peter Daszak
b6
Subject: Re: Study from 2007 shows SARS-infected civets on farms in Hubei

Yes, people are already claiming that the lack of a furin cleavage cite in these viruses means that it must have been inserted into SARS-CoV-2.

They must have a large team of engineers on hand so they can regularly move the goal posts.

PROFESSOR EDWARD C. HOLMES FAA FRS
ARC Australian Laureate Fellow

THE UNIVERSITY OF SYDNEY
Marie Bashir Institute for Infectious Diseases & Biosecurity,
School of Life & Environmental Sciences and School of Medical Sciences,
The University of Sydney | Sydney | NSW | 2006 | Australia
T b6
E

On 18 Sep 2021, at 12:56 pm, Wang Linfa b6 wrote:

Almost identical SARS-CoV-2 RBD in several bat sarbecoviruses! This is as close as you can get for a natural RBD origin!

Also, the paper concluded that SARS-CoV-2 genome fragments are found in different sarbecoviruses, very similar to the PloS Path paper for SARS-CoV-1.

All we need is to find a sarbecovirus with a furin cleavage site and no more debate on the natural origin of SARS-CoV-2!

Linfa (Lin-Fa) WANG, PhD FTSE FAAM
Professor
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: b6

From: Edward Holmes b6
Sent: Thursday, 16 September 2021 3:31 PM
To: Jason Gale <j.gale@bloomberg.net>
Cc: Stephen Goldstein b6
b6; Peter Daszak
b6; Wang Linfa
Subject: Re: Study from 2007 shows SARS-infected civets on farms in Hubei

- External Email -

Dismantles one key argument of the leakers - how could a virus get from Yunnan to Wuhan - in one simple move.

PROFESSOR EDWARD C. HOLMES FAA FRS
ARC Australian Laureate Fellow

THE UNIVERSITY OF SYDNEY
Marie Bashir Institute for Infectious Diseases & Biosecurity,
School of Life & Environmental Sciences and School of Medical Sciences,
The University of Sydney | Sydney | NSW | 2006 | Australia
T b6
E

On 16 Sep 2021, at 2:26 pm, Jason Gale (BLOOMBERG/ NEWSROOM:) <j.gale@bloomberg.net> wrote:

And there's this:
"The discovery of civet-CoVs in the Hubei province should not be a surprise as SARS-CoV-like viruses were recently found in a bat species in the same province"

From: b6 At: 09/16/21 14:24:33 UTC+10:00
To: Jason Gale (BLOOMBERG/ NEWSROOM:)
Cc: b6
b6
Subject: Re: Study from 2007 shows SARS-infected civets on farms in Hubei

Just stumbled across it reading the discussion of another paper honestly. It's been cited since - there are certainly people who remembered it but I did not know of it and clearly had not penetrated the public origins discussion.

Stephen

Sent from my iPhone

On Sep 15, 2021, at 10:22 PM, Jason Gale (BLOOMBERG/ NEWSROOM:) <j.gale@bloomberg.net> wrote:

Well done, Stephen for finding this:https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1900161/

Jason Gale, MHlthSec
Senior editor & chief biosecurity correspondent
| Bloomberg News
Level 30, 120 Collins St., Melbourne VIC 3000
Tel. (landline) +61-3-9228-8783 | Mobile b6
b6
@jwgale |
Linkedin: http://www.linkedin.com/pub/jason-gale/6/249/a56

<210918-preprint-Lao-RBD very close to SARS-CoV-2.pdf>

From: William B. Karesh [b6]
Sent: 11/22/2021 5:02:13 PM
To: Morens, David (NIH/NIAID) [E] [b6
(b6)]
Subject: Re: figure for World Bank report

perfect, thanks again.

BK

On Nov 22, 2021, at 11:56 AM, Morens, David (NIH/NIAID) [E] b6 wrote:

Yes, that would work, thanks

<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
☎ b6 (assistant: Whitney Robinson)
📠 301 496 4409
💻 b6

<image002.jpg>

From: William B. Karesh b6
Sent: Monday, November 22, 2021 11:54 AM

To: Morens, David (NIH/NIAID) [E] b6
Cc: Catherine Machalaba b6 ; Daniel Mira-Salama
b6
Subject: Re: figure for World Bank report

Yes, both received.

If we use the more recent one (post 2020 publication) should we cite “Morens and Fauci, NIH, 2021” ?

BK

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

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018 USA

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www.ecohealthalliance.org

President, OIE Working Group on Wildlife

Co-chair, IUCN Species Survival Commission - Wildlife Health Specialist Group

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

> On Nov 22, 2021, at 11:49 AM, Morens, David (NIH/NIAID) [E]
> b6 wrote:
>
> Billy, Did you get both? You are free to use either one, just cite us as the source.
>
> <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
☎ b6 (assistant: Whitney Robinson)
📠 301 496 4409
💻 b6

<image002.jpg>

From: William B. Karesh b6
Sent: Monday, November 22, 2021 11:48 AM
To: Morens, David (NIH/NIAID) [E] b6
Cc: Catherine Machalaba b6; Daniel Mira-Salama b6
Subject: Re: figure for World Bank report

Beautiful!! Thanks so much.

BK

> On Nov 22, 2021, at 11:23 AM, Morens, David (NIH/NIAID) [E] b6 wrote:
>
> Billy, this is our updated version of what I just sent, made in June 2021. Let me know if this big file gets through to all.
>
> *<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
☎ b6 (assistant: Whitney Robinson)
📠 301 496 4409
💻 b6

<image002.jpg>

From: William B. Karesh b6
Sent: Monday, November 22, 2021 7:27 AM
To: Morens, David (NIH/NIAID) [E] b6
Cc: Catherine Machalaba b6; Daniel Mira-Salama b6
Subject: Re: figure for World Bank report

Thanks David !!!

If you could share the original with the three of us, Daniel can check to see if it will serve the purpose.

Thanks again,

Billy

On Nov 22, 2021, at 7:21 AM, Morens, David (NIH/NIAID) [E] b6 wrote:

Billy, this map was reconstructed from our original by the graphics department at the journal Cell. They did this purely so they could copyright it.

You could contact Cell, abd they will charge you. Or else we can give you the original with you can have for free. The original has all the same info and the same color code, but is less spread out vertically and differs in other minor ways

Let me know. My best to Peter and the gang. David

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

> On Nov 22, 2021, at 06:46, William B. Karesh b6 wrote:
>
> Dear David,
>
> Hope this finds you well.
>
> We are in the final stages of printer's proofs of a report on EID’s in Asia we did for the World Bank. We want to include your EID map from 2020 (attached), but the printer’s tell us that our version is not high enough resolution. Would you happen to have high resolution version that could be used?
>
> Hope you have a great Thanksgiving, all the best,
>
> Billy
>
> William B. Karesh, D.V.M
> Executive Vice President for Health and Policy
>
> EcoHealth Alliance
> 520 Eighth Avenue, Suite 1200

New York, NY 10018 USA

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www.ecohealthalliance.org

President, OIE Working Group on Wildlife

Co-chair, IUCN Species Survival Commission - Wildlife Health Specialist Group

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

<PastedGraphic-1.tiff><PastedGraphic-1.tiff>

<Figure 1 11-22-2021.tif>

From: Peter Daszak [b6]
Sent: 6/23/2021 3:51:14 PM
To: Morens, David (NIH/NIAID) [E] [b6 b6]; Keusch, Jerry [b6]; Rich Roberts [b6]
Subject: Bizarre witness list! RE: House Select Subcommittee Republicans Announce Expert Witness Forum on COVID-19 Origins

Wow – they're going straight to a witness (Dr. Stephen Quay) who's got his own page on "Quackwatch": https://quackwatch.org/cases/fdawarning/prod/fda-warning-letters-about-products-2013/atossa/

He's also had his book, which promotes 'self-cures' for COVID-19 removed from Amazon: https://www.prnewswire.com/news-releases/potential-life-saving-covid-19-survival-manual-removed-from-amazon-kindle-store-three-days-before-official-launch-301071518.html

This is the person who's published in pre-print form, a completely ridiculous "Bayesian analysis" of the probability of COVID originating in a lab – surprise, surprise he estimates that at a 99.8% probability, based on some seriously wayward assumptions: https://www.prnewswire.com/news-releases/new-study-by-dr-steven-quay-concludes-that-sars-cov-2-came-from-a-laboratory-301217952.html

The PR newswire links are his own press releases – he's funding these at a cost of a few thousand each to get the message out. I've known about his quackery for a good few months, but it lliterally took me 5 minutes to find these links. The House Republicans are clearly not at all bothered enough to even do a google search. I hope that no serious people will attend this briefing – it's a mockery of public discourse.

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-6507
USA

Tel.: b6
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

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

---

From: Morens, David (NIH/NIAID) [E] b6
Sent: Wednesday, June 23, 2021 10:46 AM
To: Peter Daszak (b6) b6; Keusch, Jerry (b6)

b6; Rich Roberts (b6) b6

Subject: FW: House Select Subcommittee Republicans Announce Expert Witness Forum on COVID-19 Origins

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

☎ b6 (assistant: Whitney Robinson)
📠 301 496 4409
💻 b6

From: Folkers, Greg (NIH/NIAID) [E] b6
Sent: Wednesday, June 23, 2021 10:07 AM
Subject: House Select Subcommittee Republicans Announce Expert Witness Forum on COVID-19 Origins

Press Release Published: Jun 23, 2021

Select Subcommittee Republicans Announce Expert Witness Forum on COVID-19 Origins

Forum to be held with expert witnesses on Tuesday, June 29

WASHINGTON—On **Tuesday, June 29 at 12:00 p.m. ET**, Republican Whip and Select Subcommittee on the Coronavirus Crisis Ranking Member Steve Scalise (R-La.), House Committee on Oversight and Reform Ranking Member James Comer (R-Ky.), and Select Subcommittee Republican lawmakers will hold a forum with expert witnesses to examine the origins of the coronavirus. For more than a year now, Republicans have repeatedly called on Democrats to investigate the mounting evidence showing the virus originated from the Wuhan Institute of Virology (WIV) lab, but Democrats continue refusing to launch an investigation.

"The left-wing media called it a 'fringe conspiracy theory,' Big Tech censored it, activists in white lab coats dismissed it and Democrats ignored it, but there is growing evidence Communist China started the pandemic, covered it up, and is responsible for the deaths of more than 600,000 Americans and millions more worldwide," **said Scalise and Comer**. "Despite Speaker Pelosi's efforts to create diversions and cover this up, the American people deserve the truth and are demanding accountability, and House Republicans will insist on getting these answers.

"The House Democrat majority's refusal to follow the science, listen to the experts, and investigate the origins of COVID-19 is a dereliction of their duty. Next week, Select Subcommittee Republicans will hold a forum with expert witnesses to advance our investigation into the origins of COVID-19," **added Scalise and Comer**. "The American people deserve to know the truth, even if Washington Democrats refuse to seek it."

It was recently **reported** that three researchers from the Wuhan lab became ill with symptoms consistent with COVID-19 and sought hospital care in November 2019. Additionally, Dr. Fauci's recently released emails from February 2020 reveal that scientists raised the possibility of a lab leak and also expressed concern the virus appeared to be engineered.

WHAT: Select Subcommittee expert forum entitled "Led By Science: The COVID-19 Origin Story"

WHEN: Tuesday, June 29 at 12:00 p.m. ET

WHERE: HVC-215, Capitol Visitors Center

WHO:

Witness Panel I

- **The Honorable Brett P. Giroir, former Assistant Secretary for Health, U.S. Department of Health and Human Services: Admiral Giroir brings firsthand knowledge about the public health response to the COVID-19 pandemic. As COVID-19 testing czar, he oversaw creating a nationwide testing apparatus from scratch which was made particularly difficult by China's lack of transparency. Admiral Giroir will also discuss the investigatory failures of the World Health Organization and why a U.S.-led origins investigation is vital.**
- **Dr. David Asher, Senior Fellow, Hudson Institute: Dr. Asher has decades of national security experience and most recently led the U.S. Department of State's COVID-19**

origins investigation. His testimony will provide inside information into the origins investigation and the role of the Chinese government's efforts to block a thorough and impartial investigation.

- **Dr. Richard Muller, Emeritus Professor of Physics, University of California Berkeley: Dr. Muller is an acclaimed scientist that used his own research to study available data in attempting to determine the origins of COVID-19. He recently penned an op-ed in the *Wall Street Journal* pointing out there is strong evidence COVID-19 was developed in a laboratory using gain-of-function acceleration.**
- **Dr. Steven Quay, Founder, Atossa Therapeutics: Dr. Quay is one of a growing number of scientists dedicated to finding the origins of COVID-19. He has conducted his own research using the publicly available viral data and reached conclusions apart from outside influence. He brings significant scientific expertise to this endeavor including over 87 patents and hundreds of published scientific articles.**

Member Panel

- **The Honorable Cathy McMorris Rodgers, Member of Congress**
- **The Honorable Michael McCaul, Member of Congress**
- **The Honorable Devin Nunes, Member of Congress**
- **The Honorable Mike Gallagher, Member of Congress**

Witness Panel II (invited but hasn't yet accepted)

- **The Honorable Francis Collins, Director, National Institutes of Health**
- **Dr. Anthony Fauci, Director, National Institute of Allergy and Infectious Diseases**
- **Dr. David Hassell, Chairman, P3CO**

WATCH: A livestream will be available **HERE**.

From: Morens, David (NIH/NIAID) [E] [b6
b6]
Sent: 8/5/2021 10:39:21 PM
To: Roberts, Rich [b6]
CC: Edward Holmes [b6]; Peter Daszak (b6)
[b6]; Keusch, Jerry (b6) [b6]; Kessler, Robert
(b6) [b6]
BCC: Morens, David (NIH/NIAID) [E] [b6
b6]
Subject: Re: CNN: Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt https://protect-au.mimecast.com/s/xCyoCvl1rKi7NAywGIQWvWo?domain=cnn.it

I think Shakespeare needs to be updated. "Killed all the lawyers" should perhaps be changed to "Kill all the politicians". But i repeat myself….. d

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

> On Aug 5, 2021, at 18:28, Roberts, Rich b6 wrote:
>
> Me too, but until we get rid of the politicians that may not happen.
>
> Rich
>
> Richard J. Roberts
> New England Biolabs
> 240 County Road
> Ipswich, MA 01938-2723
> USA
> Tel: b6
> Fax: (978) 412 9910
> email: b6
>
> **From:** Morens, David (NIH/NIAID) [E] b6
> **Sent:** Thursday, August 5, 2021 5:42 PM
> **To:** Edward Holmes b6
> **Cc:** Peter Daszak (b6) b6; Keusch, Jerry
> (b6) b6; Kessler, Robert (b6)
> b6; Roberts, Rich b6
> **Subject:** Re: CNN: Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt https://protect-au.mimecast.com/s/xCyoCvl1rKi7NAywGIQWvWo?domain=cnn.it
>
> EXTERNAL SENDER
>
> I take some pleasure in knowing that in the end they will all kick themselves for having wasted their time.
>
> Sent from my iPhone

David M Morens
OD, NIAID, NIH

On Aug 5, 2021, at 17:29, Edward Holmes b6 wrote:

Yes, I hope that means we can put that particular issue to bed.

Professor Edward C. Holmes FAA FRS
The University of Sydney

On 6 Aug 2021, at 7:26 am, Morens, David (NIH/NIAID) [E] b6 wrote:

<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

☎ b6 (assistant: Whitney Robinson)
📠 301 496 4409
💻 b6

<image002.jpg>

From: Folkers, Greg (NIH/NIAID) [E] b6
Sent: Thursday, August 5, 2021 4:18 PM
Subject: CNN: Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt https://cnn.it/3fzBbsp

Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt

By Katie Bo Williams, Zachary Cohen and Natasha Bertrand, CNN

Updated 9:02 AM ET, Thu August 5, 2021

*Washington (CNN)*US intelligence agencies are digging through a treasure trove of genetic data that could be key to uncovering the origins of the coronavirus -- as soon as they can decipher it.

This giant catalog of information contains genetic blueprints drawn from virus samples studied at the lab in Wuhan, China which some officials believe may have been the source of the Covid-19 outbreak, multiple people familiar with the matter tell CNN.

It's unclear exactly how or when US intelligence agencies gained access to the information, but the machines involved in creating and processing this kind of genetic data from viruses are typically connected to external cloud-based servers -- leaving open the possibility they were hacked, sources said.

Still, translating this mountain of raw data into usable information -- which is only one part of the intelligence community's 90-day push to uncover the pandemic's origins -- presents a range of challenges, including harnessing enough computing power to process it all. To do that, intelligence agencies are relying on supercomputers at the Department of Energy's National Labs, a collection of 17 elite government research institutions.

There's also a manpower issue. Not only do intelligence agencies need government scientists skilled enough to interpret complex genetic sequencing data and who have the proper security clearance, they also need to speak Mandarin, since the information is written in Chinese with a specialized vocabulary.

"Obviously there are scientists who are (security) cleared," one source familiar with the intelligence told CNN. "But Mandarin-speaking ones who are cleared? That's a very small pool. And not just any scientists, but ones who specialize in bio? So you can see how this quickly becomes difficult."

Officials conducting the 90-day review hope this information will help answer the question of how the virus jumped from animals to humans. Unlocking that mystery is essential to ultimately determining whether Covid-19 leaked from the lab or was transmitted to humans from animals in the wild, multiple sources told CNN.

Investigators both inside and outside the government have long sought genetic data from 22,000 virus samples that were being studied at the Wuhan Institute of Virology. That data was removed from the internet by Chinese officials in September 2019, and China has since refused to turn over this and other raw data on early coronavirus cases to the World Health Organization and the US.

The question for investigators is whether the WIV or other labs in China possessed virus samples or other contextual information that could help them trace the coronavirus' evolutionary history.

Two scientists who study coronaviruses told CNN they are skeptical that there is any genetic data either in the tranche of 22,000 samples or any other database from the WIV that scientists don't already know about.

"Basically in [a 2020 research paper published in Nature], the WIV talked about all the sequences they had up until a certain point in time -- it's what most scientists virologists believe, that's pretty much what they had," said Dr. Robert Garry, a virologist at the Tulane University School of Medicine.

A source familiar with the US investigation would neither confirm nor deny that any of the data pertaining to those 22,000 samples is among what US intelligence agencies are currently analyzing.

No 'smoking gun'

Sources familiar with the effort say filling in that missing genetic link won't be enough to definitively prove whether the virus originated in the lab at Wuhan or first emerged naturally. Officials will still need to piece together other contextual clues to determine the true origins of the pandemic.

But it is a critical puzzle piece that the Biden administration has been prioritizing.

"The most prized technical data in this context are genetic sequences, database entries and contextual information about the provenance of the samples and the time and context in which they were acquired -- information people would use to place them in a narrative of the origins of SARS, Covid," one source familiar with the investigation told CNN.

For now, senior intelligence officials still say that they are genuinely split between the two prevailing theories on the pandemic's origins, or some combination of both scenarios. CNN reported last month that senior Biden administration officials overseeing the 90-day review now believe the theory that the virus accidentally escaped from a lab in Wuhan is at least as credible as the possibility that it emerged naturally in the wild --

a dramatic shift from a year ago, when Democrats publicly downplayed the so-called lab leak theory.

Multiple sources told CNN that absent an unexpected windfall of new information, officials don't expect to uncover a "smoking gun" -- like intercepted communications, for example -- that would offer definitive proof for either theory. The Biden administration's 90-day push is predicated on the expectation that science, not intelligence will be the key.

Intelligence officials are tasked with addressing several "scientific knowledge gaps" about the virus' evolution, according to the collection guidance governing the 90-day push, distributed to more than a dozen agencies on June 11 by the Office of the Director of National Intelligence and obtained by CNN.

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But former Director of National Intelligence John Ratcliffe told CNN that the US intelligence community already had sufficient collection on the topic of Covid origins.

"Obviously the more, the better. But we've had extraordinary insight into this topic for many months, much more than has been declassified. Pretending we didn't is political theater and a classic example of a politician trying to buy time by using the IC as a scapegoat," he told CNN in a statement.

Digging into the science

That's where the genomic data from the Wuhan lab could come in.

The genetic code of a given virus is the signature that allows scientists to tell the difference between the Delta and Beta variants of the coronavirus, for example. It can also offer clues as to how the virus has adapted or mutated over time, including whether it shows signs of human manipulation -- a kind of genetic history.

Many scientists continue to believe that the most likely scenario is that the virus jumped from animals to humans naturally. But despite testing thousands of animals, researchers still haven't identified the intermediate host through which the virus passed as it adapted to humans.

But some researchers, intelligence officials and Republican lawmakers believe that researchers at the WIV might have genetically altered a virus in the lab, using a controversial kind of research known as "gain of function" that could have infected researchers who then spread it in their community.

It's also plausible that the initial infection took place naturally outside of the lab, perhaps while a scientist was collecting a sample from an animal in the wild, and that scientist then spread the virus unknowingly when he returned to the lab with the samples, multiple sources familiar with the intelligence explained.

"If it was the latter, it was likely brought into a lab to study because someone got sick ... which means there were an unknowable number of other people who were already sick," the source familiar with the probe said.
Understanding exactly which viruses researchers at the WIV were working on could provide important evidence for any one of these theories. It's one of the reasons that investigators on Capitol Hill and elsewhere have been keenly focused on the database that was taken offline in 2019.

But it might not prove anything definitively, sources familiar with the intelligence say. Even if scientists in the intelligence community are able to use the data from the lab to stitch together a complete genetic history that shows how the virus mutated, they might not have enough information about how it was handled by the Chinese lab to determine with a high level of confidence that it leaked.

"Despite having that complete history of variants, [officials might] lack the contextual information to make sense of it in a narrative way," the source familiar with the investigation explained.
"Even a complete sequence history is difficult to obtain. And doesn't really tell us anything about the origins of the pandemic itself without the context," this person added.

Some Republicans on Capitol Hill have jumped into the uncertainty with their own report claiming that "the preponderance of evidence suggests" the coronavirus was "accidentally" released from a lab in Wuhan in 2019 -- an assertion that goes far beyond the intelligence community's current view of the matter.

90 days -- and then what?

It's possible that at the end of Biden's 90-day push, the intelligence community won't have reached what's known as a "high-confidence" assessment as to the pandemic's origins. Administration officials have previously suggested to CNN that it's possible a second review could be ordered at the end of the 90 days.

A bipartisan group of lawmakers on the Senate Intelligence and Foreign Relations Committees earlier this week sent a letter urging the administration to continue to prioritize the hunt until such a judgment can be made in order to prevent future pandemics.

But the lawmakers also zeroed in on a related focus for intelligence officials probing the pandemic's origins: China's "efforts to conceal the severity and scope of the outbreak of the SARS-CoV-2 virus that caused the COVID-19 pandemic."
"We also believe that the investigation should address PRC efforts to prevent international inquiries into the origins of SARS-CoV-2, and other actions PRC authorities have taken to obscure the nature of the virus and its transmission," the lawmakers said.

Republican lawmakers in the House, meanwhile, have latched onto the theory that the virus escaped from a lab. GOP lawmakers in a report released Monday by Rep. Michael McCaul of Texas have claimed that "the preponderance of evidence suggests" the coronavirus was "accidentally" released from a lab in Wuhan in 2019.

Intelligence officials say it's still far too soon to say.

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b6]
Sent: 8/5/2021 9:42:12 PM
To: Edward Holmes [b6]
CC: Peter Daszak (b6) [b6]; Keusch, Jerry (b6)
[b6]; Kessler, Robert (b6) [b6]; Rich Roberts
(b6) [b6]
Subject: Re: CNN: Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt https://protect-au.mimecast.com/s/xCyoCvl1rKi7NAywGIQWvWo?domain=cnn.it

I take some pleasure in knowing that in the end they will all kick themselves for having wasted their time.

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>>
>> ☎ b6 (assistant: Whitney Robinson)
>> 📠 301 496 4409
>> 💻 b6

<image002.jpg>

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Sent: Thursday, August 5, 2021 4:18 PM
Subject: CNN: Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt https://cnn.it/3fzBbsp

Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt

By Katie Bo Williams, Zachary Cohen and Natasha Bertrand, CNN

Updated 9:02 AM ET, Thu August 5, 2021

*Washington (CNN)*US intelligence agencies are digging through a treasure trove of genetic data that could be key to uncovering the origins of the coronavirus -- as soon as they can decipher it.

This giant catalog of information contains genetic blueprints drawn from virus samples studied at the lab in Wuhan, China which some officials believe may have been the source of the Covid-19 outbreak, multiple people familiar with the matter tell CNN.

It's unclear exactly how or when US intelligence agencies gained access to the information, but the machines involved in creating and processing this kind of genetic data from viruses are typically connected to external cloud-based servers -- leaving open the possibility they were hacked, sources said.

Still, translating this mountain of raw data into usable information -- which is only one part of the intelligence community's 90-day push to uncover the pandemic's origins -- presents a range of challenges, including harnessing enough computing power to process it all. To do that, intelligence agencies are relying on supercomputers at the Department of Energy's National Labs, a collection of 17 elite government research institutions.

There's also a manpower issue. Not only do intelligence agencies need government scientists skilled enough to interpret complex genetic sequencing data and who have the proper security clearance, they also need to speak Mandarin, since the information is written in Chinese with a specialized vocabulary.

"Obviously there are scientists who are (security) cleared," one source familiar with the intelligence told CNN. "But Mandarin-speaking ones who are cleared? That's a very small pool. And not just any scientists, but ones who specialize in bio? So you can see how this quickly becomes difficult."

Officials conducting the 90-day review hope this information will help answer the question of how the virus jumped from animals to humans. Unlocking that mystery is essential to ultimately determining whether Covid-19 leaked from the lab or was transmitted to humans from animals in the wild, multiple sources told CNN.

Investigators both inside and outside the government have long sought genetic data from 22,000 virus samples that were being studied at the Wuhan Institute of Virology. That data was removed from the internet by Chinese officials in September 2019, and China has since refused to turn over this and other raw data on early coronavirus cases to the World Health Organization and the US.

The question for investigators is whether the WIV or other labs in China possessed virus samples or other contextual information that could help them trace the coronavirus' evolutionary history.

Two scientists who study coronaviruses told CNN they are skeptical that there is any genetic data either in the tranche of 22,000 samples or any other database from the WIV that scientists don't already know about.

"Basically in [a 2020 research paper published in Nature], the WIV talked about all the sequences they had up until a certain point in time -- it's what most scientists virologists believe, that's pretty much what they had," said Dr. Robert Garry, a virologist at the Tulane University School of Medicine.

A source familiar with the US investigation would neither confirm nor deny that any of the data pertaining to those 22,000 samples is among what US intelligence agencies are currently analyzing.

No 'smoking gun'

Sources familiar with the effort say filling in that missing genetic link won't be enough to definitively prove whether the virus originated in the lab at Wuhan or first emerged naturally. Officials will still need to piece together other contextual clues to determine the true origins of the pandemic.

But it is a critical puzzle piece that the Biden administration has been prioritizing.
"The most prized technical data in this context are genetic sequences, database entries and contextual information about the provenance of the samples and the time and context in which they were acquired -- information people would use to place them in a narrative of the origins of SARS, Covid," one source familiar with the investigation told CNN.

For now, senior intelligence officials still say that they are genuinely split between the two prevailing theories on the pandemic's origins, or some combination of both scenarios. CNN reported last month that senior Biden administration officials overseeing the 90-day review now believe the theory that the virus accidentally escaped from a lab in Wuhan is at least as credible as the possibility that it emerged naturally in the wild -- a dramatic shift from a year ago, when Democrats publicly downplayed the so-called lab leak theory.

Multiple sources told CNN that absent an unexpected windfall of new information, officials don't expect to uncover a "smoking gun" -- like intercepted communications, for example -- that would offer definitive proof for either theory. The Biden administration's 90-day push is predicated on the expectation that science, not intelligence will be the key.

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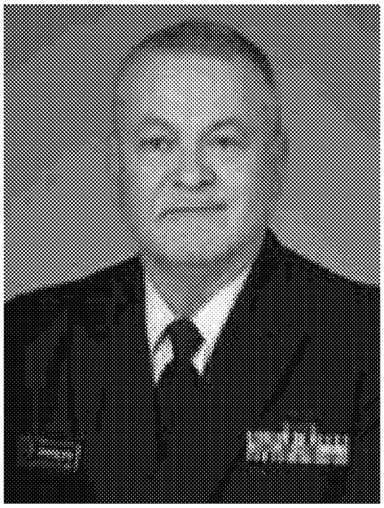

David

From: Morens, David (NIH/NIAID) [E] [b6

b6]

Sent: 11/22/2021 4:22:15 PM

To: William B. Karesh [b6]

CC: Catherine Machalaba [b6]; Daniel Mira-Salama [b6]

Subject: RE: figure for World Bank report

Attachments: Figure 1 8-11-2020.tif

Billy, this is the first of two images, the second of which will come in a minute. This is the image we gave Cell in summer, 2020.

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

☎ b6 (assistant: Whitney Robinson)
📠 301 496 4409
💻 b6

From: William B. Karesh b6
Sent: Monday, November 22, 2021 7:27 AM
To: Morens, David (NIH/NIAID) [E] b6
Cc: Catherine Machalaba b6; Daniel Mira-Salama b6
Subject: Re: figure for World Bank report

Thanks David !!!

If you could share the original with the three of us, Daniel can check to see if it will serve the purpose.

Thanks again,

Billy

> On Nov 22, 2021, at 7:21 AM, Morens, David (NIH/NIAID) [E] b6 wrote:
>
> Billy, this map was reconstructed from our original by the graphics department at the journal Cell. They did this purely so they could copyright it.
>
> You could contact Cell, abd they will charge you. Or else we can give you the original with you can have for free. The original has all the same info and the same color code, but is less spread out vertically and differs in other minor ways
>
> Let me know. My best to Peter and the gang. David
>
> Sent from my iPhone
> David M Morens
> OD, NIAID, NIH
>
>> On Nov 22, 2021, at 06:46, William B. Karesh b6 wrote:
>>
>> Dear David,
>>
>> Hope this finds you well.
>>
>> We are in the final stages of printer's proofs of a report on EID's in Asia we did for the World Bank. We want to include your EID map from 2020 (attached), but the printer's tell us that our version is not high enough resolution. Would you happen to have high resolution version that could be used?
>>
>> Hope you have a great Thanksgiving, all the best,
>>
>> Billy

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

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018 USA

[redacted] b6 (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

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

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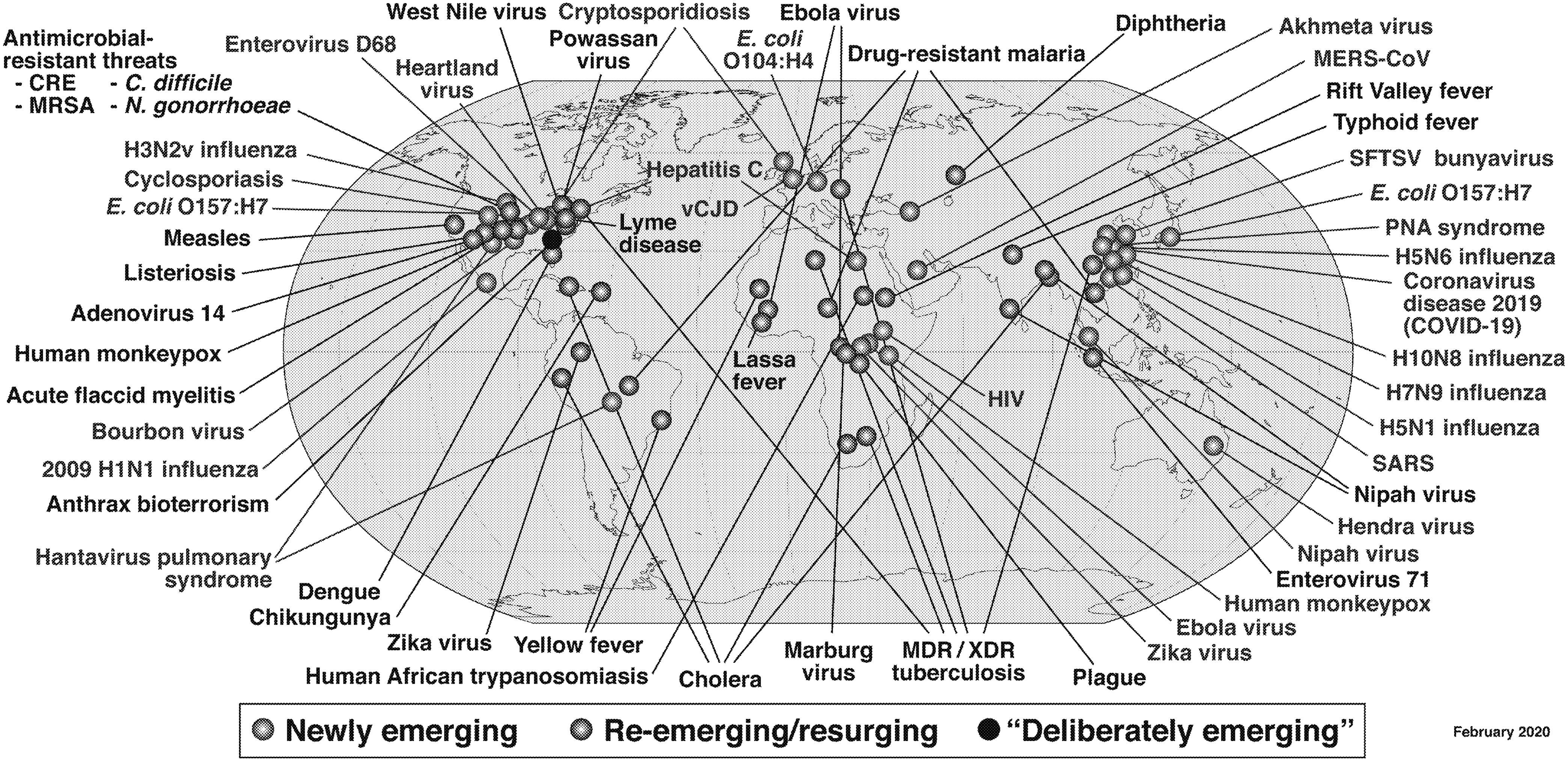

February 2020

From: Morens, David (NIH/NIAID) [E] [b6 b6]

Sent: 9/18/2021 3:43:35 PM

To: Peter Daszak [b6]; Wang Linfa [b6]; Edward Holmes [b6]; Jason Gale [j.gale@bloomberg.net]

CC: Stephen Goldstein [b6]; b6 Garry, Robert F [b6 Administrative Group (b6]; b6; b6; Robert Kessler [b6]; David Morens [b6]; b6

Subject: RE: Study from 2007 shows SARS-infected civets on farms in Hubei

Yes, this is dynamite,. and all the more reason that more work needs to be done to characterize the bat sarbecovirus "universe" all over the region.

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
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Bethesda, MD 20892-2520

☎ b6 (assistant: Whitney Robinson)
📠 301 496 4409
💻 b6

From: Peter Daszak b6
Sent: Saturday, September 18, 2021 10:09 AM
To: Wang Linfa b6; Edward Holmes b6; Jason Gale <j.gale@bloomberg.net>
Cc: Stephen Goldstein b6; Garry, Robert F b6; b6; Morens, David (NIH/NIAID) [E] b6; Robert Kessler b6; David Morens b6; b6
Subject: RE: Study from 2007 shows SARS-infected civets on farms in Hubei
Importance: High

Yes – saw that paper Jason – really interesting

I looked through the paper and it's yet another game changer. So far, in the last few weeks/months, we've got the following new evidence supporting emergence via bat-to-intermediate host-to-human origin for COVID-19 (I've probably missed something):

Multiple new, SARS-CoV-2 related CoVs in SE Asia (Cambodia, Thailand, Japan, China etc.). I know of other work in review describing other related viruses in SE Asia also. We're also finding further novel SARS-CoV-2 related bat viruses in Malaysia, Thailand.
New evidence that live animals of the type that carry CoVs were present in the Wuhan markets (including Huanan).
Evidence from other bat SARSr-CoVs that mutations occur where there FCS is found (eg. RmYN02) https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7211627/
a rat alpha-CoV with an FCS in wildlife farms, hotels and train stations in S. China, showing that FCS insertions are more common in nature than previously thought. https://journals.asm.org/doi/epdf/10.1128/JVI.01173-21
Epidemiological analysis of early cases supporting early origin close to Huanan market, not WIV https://www.cell.com/cell/fulltext/S0092-8674(21)00991-0
Phylogenetic analyses suggesting there may have been multiple introductions into the human population, supporting presence of a virus circulating in animals rather than a lab leak (@virology paper)
Our work showing a very large interface for bat SARSr-CoV spillover in a v. densly population region, and potential for large numbers of missing cases each year https://www.medrxiv.org/content/10.1101/2021.09.09.21263359v1
This paper showing ACE2 binding for bat SARS-CoV-2 related CoVs. https://www.researchsquare.com/article/rs-871965/v1

On the lab leak side, we have convoluted accusations based on interpretations of intent about how Chinese scientists submitted genomes, wrote the papers, or how me and other scientists had collaborations with Chinese scientists. But, as far as new evidence goes, I could only find this:

- None

Of course, the momentum on the lab leak side will continue, with books by Sharri Markison, Alina Chan/Matt Ridley, Op Eds that criticize scientists, 70+ FoIAs by one organization alone, many other FoIAs on their way, 900 pages of FoIA'd grants and reports from EHA/NIAID showing zero evidence of lab leak.

This rate of research even in a pandemic is remarkable and suggests that we'll pretty quickly have such overwhelming evidence for the 'natural' origins that most people will move on from the lab leak.

(Off-the-record) However, the damage they leave behind is already horrific and will be worse by the time they decide to find another issue to focus on.

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-6507
USA

Tel.: b6
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

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

From: Wang Linfa b6
Sent: Friday, September 17, 2021 10:56 PM
To: Edward Holmes b6; Jason Gale <j.gale@bloomberg.net>
Cc: Stephen Goldstein b6;
b6; Peter Daszak b6;
b6
Subject: RE: Study from 2007 shows SARS-infected civets on farms in Hubei

Almost identical SARS-CoV-2 RBD in several bat sarbecoviruses! This is as close as you can get for a natural RBD origin!

Also, the paper concluded that SARS-CoV-2 genome fragments are found in different sarbecoviruses, very similar to the PloS Path paper for SARS-CoV-1.

All we need is to find a sarbecovirus with a furin cleavage site and no more debate on the natural origin of SARS-CoV-2!

Linfa (Lin-Fa) WANG, PhD FTSE FAAM
Professor
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: b6

From: Edward Holmes b6
Sent: Thursday, 16 September 2021 3:31 PM
To: Jason Gale <j.gale@bloomberg.net>
Cc: Stephen Goldstein b6
b6; Peter Daszak b6;

b6 Wang Linfa b6

Subject: Re: Study from 2007 shows SARS-infected civets on farms in Hubei

- External Email -

Dismantles one key argument of the leakers - how could a virus get from Yunnan to Wuhan - in one simple move.

PROFESSOR EDWARD C. HOLMES FAA FRS
ARC Australian Laureate Fellow

THE UNIVERSITY OF SYDNEY
Marie Bashir Institute for Infectious Diseases & Biosecurity,
School of Life & Environmental Sciences and School of Medical Sciences,
The University of Sydney | Sydney | NSW | 2006 | Australia
T
E b6

> On 16 Sep 2021, at 2:26 pm, Jason Gale (BLOOMBERG/ NEWSROOM:) <j.gale@bloomberg.net> wrote:
>
> And there's this:
> *"The discovery of civet-CoVs in the Hubei province should not be a surprise as SARS-CoV-like viruses were recently found in a bat species in the same province"*
>
> From: b6 At: 09/16/21 14:24:33 UTC+10:00
> To: Jason Gale (BLOOMBERG/ NEWSROOM:)
> Cc: b6,
> b6,
> Subject: Re: Study from 2007 shows SARS-infected civets on farms in Hubei
>
>> Just stumbled across it reading the discussion of another paper honestly. It's been cited since - there are certainly people who remembered it but I did not know of it and clearly had not penetrated the public origins discussion.
>>
>> Stephen
>>
>> Sent from my iPhone
>>
>>> On Sep 15, 2021, at 10:22 PM, Jason Gale (BLOOMBERG/ NEWSROOM:) <j.gale@bloomberg.net> wrote:

Well done, Stephen for finding this:
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1900161/

Jason Gale, MHlthSec
Senior editor & chief biosecurity correspondent | Bloomberg News
Level 30, 120 Collins St., Melbourne VIC 3000
Tel. (landline) +61-3-9228-8783 | Mobile b6
@jwgale | Linkedin: http://www.linkedin.com/pub/jason-gale/6/249/a56

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BCC: Morens, David (NIH/NIAID) [E] [b6 b6]
Subject: Re: CNN: Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt https://protect-au.mimecast.com/s/xCyoCvl1rKi7NAywGIQWvWo?domain=cnn.it

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There's also a manpower issue. Not only do intelligence agencies need government scientists skilled enough to interpret complex genetic sequencing data and who have the proper security clearance, they also need to speak Mandarin, since the information is written in Chinese with a specialized vocabulary.

"Obviously there are scientists who are (security) cleared," one source familiar with the intelligence told CNN. "But Mandarin-speaking ones who are cleared? That's a very small pool. And not just any scientists, but ones who specialize in bio? So you can see how this quickly becomes difficult."

Officials conducting the 90-day review hope this information will help answer the question of how the virus jumped from animals to humans. Unlocking that mystery is essential to ultimately determining whether Covid-19 leaked from the lab or was transmitted to humans from animals in the wild, multiple sources told CNN.

Investigators both inside and outside the government have long sought genetic data from 22,000 virus samples that were being studied at the Wuhan Institute of Virology. That data was removed from the internet by Chinese officials in September 2019, and China has since refused to turn over this and other raw data on early coronavirus cases to the World Health Organization and the US.

The question for investigators is whether the WIV or other labs in China possessed virus samples or other contextual information that could help them trace the coronavirus' evolutionary history.

Two scientists who study coronaviruses told CNN they are skeptical that there is any genetic data either in the tranche of 22,000 samples or any other database from the WIV that scientists don't already know about.

"Basically in [a 2020 research paper published in Nature], the WIV talked about all the sequences they had up until a certain point in time -- it's what most scientists virologists believe, that's pretty much what they had," said Dr. Robert Garry, a virologist at the Tulane University School of Medicine.

A source familiar with the US investigation would neither confirm nor deny that any of the data pertaining to those 22,000 samples is among what US intelligence agencies are currently analyzing.

No 'smoking gun'

Sources familiar with the effort say filling in that missing genetic link won't be enough to definitively prove whether the virus originated in the lab at Wuhan or first emerged naturally. Officials will still need to piece together other contextual clues to determine the true origins of the pandemic.

But it is a critical puzzle piece that the Biden administration has been prioritizing.
"The most prized technical data in this context are genetic sequences, database entries and contextual information about the provenance of the samples and the time and context in which they were acquired -- information people would use to place them in a narrative of the origins of SARS, Covid," one source familiar with the investigation told CNN.

For now, senior intelligence officials still say that they are genuinely split between the two prevailing theories on the pandemic's origins, or some combination of both scenarios. CNN reported last month that senior Biden administration officials overseeing the 90-day review now believe the theory that the virus accidentally escaped from a lab in Wuhan is at least as credible as the possibility that it emerged naturally in the wild -- a dramatic shift from a year ago, when Democrats publicly downplayed the so-called lab leak theory.

Multiple sources told CNN that absent an unexpected windfall of new information, officials don't expect to uncover a "smoking gun" -- like intercepted communications, for example -- that would offer definitive proof for either theory. The Biden administration's 90-day push is predicated on the expectation that science, not intelligence will be the key.

Intelligence officials are tasked with addressing several "scientific knowledge gaps" about the virus' evolution, according to the collection guidance governing the 90-day push, distributed to more than a dozen agencies on June 11 by the Office of the Director of National Intelligence and obtained by CNN.

The memo instructs the intelligence community to "expand its collection" and consider data already in its possession to identify both the initial host of the coronavirus and any species that it may have passed through as it adapted to humans -- or to find as "any progenitor virus and/or virus that could serve as backbone for genetic engineering purposes."

But former Director of National Intelligence John Ratcliffe told CNN that the US intelligence community already had sufficient collection on the topic of Covid origins.

"Obviously the more, the better. But we've had extraordinary insight into this topic for many months, much more than has been declassified. Pretending we didn't is political theater and a classic example of a politician trying to buy time by using the IC as a scapegoat," he told CNN in a statement.

Digging into the science

That's where the genomic data from the Wuhan lab could come in.

The genetic code of a given virus is the signature that allows scientists to tell the difference between the Delta and Beta variants of the coronavirus, for example. It can also offer clues as to how the virus has adapted or mutated over time, including whether it shows signs of human manipulation -- a kind of genetic history.

Many scientists continue to believe that the most likely scenario is that the virus jumped from animals to humans naturally. But despite testing thousands of animals, researchers still haven't identified the intermediate host through which the virus passed as it adapted to humans.

But some researchers, intelligence officials and Republican lawmakers believe that researchers at the WIV might have genetically altered a virus in the lab, using a controversial kind of research known as "gain of function" that could have infected researchers who then spread it in their community.

It's also plausible that the initial infection took place naturally outside of the lab, perhaps while a scientist was collecting a sample from an animal in the wild, and that scientist then spread the virus unknowingly when he returned to the lab with the samples, multiple sources familiar with the intelligence explained.

"If it was the latter, it was likely brought into a lab to study because someone got sick ... which means there were an unknowable number of other people who were already sick," the source familiar with the probe said.
Understanding exactly which viruses researchers at the WIV were working on could provide important evidence for any one of these theories. It's one of the reasons that investigators on Capitol Hill and elsewhere have been keenly focused on the database that was taken offline in 2019.

But it might not prove anything definitively, sources familiar with the intelligence say. Even if scientists in the intelligence community are able to use the data from the lab to stitch together a complete genetic history that shows how the virus mutated, they might not have enough information about how it was handled by the Chinese lab to determine with a high level of confidence that it leaked.

"Despite having that complete history of variants, [officials might] lack the contextual information to make sense of it in a narrative way," the source familiar with the investigation explained.
"Even a complete sequence history is difficult to obtain. And doesn't really tell us anything about the origins of the pandemic itself without the context," this person added.

Some Republicans on Capitol Hill have jumped into the uncertainty with their own report claiming that "the preponderance of evidence suggests" the coronavirus was "accidentally" released from a lab in Wuhan in 2019 -- an assertion that goes far beyond the intelligence community's current view of the matter.

90 days -- and then what?

It's possible that at the end of Biden's 90-day push, the intelligence community won't have reached what's known as a "high-confidence" assessment as to the pandemic's origins. Administration officials have previously suggested to CNN that it's possible a second review could be ordered at the end of the 90 days.

A bipartisan group of lawmakers on the Senate Intelligence and Foreign Relations Committees earlier this week sent a letter urging the administration to continue to prioritize the hunt until such a judgment can be made in order to prevent future pandemics.

But the lawmakers also zeroed in on a related focus for intelligence officials probing the pandemic's origins: China's "efforts to conceal the severity and scope of the outbreak of the SARS-CoV-2 virus that caused the COVID-19 pandemic."
"We also believe that the investigation should address PRC efforts to prevent international inquiries into the origins of SARS-CoV-2, and other actions PRC authorities have taken to obscure the nature of the virus and its transmission," the lawmakers said.

Republican lawmakers in the House, meanwhile, have latched onto the theory that the virus escaped from a lab. GOP lawmakers in a report released Monday by Rep. Michael McCaul of Texas have claimed that "the preponderance of evidence suggests" the coronavirus was "accidentally" released from a lab in Wuhan in 2019.

Intelligence officials say it's still far too soon to say.

From: Morens, David (NIH/NIAID) [E] [b6 b6]
Sent: 8/12/2021 8:14:14 PM
To: Keusch, Gerald T [b6]; Edward Holmes [b6]
CC: Peter Daszak (b6) [b6]; Kessler, Robert (b6) [b6]; Rich Roberts (b6) [b6]
Subject: RE: CNN: Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt https://protect-au.mimecast.com/s/xCyoCvl1rKi7NAywGIQWvWo?domain=cnn.it

Here are a few, some of which have some issues with them but together look at the problem from different angles

These should all be quickly findable but if not I should have pdfs on all

Lytras pre-print 15 July 2021
Hassanin Nature Sci Rep 12 July 2021
Otto Current Biol 2021
Zhou Cell 2021;184:1-12
Kumar Molec Biol Evol 2021, 4 May
MacLean PLoS Biol 2021, 12 March
Wacharapluesdee Nature Comm 2021, 9 Feb
Boni Nature Microbiol 2020 29 July
Li X, Sci Adv 2020, I July
Zhang & Holmes Cell 2020 16 April
Anderson Nature Med 2020 April

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

☎ b6 (assistant: Whitney Robinson)
📠 301 496 4409
💻 b6

From: Keusch, Gerald T b6
Sent: Thursday, August 12, 2021 3:30 PM
To: Edward Holmes b6; Morens, David (NIH/NIAID) [E] b6
Cc: Peter Daszak (b6) b6; Kessler, Robert (b6) b6; Rich Roberts (b6) b6
Subject: RE: CNN: Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt https://protect-au.mimecast.com/s/xCyoCvl1rKi7NAywGIQWvWo?domain=cnn.it

I just found the in press Cell paper via PubMed, so I have that reference. However, I would be grateful if you have any suggestion for another high quality peer-reviewed paper in a reputable journal that strengthens the case for the evolution of the virus in nature or in particular addressing how it reached humans.

Jerry Keusch

From: Keusch, Gerald T
Sent: Thursday, August 12, 2021 12:25 PM
To: Edward Holmes b6; Morens, David (NIH/NIAID) [E] b6
Cc: Peter Daszak (b6) b6; Kessler, Robert (b6) b6; Rich Roberts (b6) b6
Subject: RE: CNN: Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt https://protect-au.mimecast.com/s/xCyoCvl1rKi7NAywGIQWvWo?domain=cnn.it

Dear Eddie,

I am currently drafting a potential reply to the letter in Lancet that Peter, I and 22 others published in Lancet last month (attached for your convenience). We have been invited to respond to a letter from a group of French scientists stating that “There is no scientifically validated evidence that directly supports a natural origin”. While we don’t want to engage in an endless series of back and forth arguments in the Lancet we are considering a brief response to focus on the real evidence there is. To that we would cite just one reference, your recent review (the French included 15 references, not including yours, as they clearly submitted before your paper appeared as a preprint. I would obviously like to have a peer-reviewed citation even if just in press, so I would greatly appreciate it if you could update me on the status of your paper and whether or not there is a new citation for your exceptional review.

Thanks in advance, Jerry Keusch

From: Edward Holmes b6
Sent: Thursday, August 5, 2021 5:29 PM
To: Morens, David (NIH/NIAID) [E] b6
Cc: Peter Daszak (b6) <b6; Keusch, Gerald T b6; Kessler, Robert (b6) <b6; Rich Roberts (b6) b6
Subject: Re: CNN: Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt https://protect-au.mimecast.com/s/xCyoCvl1rKi7NAywGIQWvWo?domain=cnn.it

Yes, I hope that means we can put that particular issue to bed.

Professor Edward C. Holmes FAA FRS
The University of Sydney

> On 6 Aug 2021, at 7:26 am, Morens, David (NIH/NIAID) [E] b6 wrote:
>
> <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

☎ b6 (assistant: Whitney Robinson)
📠 301 496 4409
💻 b6

<image002.jpg>

From: Folkers, Greg (NIH/NIAID) [E] b6
Sent: Thursday, August 5, 2021 4:18 PM
Subject: CNN: Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt
https://cnn.it/3fzBbsp

Exclusive: Intel agencies scour reams of genetic data from Wuhan lab in Covid origins hunt

By Katie Bo Williams, Zachary Cohen and Natasha Bertrand, CNN

Updated 9:02 AM ET, Thu August 5, 2021

*Washington (CNN)*US intelligence agencies are digging through a treasure trove of genetic data that could be key to uncovering the origins of the coronavirus -- as soon as they can decipher it.

This giant catalog of information contains genetic blueprints drawn from virus samples studied at the lab in Wuhan, China which some officials believe may have been the source of the Covid-19 outbreak, multiple people familiar with the matter tell CNN.

It's unclear exactly how or when US intelligence agencies gained access to the information, but the machines involved in creating and processing this kind of genetic data from viruses are typically connected to external cloud-based servers -- leaving open the possibility they were hacked, sources said.

Still, translating this mountain of raw data into usable information -- which is only one part of the intelligence community's 90-day push to uncover the pandemic's origins -- presents a range of challenges, including harnessing enough computing power to process it all. To do that, intelligence agencies are relying on supercomputers at the Department of Energy's National Labs, a collection of 17 elite government research institutions.

There's also a manpower issue. Not only do intelligence agencies need government scientists skilled enough to interpret complex genetic sequencing data and who have the proper security clearance, they also need to speak Mandarin, since the information is written in Chinese with a specialized vocabulary.

"Obviously there are scientists who are (security) cleared," one source familiar with the intelligence told CNN. "But Mandarin-speaking ones who are cleared? That's a very small pool. And not just any scientists, but ones who specialize in bio? So you can see how this quickly becomes difficult."

Officials conducting the 90-day review hope this information will help answer the question of how the virus jumped from animals to humans. Unlocking that mystery is essential to ultimately determining whether Covid-19 leaked from the lab or was transmitted to humans from animals in the wild, multiple sources told CNN.

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The question for investigators is whether the WIV or other labs in China possessed virus samples or other contextual information that could help them trace the coronavirus' evolutionary history.

Two scientists who study coronaviruses told CNN they are skeptical that there is any genetic data either in the tranche of 22,000 samples or any other database from the WIV that scientists don't already know about.

"Basically in [a 2020 research paper published in Nature], the WIV talked about all the sequences they had up until a certain point in time -- it's what most scientists virologists believe, that's pretty much what they had," said Dr. Robert Garry, a virologist at the Tulane University School of Medicine.

A source familiar with the US investigation would neither confirm nor deny that any of the data pertaining to those 22,000 samples is among what US intelligence agencies are currently analyzing.

No 'smoking gun'

Sources familiar with the effort say filling in that missing genetic link won't be enough to definitively prove whether the virus originated in the lab at Wuhan or first emerged naturally. Officials will still need to piece together other contextual clues to determine the true origins of the pandemic.

But it is a critical puzzle piece that the Biden administration has been prioritizing.
"The most prized technical data in this context are genetic sequences, database entries and contextual information about the provenance of the samples and the time and context in which they were acquired -- information people would use to place them in a narrative of the origins of SARS, Covid," one source familiar with the investigation told CNN.

For now, senior intelligence officials still say that they are genuinely split between the two prevailing theories on the pandemic's origins, or some combination of both scenarios. CNN reported last month that senior Biden administration officials overseeing the 90-day review now believe the theory that the virus accidentally escaped from a lab in Wuhan is at least as credible as the possibility that it emerged naturally in the wild -- a dramatic shift from a year ago, when Democrats publicly downplayed the so-called lab leak theory.

Multiple sources told CNN that absent an unexpected windfall of new information, officials don't expect to uncover a "smoking gun" -- like intercepted communications, for example -- that would offer definitive proof for either theory. The Biden administration's 90-day push is predicated on the expectation that science, not intelligence will be the key.

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But it might not prove anything definitively, sources familiar with the intelligence say. Even if scientists in the intelligence community are able to use the data from the lab to stitch together a complete genetic history that shows how the virus mutated, they might not have enough information about how it was handled by the Chinese lab to determine with a high level of confidence that it leaked.

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"We also believe that the investigation should address PRC efforts to prevent international inquiries into the origins of SARS-CoV-2, and other actions PRC authorities have taken to obscure the nature of the virus and its transmission," the lawmakers said.

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Intelligence officials say it's still far too soon to say.

From: Jason Gale (BLOOMBERG/ NEWSROOM:) [j.gale@bloomberg.net]
Sent: 9/18/2021 4:11:32 PM
To: b6
CC: b6; Garry, Robert F b6
b6]; b6;
b6; Morens, David (NIH/NIAID) [E] b6
b6];
b6
Subject: RE: Study from 2007 shows SARS-infected civets on farms in Hubei

Oh wow. Awesome summary! Thanks, David. Btw, we're all off the record here.

----- Original Message -----
From: Peter Daszak b6
To: JASON GALE, b6
CC: b6,
b6
At: 09/19/21 00:12:34 UTC+10:00

Yes – saw that paper Jason – really interesting

I looked through the paper and it's yet another game changer. So far, in the last few weeks/months, we've got the following new evidence supporting emergence via bat-to-intermediate host-to-human origin for COVID-19 (I've probably missed something):

- Multiple new, SARS-CoV-2 related CoVs in SE Asia (Cambodia, Thailand, Japan, China etc.). I know of other work in review describing other related viruses in SE Asia also. We're also finding further novel SARS-CoV-2 related bat viruses in Malaysia, Thailand.

- New evidence that live animals of the type that carry CoVs were present in the Wuhan markets (including Huanan).

- Evidence from other bat SARSr-CoVs that mutations occur where there FCS is found (eg. RmYN02) https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7211627/

- a rat alpha-CoV with an FCS in wildlife farms, hotels and train stations in S. China, showing that FCS insertions are more common in nature than previously thought. https://journals.asm.org/doi/epdf/10.1128/JVI.01173-21

- Epidemiological analysis of early cases supporting early origin close to Huanan market, not WIV https://www.cell.com/cell/fulltext/S0092-8674(21)00991-0

- Phylogenetic analyses suggesting there may have been multiple introductions into the human population, supporting presence of a virus circulating in animals rather than a lab leak (@virology paper)

- Our work showing a very large interface for bat SARSr-CoV spillover in a v. densly population region, and potential for large numbers of missing cases each year https://www.medrxiv.org/content/10.1101/2021.09.09.21263359v1

- This paper showing ACE2 binding for bat SARS-CoV-2 related CoVs. https://www.researchsquare.com/article/rs-871965/v1

On the lab leak side, we have convoluted accusations based on interpretations of intent about how Chinese scientists submitted genomes, wrote the papers, or how me and other scientists had collaborations with Chinese scientists. But, as far as new evidence goes, I could only find this:

- None

Of course, the momentum on the lab leak side will continue, with books by Sharri Markison, Alina Chan/Matt Ridley, Op Eds that criticize scientists, 70+ FoIAs by one organization alone, many other FoIAs on their way, 900 pages of FoIA'd grants and reports from EHA/NIAID showing zero evidence of lab leak.

This rate of research even in a pandemic is remarkable and suggests that we'll pretty quickly have such overwhelming evidence for the 'natural' origins that most people will move on from the lab leak.

(Off-the-record) However, the damage they leave behind is already horrific and will be worse by the time they decide to find another issue to focus on.

Cheers,

Peter

Peter Daszak

President

EcoHealth Alliance

520 Eighth Avenue, Suite 1200

New York, NY 10018-6507

USA

Tel.: b6

Website: www.ecohealthalliance.org

Twitter: @PeterDaszak

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

---

From: Wang Linfa b6
Sent: Friday, September 17, 2021 10:56 PM
To: Edward Holmes b6; Jason Gale <j.gale@bloomberg.net>
Cc: Stephen Goldstein b6;
b6; Peter Daszak
b6
Subject: RE: Study from 2007 shows SARS-infected civets on farms in Hubei

Almost identical SARS-CoV-2 RBD in several bat sarbecoviruses! This is as close as you can get for a natural RBD origin!

Also, the paper concluded that SARS-CoV-2 genome fragments are found in different sarbecoviruses, very similar to the PloS Path paper for SARS-CoV-1.

All we need is to find a sarbecovirus with a furin cleavage site and no more debate on the natural origin of SARS-CoV-2!

Linfa (Lin-Fa) WANG, PhD FTSE FAAM

Professor

Programme in Emerging Infectious Disease

Duke-NUS Medical School,

8 College Road, Singapore 169857

Tel: b6

From: Edward Holmes b6
Sent: Thursday, 16 September 2021 3:31 PM
To: Jason Gale <j.gale@bloomberg.net>
Cc: Stephen Goldstein b6;
b6; Peter Daszak
b6
Wang Linfa b6
Subject: Re: Study from 2007 shows SARS-infected civets on farms in Hubei

▓- External Email -

Dismantles one key argument of the leakers - how could a virus get from Yunnan to Wuhan - in one simple move.

--

PROFESSOR EDWARD C. HOLMES FAA FRS
ARC Australian Laureate Fellow

THE UNIVERSITY OF SYDNEY
Marie Bashir Institute for Infectious Diseases & Biosecurity,
School of Life & Environmental Sciences and School of Medical Sciences,
The University of Sydney | Sydney | NSW | 2006 | Australia
T
E b6

On 16 Sep 2021, at 2:26 pm, Jason Gale (BLOOMBERG/ NEWSROOM:) <j.gale@bloomberg.net> wrote:

And there's this:

"The discovery of civet-CoVs in the Hubei province should not be a surprise as SARS-CoV-like viruses were recently found in a bat species in the same province"

From: b6 At: 09/16/21 14:24:33 UTC+10:00

To: Jason Gale (BLOOMBERG/ NEWSROOM:)
Cc: b6,
b6
Subject: Re: Study from 2007 shows SARS-infected civets on farms in Hubei

Just stumbled across it reading the discussion of another paper honestly. It's been cited since - there are certainly people who remembered it but I did not know of it and clearly had not penetrated the public origins discussion.

Stephen

Sent from my iPhone

On Sep 15, 2021, at 10:22 PM, Jason Gale (BLOOMBERG/ NEWSROOM:) <j.gale@bloomberg.net> wrote:

Well done, Stephen for finding this: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1900161/

Jason Gale, MHlthSec
Senior editor & chief biosecurity correspondent | Bloomberg News
Level 30, 120 Collins St., Melbourne VIC 3000
Tel. (landline) +61-3-9228-8783 | Mobile b6 [redacted] b6 [redacted]
@jwgale | Linkedin: http://www.linkedin.com/pub/jason-gale/6/249/a56

From: Garry, Robert F [b6]
Sent: 9/18/2021 2:26:15 PM
To: Peter Daszak [b6]
CC: Wang Linfa [b6]; Edward Holmes [b6]; Jason Gale [j.gale@bloomberg.net]; Stephen Goldstein [b6]; b6; b6; Morens, David (NIH/NIAID) [E] b6 b6]; Robert Kessler b6]; David Morens [b6]; b6
Subject: Re: Study from 2007 shows SARS-infected civets on farms in Hubei

Excellent summary - I'd add an intelligence community report despite some of the most biased news coverage I've ever seen. Reading the report it's clear that the Ic including the top committee also leans heavily to natural - zip zero nada evidence for lab leak - all that's left for lab leakers is thd Relman Special - that wiv had sc2 in a freezer and didn't know they had it - some lab person got infected and touched of transmission chains in multiple wet markets

Sent from my iPhone

> On Sep 18, 2021, at 9:12 AM, Peter Daszak b6 wrote:

> Yes – saw that paper Jason – really interesting
>
> I looked through the paper and it's yet another game changer. So far, in the last few weeks/months, we've got the following new evidence supporting emergence via bat-to-intermediate host-to-human origin for COVID-19 (I've probably missed something):
>
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On the lab leak side, we have convoluted accusations based on interpretations of intent about how Chinese scientists submitted genomes, wrote the papers, or how me and other scientists had collaborations with Chinese scientists. But, as far as new evidence goes, I could only find this:

- None

Of course, the momentum on the lab leak side will continue, with books by Sharri Markison, Alina Chan/Matt Ridley, Op Eds that criticize scientists, 70+ FoIAs by one organization alone, many other FoIAs on their way, 900 pages of FoIA'd grants and reports from EHA/NIAID showing zero evidence of lab leak.

This rate of research even in a pandemic is remarkable and suggests that we'll pretty quickly have such overwhelming evidence for the 'natural' origins that most people will move on from the lab leak.

(Off-the-record) However, the damage they leave behind is already horrific and will be worse by the time they decide to find another issue to focus on.

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-6507
USA

Tel.: b6
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

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

From: Wang Linfa b6
Sent: Friday, September 17, 2021 10:56 PM
To: Edward Holmes b6; Jason Gale <j.gale@bloomberg.net>
Cc: Stephen Goldstein b6; b6; Peter Daszak b6; b6
Subject: RE: Study from 2007 shows SARS-infected civets on farms in Hubei

Almost identical SARS-CoV-2 RBD in several bat sarbecoviruses! This is as close as you can get for a natural RBD origin!

Also, the paper concluded that SARS-CoV-2 genome fragments are found in different sarbecoviruses, very similar to the PloS Path paper for SARS-CoV-1.

All we need is to find a sarbecovirus with a furin cleavage site and no more debate on the natural origin of SARS-CoV-2!

Linfa (Lin-Fa) WANG, PhD FTSE FAAM
Professor
Programme in Emerging Infectious Disease
Duke-NUS Medical School,
8 College Road, Singapore 169857
Tel: b6

From: Edward Holmes b6
Sent: Thursday, 16 September 2021 3:31 PM
To: Jason Gale <j.gale@bloomberg.net>
Cc: Stephen Goldstein b6;
b6; Peter Daszak b6;
b6; Wang Linfa b6
Subject: Re: Study from 2007 shows SARS-infected civets on farms in Hubei

[redacted]- External Email -

Dismantles one key argument of the leakers - how could a virus get from Yunnan to Wuhan - in one simple move.

PROFESSOR EDWARD C. HOLMES FAA FRS
ARC Australian Laureate Fellow

THE UNIVERSITY OF SYDNEY
Marie Bashir Institute for Infectious Diseases & Biosecurity,
School of Life & Environmental Sciences and School of Medical Sciences,
The University of Sydney | Sydney | NSW | 2006 | Australia
T b6
E

> On 16 Sep 2021, at 2:26 pm, Jason Gale (BLOOMBERG/ NEWSROOM:) <j.gale@bloomberg.net> wrote:
>
> `And there's this:`
> *"The discovery of civet-CoVs in the Hubei province should not be a surprise as SARS-CoV-like viruses were recently found in a bat species in the same province"*
>
> `From: b6 At: 09/16/21 14:24:33 UTC+10:00`

To: Jason Gale (BLOOMBERG/ NEWSROOM:)
Cc: b6,
b6
Subject: Re: Study from 2007 shows SARS-infected civets on farms in Hubei

Just stumbled across it reading the discussion of another paper honestly. It's been cited since - there are certainly people who remembered it but I did not know of it and clearly had not penetrated the public origins discussion.

Stephen

Sent from my iPhone

> On Sep 15, 2021, at 10:22 PM, Jason Gale (BLOOMBERG/ NEWSROOM:) <j.gale@bloomberg.net> wrote:
>
> Well done, Stephen for finding this: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1900161/
>
> ---
>
> Jason Gale, MHlthSec
> Senior editor & chief biosecurity correspondent | Bloomberg News
> Level 30, 120 Collins St., Melbourne VIC 3000
> Tel. (landline) +61-3-9228-8783 | Mobile b6
> b6
> @jwgale | Linkedin: http://www.linkedin.com/pub/jason-gale/6/249/a56

small organizations from malicious activity, human error and technology failure; and to lead the movement toward building a more resilient world. To find out more, visit our website.

From: Morens, David (NIH/NIAID) [E]
Sent: Wed, 11 Dec 2019 22:29:57 +0000
To: Ellen Carlin
Bcc: Morens, David (NIH/NIAID) [E]
Subject: Re: Journal contact?
Attachments: Carlin et al Building resilience Draft 10.31.19.docx, ATT00001.htm

Ellen, i have contacts at nejm, jid, and several other journals but not lancet. (b)(6) left and although i knew (b)(6) slightly, i don't think i can do any good there.

I agree: go big. Sometimes you hit a bulls eye, other times not

But your work is good, and it will be published, read, and considered. I mean, after all, this is important stuff

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

On Dec 11, 2019, at 15:03, Ellen Carlin (b)(6) wrote:

Hi David! I hope all is well.

I wanted to ask if you know any editors at The Lancet who might be receptive to an email from you about our paper (attached)? Billy tried an editor he knows there but has received no response. We thought a pre-submission inquiry would be better than a cold submission.

I also thought if The Lancet is a no-go, perhaps you might have a contact at NEJM or another high-impact journal? NEJM has a Commentary article type. I figure we should go big if we can!

Thanks!!
Ellen

Ellen P. Carlin, DVM
Senior Health and Policy Specialist

EcoHealth Alliance
(b)(6) (direct)
(mobile)
(b)(6)
www.ecohealthalliance.org

Research Associate, Smithsonian Conservation Biology Institute
Adjunct Research Scientist, Columbia University National Center for Disaster Preparedness
Courtesy Lecturer, Cornell University College of Veterinary Medicine

EcoHealth Alliance leads cutting-edge scientific research into the critical connections between human and wildlife health and delicate ecosystems. With this science, we develop solutions that prevent pandemics and promote conservation.

Title

Global health security: targeting investments toward unmet needs

Authors

Ellen P. Carlin, DVM
EcoHealth Alliance, 460 West 34th Street, New York, NY 10001
(b)(6)

Catherine Machalaba, MPH
EcoHealth Alliance, 460 West 34th Street, New York, NY 10001

Kanya C. Long, PhD
University of California San Diego, 6304 Atkinson Hall, La Jolla, CA 92093
Dr. Long was a fellow at the World Bank at the time of the study.

Franck C. J. Berthe, DVM
World Bank, 1818 H Street, NW, Washington, DC 20433

David Morens, MD
National Institutes of Allergy and Infectious Diseases, 5601 Fishers Lane, Bethesda, MD 20892

William B. Karesh, DVM
EcoHealth Alliance, 460 West 34th Street, New York, NY 10001

As the second largest Ebola outbreak in history finally appears to be waning in the Democratic Republic of the Congo, a global reckoning is due. Understanding why especially dangerous pathogens are emerging with increasing frequency continues to take a back seat to response and response preparedness. This crisis-centered approach is bound to keep us trapped in a perpetual cycle of panic and neglect.[1]

To document this dynamic and reveal its extent, we collated the functions needed for effective defenses against major biological incidents and assessed which areas are receiving insufficient attention.[2] Our organizing construct included four "pillars"—prevent, detect, respond, and recover. Through extensive review of the scientific and gray literature, and with expert input via roundtable discussions, interviews, and peer review, we identified 60 functions that undergird these four pillars and to which countries must have sufficient access to optimize their health security. We also identified 22 major initiatives global in architecture or oversight and designed to support the development of local, country, or regional capacities. We then mapped the initiatives to the pillars to reveal areas of global neglect (Figure 1).

[Insert Figure 1 here]

As the figure shows, activities directed at prevention are minimal in number. We defined prevention as a multi-dimensional concept that captures prevention of 1) epidemics at pre-initiation (*before* pathogens emerge into people); 2) bioweapons development and deployment; and 3) accidental releases of pathogens, such as from laboratories. The majority of funded efforts do not address prevention at all, and even fewer deal with the underlying risk factors that lead to epidemic emergence. Most programs view epidemic prevention narrowly (i.e., preventing small outbreaks from growing) rather than addressing what drives outbreaks to occur in the first place. The latter entails politically challenging decisions about societal priorities ranging from land use and agricultural practices to urbanization and climate change.

Few efforts address recovery, and the very inclusion of recovery as a core pillar in our construct is novel among frameworks. (A recent World Bank publication on which some of the authors worked, which is designed to strengthen human, animal, and environmental public health systems at their interface, is one of the only examples and has not yet been adopted into global efforts.[3]) Since strong recovery from one epidemic event can pre-empt future outbreaks, systematic and sustained attention to this pillar is badly needed.

We also found two strategic points of concern. One is that, by current design, global health security implementation efforts and their attached financing tackle particular objectives—vaccine development, regional surveillance, training—while no governance effort or strategic inter-institutional guiding framework aligns them toward a commonly defined set of goals. The other is that there seems to be a tendency to view biothreats in terms of the single end consequence that worries people the most: our own health. The problem with this approach is that it drives reverse engineering of structures and decisions to deal with only human health consequences, and forward engineering of response activity tailored to human health needs. Defense, environment, and animal health are often treated as needs outside of human health security frameworks, even though their full inclusion would restore the breadth of the health *security* concept. Ebola in DRC exists at this nexus: viral circulation in an ecological environment that supports spillover and a fragile, violent, and conflict-ridden setting that hampers both prevention and response.

The international community's approaches diverge from what may be fundamentally needed to grapple with the new epidemic threat reality and ultimately stave off its worst consequences. Some of the functions we identified require less investment than others to achieve great benefit—addressing drivers of epidemics is a case in point. The World Bank estimates that an annual expenditure of ~$3.4 billion to prevent one in every eight severe pandemics will save $30 billion.[4] Assessing cost-benefits and returns on investment of particular activities is precisely what a unifying strategic framework could do. The release of the 2019 Global Health Security Index, which finds among 195 countries assessed an average preparedness score of 40·2 out of a possible 100, may provide new impetus to act.[5] A substantial but feasible rethinking of the orientation of global and national investment is achievable within the major guiding frameworks and efforts that are already underway. As the Global Health Security Agenda embarks on its second five years, this is a timely opportunity to strengthen neglected lines of effort and support a holistic approach to dealing with the global health challenge of epidemic disease.

Acknowledgements

This work was funded by the Smith Richardson Foundation, which had no other role in the development of the study.

References

1. World Bank. *From panic and neglect to investing in health security: Financing pandemic preparedness at a national level.* Washington, DC: World Bank;2017.
2. Carlin EP, Machalaba C, Berthe FCJ, Long KC, Karesh WB. *Building resilience to biothreats: An assessment of unmet core global health security needs.* New York, NY: EcoHealth Alliance;2019.
3. World Bank. *Operational framework for strengthening human, animal and environmental public health systems at their interface.* Washington, DC: World Bank Group;2018.
4. World Bank. *People, pathogens, and our planet: The economics of one health, volume 2.* Washington, DC: World Bank;June 2012.
5. Nuclear Threat Initiative. *Global health security index: Building collective action and accountability.* Washington, DC: Nuclear Threat Initiative;2019.

Figure 1: Mapping of global health security initiatives to core needs

Initiative	[redacted]	[redacted]	[redacted]
Australia Group	[redacted]	[redacted]	[redacted]
CEPI*	[redacted]	[redacted]	[redacted]
CP3	[redacted]	[redacted]	[redacted]
Gavi†	[redacted]	[redacted]	[redacted]
GLASS	[redacted]	[redacted]	[redacted]
GLEWS‡	[redacted]	[redacted]	[redacted]
Global Financing Facility	[redacted]	[redacted]	[redacted]
Global Fund	[redacted]	[redacted]	[redacted]
GHSA§	[redacted]	[redacted]	[redacted]
GHSI	[redacted]	[redacted]	[redacted]
Global Partnership	[redacted]	[redacted]	[redacted]
International Reagent Resource	[redacted]	[redacted]	[redacted]
OIE WAHIS	[redacted]	[redacted]	[redacted]
Proliferation Security Initiative	[redacted]	[redacted]	[redacted]
World Bank PEF‖	[redacted]	[redacted]	[redacted]
World Bank Pandemic Preparedness Plan	[redacted]	[redacted]	[redacted]
WEF Epidemics Readiness Accelerator	[redacted]	[redacted]	[redacted]
WHO CFE	[redacted]	[redacted]	[redacted]
WHO Global Influenza Programme	[redacted]	[redacted]	[redacted]
WHO GOARN	[redacted]	[redacted]	[redacted]
WHO Health Emergencies Program	[redacted]	[redacted]	[redacted]
WHO R&D Blueprint	[redacted]	[redacted]	[redacted]

Major global health security initiatives were mapped to four pillars of global health security activity: prevent, detect, respond, and recover, revealing a predominance of focus on detection and response. Figure reprinted from Carlin EP, Machalaba C, Berthe FCJ, et al. *Building Resilience to Biothreats: An assessment of unmet core global health security needs*. EcoHealth Alliance. 2019.

*Committed to funding through Phase 2 investigational stockpiles; not funded for Phase 3 or linked to a system for procurement, distribution, or dispensing. †To the extent that Gavi covers Prevent it is for the specific prevention of yellow fever spillover through vaccination in high-risk areas; does not address drivers. ‡Predominantly focused on risk monitoring and information alerts for Rift Valley fever in livestock. §Addresses prevention in the sense of containing outbreaks; attention to and capacity for spillover risk management is extremely limited. ‖Disbursement of funds only applies to select viruses.

From: Peter Daszak
Sent: Fri, 9 Jul 2021 12:18:09 -0400
To: Morens, David (NIH/NIAID) [E]; Keusch, Jerry
Subject: RE: Politico: POLITICO-Harvard poll: Most Americans believe Covid leaked from lab

Bring on the Witchfinder-General! This shows how little we've improved in the public understanding of science since Medieval times..

It also demonstrates what a disastrous thing it was for David Relman and others to sign that letter to Science. It's fine to claim that as scientists we need to be honest about our doubt, but to give credence to the lab leak theory and place it on equal status to the wildlife farms is a heinous act as a scientist and a citizen.

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-6507
USA

Tel.: (b)(6)
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

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

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From: Morens, David (NIH/NIAID) [E] (b)(6)
Sent: Friday, July 9, 2021 10:32 AM
To: Peter Daszak ((b)(6)) (b)(6); Keusch, Jerry ((b)(6)) (b)(6)
Subject: FW: Politico: POLITICO-Harvard poll: Most Americans believe Covid leaked from lab

Sad….. Most small children believe in Santa Claus….. Not so sad….

David

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

From: Folkers, Greg (NIH/NIAID) [E] (b)(6)
Sent: Friday, July 9, 2021 8:52 AM
Subject: Politico: POLITICO-Harvard poll: Most Americans believe Covid leaked from lab

POLITICO-Harvard poll: Most Americans believe Covid leaked from lab

Opinion on the lab leak scenario, once seen as a fringe theory, has shifted dramatically.

By **ALICE MIRANDA OLLSTEIN**

07/09/2021 06:00 AM EDT

- Most Americans now believe that the coronavirus leaked from a laboratory in China, according to a new POLITICO-Harvard poll that found a dramatic shift in public perception of Covid-19's origins over the last year.

U.S. adults were almost twice as likely to say the virus was the result of a lab leak in China than human contact with an infected animal, which many scientists believe is the most likely scenario. The poll's findings show what was once a fringe belief held mainly among some on the political right has become accepted by most Republicans, as well as most Democrats, amid heightened scrutiny of the lab leak theory.

In March 2020, a Pew Research Center poll found 29 percent of Americans believed the virus was made in a Chinese lab and released either accidentally or intentionally. The new survey shows 52 percent believe the virus came out of a lab, including 59 percent of Republicans and 52 percent of Democrats, while 28 percent said it was from an infected animal.

The absence of a large partisan gap on the issue is particularly striking, said Bob Blendon, a professor of health policy and political analysis at the Harvard T.H. Chan School of Public Health who designed the poll.

“Usually, our polls find a big split between Republicans and Democrats, so this is unique,” he said. “More conservative media have been carrying the ‘lab leak’ issue, and it’s been a Trump talking point from the beginning, so we expected people who lean Democratic would say either ‘It’s not true’ or ‘I don’t know.’ But the belief is bipartisan.”

Blendon said Democrats likely became more receptive to the idea after President Joe Biden’s recent order that intelligence agencies investigate the virus’ origin and comments from Anthony Fauci, the White House chief medical officer, that it's worth digging into. Fauci and other scientists have cautioned the answer may never be known definitively.

“That the president thought there was enough evidence to ask intelligence agencies to put together a report sends a signal to Democrats that there might be something there,” Blendon said.

Democratic lawmakers have also faced pressure to look more closely at the lab leak scenario, though they worry Republicans will stoke uncertainty about the virus origin for political gain. Several congressional committees have launched inquiries, and the House Science Committee plans to hold its first hearing on the issue next week.

The POLITICO-Harvard poll, which will be released next week, also found there’s a high level of public interest in investigating Covid-19’s origin, with almost two-thirds of Democrats and Republicans calling the issue “extremely” or “very” important. The finding also surprised Blendon, who said the public isn’t typically invested in such a scientific inquiry.

The broad attention on the issue underscores the stakes for the Biden administration’s upcoming report on the virus origin, due in August. Even if the report concludes the virus came from nature, it could be hard to move public opinion, lawmakers and researchers like Blendon have noted.

The poll surveyed 1,009 adults from June 22-27. The margin of error was plus or minus 3.8 percentage points.

From: Morens, David (NIH/NIAID) [E]
Sent: Wed, 18 Aug 2021 21:20:37 +0000
To: Kevin Olival
Subject: Re: PRO/AH/EDR> Undiagnosed die off, deer - USA: (ID) RFI

Yes, i did see your work and think that this is an important under appreciated issue. If you have contacts in Idaho, you might want to ping them. ! d

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

On Aug 18, 2021, at 16:16, Kevin Olival (b)(6) wrote:

Hope this finds you well, and totally agree David.

We've been working with USGS, USFWS, and National Wildlife Health Center, on this issue of spillback. I can reach out to USGS colleagues and see what new testing is happening. I think you saw our paper about "spillback" risk to North American bats out a while ago? https://journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1008758

And this one: https://pubs.er.usgs.gov/publication/ofr20201060 Same applies to all N. American wildlife, to different degrees, but evidence definitely points to deer being susceptible too! https://www.nature.com/articles/d41586-021-02110-8

Cheers,
Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018

(b)(6) (direct)
(mobile)
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www.ecohealthalliance.org

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

On Aug 18, 2021, at 3:10 PM, Morens, David (NIH/NIAID) [E] (b)(6)
wrote:

Guys, these deer need to be tested for SARS-CoV-2, which has apparently been spreading from humans to deer in the US.

<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) (assistant: Whitney Robinson)
📠 301 496 4409
💻 (b)(6)

<image002.jpg>

From: ProMED <promed@isid.org>
Sent: Wednesday, August 18, 2021 1:12 PM
To: Morens, David (NIH/NIAID) [E] (b)(6)
Subject: PRO/AH/EDR> Undiagnosed die off, deer - USA: (ID) RFI

UNDIAGNOSED DIE OFF, DEER - USA: (IDAHO) REQUEST FOR INFORMATION
****
A ProMED-mail post
http://www.promedmail.org
ProMED-mail is a program of the
International Society for Infectious Diseases
http://www.isid.org

Date: Mon 16 Aug 2021
Source: KLIX News radio [edited]
https://newsradio1310.com/unknown-disease-kills-150-deer-in-north-central-idaho/

Around 150 white-tailed deer have died of some sort of disease in north central Idaho and it isn't clear what is causing it according to game officials.

Idaho Department of Fish and Game officials in the Clearwater region said reports continue to come in of dead deer in the Kamiah area, as of [13 Aug 2021]. So far, tests for bluetongue and epizootic hemorrhagic disease, and adenovirus hemorrhagic disease have come back negative in the corpses tested.

People in the area have been asked to report any dead or sick deer to Idaho Fish and Game. Officials have asked people to remove food and water sources that may cause deer to congregate out of a concern that whatever is making the animals sick is spreading from animal to animal. Idaho Fish and Game first reported deer had been dying of some sort of illness on [5 Aug 2021] and began running tests. Idaho Fish and Game said it appeared to be a localized situation.

--
Communicated by:
ProMED from HealthMap Alerts
promed@promedmail.org

[Hemorrhagic disease (HD) in cervids, caused by viruses in either the epizootic hemorrhagic disease virus (EHDV) group or the bluetongue virus (BTV) group, is the most important disease of white-tailed deer and is more common in the eastern USA. In western states, an adenovirus (CdAdV-1 or OdAdV-1) causes fatal hemorrhagic disease in black-tailed deer and moose. Tests to detect those diseases were negative and there are no data on signs or pathological findings to speculate a possible cause. We await the results of any studies being conducted by the Idaho Department of Fish and Game. - Mod.PMB

HealthMap/ProMED map of Idaho, United States:
http://healthmap.org/promed/p/68515]

[See Also:
Epizootic hemorrhagic disease - USA: (NY) deer
http://promedmail.org/post/20210811.8585742
Adenovirus hemorrhagic disease - USA (03): (WA) deer
http://promedmail.org/post/20210806.8573558
2015

Bluetongue - USA (03): (ID) cervid
http://promedmail.org/post/20151009.3703577
2003

Epizootic hemorrhagic disease, cervids - USA (ID)
http://promedmail.org/post/20030809.1974]
....sb/pmb/mj/jh
##

##
##

From: Morens, David (NIH/NIAID) [E]
Sent: Fri, 9 Jul 2021 20:53:04 +0000
To: Keusch, Gerald T; Peter Daszak
Subject: RE: Politico: POLITICO-Harvard poll: Most Americans believe Covid leaked from lab

In my experience these folks are bean counters but they know honest people when they see them. They don't go nuts over minor issues, which evberyone has. Not to worry…..

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
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Bethesda, MD 20892-2520
☎ (b)(6) (assistant: Whitney Robinson)
📠 301 496 4409
💻 (b)(6)

From: Keusch, Gerald T (b)(6)
Sent: Friday, July 9, 2021 4:05 PM
To: Peter Daszak (b)(6); Morens, David (NIH/NIAID) [E]
(b)(6)
Subject: RE: Politico: POLITICO-Harvard poll: Most Americans believe Covid leaked from lab

There is only one response, bite your tongue and comply with their inspection.

Gerald T. Keusch, M.D.
Professor of Medicine
Associate Director
National Emerging Infectious Diseases Laboratory
Boston University, Boston MA 02118

From: Peter Daszak (b)(6)
Sent: Friday, July 9, 2021 12:19 PM
To: Morens, David (NIH/NIAID) [E] (b)(6); Keusch, Gerald T (b)(6)
Subject: RE: Politico: POLITICO-Harvard poll: Most Americans believe Covid leaked from lab

By the way – we got our notice from the HHS Office of the Inspector-General today that they're going to audit us.

I'm not worried, we've done nothing wrong, but this is upsetting and a major waste of our time and of taxpayer funds.

Advice welcome, of course…

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance

520 Eighth Avenue, Suite 1200
New York, NY 10018-6507
USA

Tel.: (b)(6)
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

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

---

From: Morens, David (NIH/NIAID) [E] (b)(6)
Sent: Friday, July 9, 2021 10:32 AM
To: Peter Daszak ((b)(6)) (b)(6); Keusch, Jerry ((b)(6)) (b)(6)
Subject: FW: Politico: POLITICO-Harvard poll: Most Americans believe Covid leaked from lab

Sad….. Most small children believe in Santa Claus….. Not so sad….

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David M. Morens, M.D.
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From: Folkers, Greg (NIH/NIAID) [E] (b)(6)
Sent: Friday, July 9, 2021 8:52 AM
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POLITICO-Harvard poll: Most Americans believe Covid leaked from lab

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07/09/2021 06:00 AM EDT

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> The absence of a large partisan gap on the issue is particularly striking, said Bob Blendon, a professor of health policy and political analysis at the Harvard T.H. Chan School of Public Health who designed the poll.

“Usually, our polls find a big split between Republicans and Democrats, so this is unique,” he said. “More conservative media have been carrying the ‘lab leak’ issue, and it’s been a Trump talking point from the beginning, so we expected people who lean Democratic would say either ‘It’s not true’ or ‘I don’t know.’ But the belief is bipartisan.”

Blendon said Democrats likely became more receptive to the idea after President Joe Biden’s recent order that intelligence agencies investigate the virus’ origin and comments from Anthony Fauci, the White House chief medical officer, that it's worth digging into. Fauci and other scientists have cautioned the answer may never be known definitively.

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Democratic lawmakers have also faced pressure to look more closely at the lab leak scenario, though they worry Republicans will stoke uncertainty about the virus origin for political gain. Several congressional committees have launched inquiries, and the House Science Committee plans to hold its first hearing on the issue next week.

The POLITICO-Harvard poll, which will be released next week, also found there’s a high level of public interest in investigating Covid-19’s origin, with almost two-thirds of Democrats and Republicans calling the issue “extremely” or “very” important. The finding also surprised Blendon, who said the public isn’t typically invested in such a scientific inquiry.

The broad attention on the issue underscores the stakes for the Biden administration’s upcoming report on the virus origin, due in August. Even if the report concludes the virus came from nature, it could be hard to move public opinion, lawmakers and researchers like Blendon have noted.

The poll surveyed 1,009 adults from June 22-27. The margin of error was plus or minus 3.8 percentage points.