From: Jon Epstein [b6]
Sent: 1/18/2021 9:40:19 PM
To: Morens, David (NIH/NIAID) [E] [b6
(b6]
Subject: Re: Request for support b6 letter
Attachments: Jonathan H Epstein full CV 2021.pdf

David,
Hopefully you've received a request for a letter. I don't know what it says in terms of content or structure. If you want to send me what they ask for, I could help draft something.
Meanwhile, here's the short paragraph they asked me for (below), and my CV, if you want to use those.

Cheers,
Jon

Describe b6
b6
250 words

b6

On Sun, Jan 17, 2021 at 1:52 PM Morens, David (NIH/NIAID) [E] b6 wrote:

> Jon, yes, absolutely, I will be happy to fo so. Please get me all materials/info asap. D
>
> Sent from my iPhone
> David M Morens
> OD, NIAID, NIH
>
> > On Jan 17, 2021, at 13:18, Jon Epstein b6 wrote:
> >
> > Hi David,
> > I hope you're doing well. I'm applying to b6
> > b6

b6

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

The application deadline is Jan 20th, but I'm trying to find out when the reference letters are due.
Sorry for the last minute request, and I'll absolutely understand if you're unable to do it.

Thanks, in advance, for considering.

Cheers,
Jon

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

b6 (direct)
(mobile)

web: ecohealthalliance.org

Twitter: @epsteinjon

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

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

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From: Morens, David (NIH/NIAID) [E] b6
(b6)
Sent: 3/25/2020 4:30:44 PM
To: Laura Spinney [b6]
BCC: Taubenberger, Jeffery (NIH/NIAID) [E] (b6)
[b6]; Peter Daszak (b6)
[b6]
Subject: RE: It takes a whole world to create a new virus, not just China | Laura Spinney | Opinion | The Guardian

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

From: Laura Spinney b6
Sent: Wednesday, March 25, 2020 12:22 PM
To: Morens, David (NIH/NIAID) [E] b6
Subject: It takes a whole world to create a new virus, not just China | Laura Spinney | Opinion | The Guardian

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

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

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

Laura Spinney Wed 25 Mar 2020 15.31 GMT

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

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

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

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

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

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

Even so, to play devil's advocate for a moment, the problem could still be regarded as uniquely Chinese. But there are two reasons why that's not true. First, with the opening up of China, its agribusiness has ceased to be wholly Chinese-owned. It is a big recipient of foreign direct investment. Second, as the American pandemic expert, David Morens, and his colleagues pointed out last month in the New England Journal of Medicine, we've been watching a similar drama unfold over a much longer timescale with influenza – the disease that has caused more pandemics in the history of humanity than any other.

Flu viruses that infect animals, including poultry and pigs, have periodically spilled over into humans ever since we domesticated those animals millennia ago. But the factory farms that produce our food today ratchet up the virulence of those flu viruses just before they spill over. This ratcheting up has been documented in Europe, Australia and the US more than it has in poor or emerging economies, and it's what gave rise to the last flu pandemic in 2009. The first cases of that pandemic were recorded in California, but nobody calls it the American flu – and it's right that they don't, if only because American farms aren't wholly American-owned either. China, for one, has invested in them.

It's not just the industries that produce our food that are creating the conditions in which new zoonoses emerge. Logging, mining, road-building and rapid urbanisation are also contributing, and the profits from those are shared internationally too. "We have created a global, human-dominated ecosystem that serves as a playground for the emergence and host-switching of animal viruses," wrote Morens et al. The resulting diseases are suffered locally at first, as is reflected in their names – Ebola and Zika virus diseases and Bolivian hemorrhagic fever, to name just three – but the irony is that some of them, such as HIV and Covid-19, go on to become global. It's hard not to see a terrible natural justice in that.

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

That doesn't mean China shouldn't be held accountable for its shortcomings. Americans know where their weak points are – they include agricultural fairs, where pigs and humans come together – and they police them ferociously. Their infectious disease experts can detect a virus circulating in a herd and generate a vaccine to it within hours. The Chinese have got better at this lately. They now vaccinate their poultry flocks against a dangerous flu virus, H7N9, which first infected humans in 2013, for example. But nearly 20 years after Sars-CoV spilled over in a wet market, those places still appear to be a liability.

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

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

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

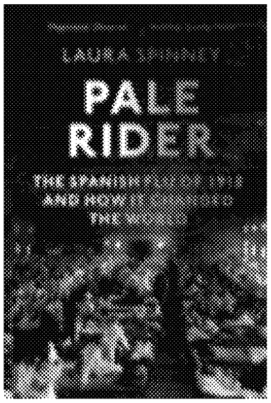
- Laura Spinney is a science journalist, novelist and author of Pale Rider: The Spanish Flu of 1918 and How it Changed the World

Laura Spinney
Writer & science journalist

Paris, France

Tel: b6
Mob: b6
Skype: b6

b6
www.lauraspinney.com



From: Morens, David (NIH/NIAID) [E] [b6 b6]
Sent: 9/11/2021 6:14:37 PM
To: Peter Daszak [b6]
CC: Gerald Keusch [redacted] b6], Robert Kessler [b6]; Kristian Andersen [b6]; Eddie Holmes [b6]; Angie Rasmussen [b6]; Jason Gale [j.gale@bloomberg.net]
Subject: Re: origins of SARS-CoV-2

She seemed like a good and diligent reporter so i was kinda pissed that she misquoted me. But as i am sure you know, this is what happens when reporters scribble down notes without thinking, and then later patch it all together and edit it down. What i said to her in an hour of interview, including many addition things not in the article, was unmistakeably NOT what she wrote, at least not in that part. Grr…. d

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

> On Sep 10, 2021, at 21:17, Peter Daszak b6 wrote:
>
> Yes – just saw that story – not much new in it and I did enjoy your quote even though I didn't know what you meant was a waste of time!! I think we all get it. In the end the give-away for this story is 1) the first pic they put up (the ubiquitous me in a car in front of the WIV with security guards) and 2) the quotes they highlight in giant font which are about the lab leak, nothing else… Tedious to be honest.
>
> I've pasted it because it's subscription only and you shouldn't be giving them money…

Members of the World Health Organization team tasked with investigating the origins of COVID-19 arrive at Wuhan Institute of Virology earlier this year.

PHOTOGRAPH BY THOMAS PETER, REUTERS

SCIENCE

CORONAVIRUS COVERAGE

Why it's so tricky to trace the origin of COVID-19

A 90-day investigation into the source of SARS-CoV-2 has shown consensus that the virus was not engineered. But many other elements remain a mystery.

BYPRIYANKA RUNWAL

PUBLISHED SEPTEMBER 10, 2021

• 20 MIN READ

After 20 months, 219 million cases, and more than four million deaths, we've learned a lot about the COVID-19 pandemic. But the most polarizing question and central mystery remains: We still don't know where the virus that started it all actually came from. Most experts were not surprised in late August when a 90-day investigation by the U.S. intelligence community came up empty-handed on the origin of the

SARS-CoV-2 virus. A brief, one-page unclassified summary released on August 27 revealed the only point on which the intelligence community agreed: that the virus was “not developed as a biological weapon.”

Understanding where, when, and how this pandemic started is important information for public health officials seeking to control its spread and even prevent future outbreaks. If the source of the virus is found to be bats or another animal, as many experts suspect, preventative measures might include curtailing contact between that animal and those living or working in close proximity. Measures could involve regular surveillance of animals and humans living where the virus is endemic to reduce the likelihood of future spillover—when a virus is transmitted to a human, directly or via a host animal, triggering an outbreak.

The results may also lead to broader policy decisions to curb deforestation and habitat fragmentation, and to block human settlements in known viral hot zones. Knowing where the pandemic virus arose could also lead to changes in human behavior, such as reducing demand for bushmeat and wildlife-derived products that drive the illegal wildlife trade. And if the virus is instead found to have leaked from a lab, that finding would no doubt spur scientists and policymakers to find safer ways to study these pathogens.

Historically looking back, we can have lab leaks.

JESSE BLOOMVIROLOGIST

That’s why scientists support a thorough, evidence-based investigation for the origins of COVID-19. But similar inquires during past epidemics have taken months to years to yield answers, and in several cases, the mystery remains unresolved.

“Science takes time,” says Arinjay Banerjee, a virologist at the University of Saskatchewan in Canada. “To go back and confidently identify the source is a difficult task.”

Earlier this year, an international World Health Organization team visited the city of Wuhan, China, to assess the evidence China had provided about the origin of SARS-CoV-2. In a report that summarized their findings, the WHO suggested that it was “likely to very likely” that the virus first spread from infected bats to humans via an intermediate host animal.

This was the case with the 2002 SARS-CoV outbreak—the first pandemic of the 21st century; the virus most likely spilled over from cave-dwelling horseshoe bats in China to palm civets sold in live animal markets, where it reached humans. Similarly, the 2012 MERS-CoV epidemic is suspected to have originated in bats and was later transmitted to dromedary camels, which infected humans.

That WHO report also deemed a laboratory leak from the Wuhan Institute of Virology, known for its work with coronaviruses, as "extremely unlikely." But the conclusion sparked backlash from scientists and governments around the world, who argued that it's still too early to rule out a lab leak based on the evidence in hand. Other experts caution that political motivations could drive people to hasty conclusions.

"There is a progenitor virus out there somewhere, and we should look for it," says David Morens, senior scientific adviser on epidemiology to Anthony Fauci, director of the National Institute of Allergy and Infectious Diseases. "But at some point, it crosses over from doing due diligence to wasting time and being crazy. We may have seen that point already."

Here's what we know so far about the scientific investigation into the origin of the pandemic, and what still needs to be done to find clear answers.

What evidence do virus detectives seek?

Tracing the origin of a virus requires extensive fieldwork, thorough forensics, and a fair bit of luck. The laborious endeavor can take years until scientists have the evidence they need to point to a source.

For diseases originating from animals, that evidence is typically a genetic match between virus sequences obtained from an animal and those from some of the first confirmed patients. The match may not be 100 percent, because viruses gather mutations or new genes over time and as they jump hosts. But with enough investigation, scientists have found nearly perfect matches of around 99 percent or better for some viruses—including the ones responsible for two previous coronavirus outbreaks.

Cat-like tree-dwelling palm civets, considered a delicacy and sold in street markets, quickly became the focus during the 2002-04 outbreak of Severe Acute Respiratory Syndrome (SARS) that emerged in China's Guangdong Province, which resulted in more than 8,000 cases and nearly 800 deaths in 29 countries. Some of the first SARS cases included several infected restaurant chefs handling a variety of animals. Blood tests of animal traders in the region showed higher prevalence of antibodies against the SARS-associated coronavirus compared to healthy controls, with the highest levels recorded among those who traded primarily in masked palm civets.

A 2003 paper also showed that the nasal swab of a masked palm civet obtained from a live animal market in Guangdong yielded a 99.8 percent match between the full genome sequence of the SARS-CoV-like virus isolated from the civet and virus from a human. This indicated that the SARS-CoV-like virus had recently infected civets at the market.

But it became evident that these furry mammals weren't the original sources, as the virus was mostly absent among farmed masked palm civets prior to reaching the markets, and it was not widely circulating in its wild populations. Suspecting bats to be the natural reservoirs, given that they harbor other zoonotic viruses, researchers sampled blood, fecal, and throat swabs of bats in regions across China and in Hong Kong.

More than 10 years later, they identified horseshoe bats in a remote cave in southwestern China's Yunnan Province sporting virus strains that contain all the genetic pieces recorded in viral genomes from human patients. It's possible the strain that precipitated the 2002 epidemic was a product of recombination of different genetic strains found in these bats.

Scientists later used lessons from tracing the origins of the SARS virus to investigate the source of the 2012 Middle East Respiratory Syndrome (MERS) coronavirus outbreak, which infected more than 2,000 people in 37 countries and killed nearly 900.

The virus was first isolated from a 60-year-old businessman who died of severe pneumonia and multi-organ failure in June 2012 in a hospital in Jeddah, Saudi Arabia. Early efforts to trace the source focused on bats. In Saudi Arabia, throat swab, urine, fecal, and blood samples from wild bats, including those occurring in the area where the first patient lived and worked, showed indications of a MERS-like coronavirus in one

Egyptian tomb bat fecal sample. But without a full genome sequence, the role of bats could not be evaluated.

Meanwhile, anecdotal reports suggested some patients had been exposed to dromedary camels or goats. A 2013 study found antibodies against MERS in blood samples collected from retired racing camels in Oman, which were missing in blood from European sheep, goats, and cattle. Similar blood surveys conducted in several countries within the Arabian Peninsula, Egypt, and Spain's Canary Islands also showed the presence of antibodies in camel blood, indicating the hoofed mammals were once infected by the virus.

But the strongest evidence of dromedary camels' involvement came from Qatar in October 2013, where a camel herd owner and his co-worker were diagnosed with MERS. Nasal swab tests indicated five of 14 camels on their farm were MERS-positive. Further, whole viral genome sequences obtained from humans and camels were 99.5 to 99.9 percent identical.

Scientists believe camels are the intermediate hosts and suspect bats to be the original reservoirs of MERS-CoV. That's because some bat species, like the vesper bats in South Africa, harbor viruses that are related to the one that causes MERS. But there's still an evolutionary gap between those bat viruses and the human or camel versions.

"We still haven't found those viruses that are very, very close," says virologist Chantal Reusken at the Dutch Institute for Public Health and the Environment in the Netherlands.

> This is all weaponized politically, which is unfortunate.
>
> DARRYL FALZARANOVIROLOGIST

What we know so far about COVID-19's origin story

One key difference with the SARS and MERS outbreaks is that scientists were able to identify the intermediate animal sources within months of their onset. For COVID-19, that link remains unknown.

In December 2019, some of the early COVID-19 cases in Wuhan were reported among vendors linked to the Huanan market, which was selling wild and farmed animals including badgers, racoon dogs, civets, hare, rats, snakes, and crocodiles.

Between January 1, when the market was closed, and March 2020, officials with the Chinese Center for Disease Control and Prevention collected more than 900 swab samples of floors, walls, or surfaces of objects from the Huanan market, its drainage system, and the surrounding markets. They found that 73 samples were SARS-CoV-2 positive.

The Chinese CDC also collected more than 2,000 fecal and body swab samples from alive or frozen animals in Huanan and other markets in Wuhan, from animals raised by some Huanan market suppliers, and from several wild animals found in nearby provinces in southern China.

According to the WHO report, all those samples tested negative for SARS-CoV-2, and in some cases, for antibodies against the virus. But this sampling missed many live animals typically sold when the markets were open. Similar tests of thousands of livestock and poultry samples collected from across China in 2018, 2019, and 2020 as part of routine animal surveillance also tested negative for SARS-CoV-2.

Last year, scientists detected SARS-CoV-2-like virus strains in Sunda pangolin tissue samples that were seized in anti-smuggling operations in southern China in 2017 and 2018. Sought for their meat and scales used in traditional Chinese medicine, these pangolins are among the world's most trafficked mammals. But with only an 85.5 to 92.4 percent match between the human SARS-CoV-2 genome sequence and those obtained from pangolins, scientists can't mark them as the relevant hosts. Also, a team surveying Wuhan's wet markets between May 2017 and November 2019 found no pangolins being sold there.

And as was the case with MERS, comparing genome sequences from early COVID-19 patients with SARS-like coronavirus sequences directly from bats hasn't yet yielded a close enough match, either.

So far, the closet relative is a coronavirus labelled RaTG13. It was discovered in Chinese horseshoe bats near a cave in Yunnan shortly after six miners fell sick and three of them died due to an unknown respiratory illness in 2012. RaTG13 shares 96.2 percent of its genome with human SARS-CoV-2. A coronavirus dubbed RmYN02 and derived from Malayan horseshoe bat poop collected in Yunnan Province in 2019 is 93.3 percent similar.

Scientists have also identified SARS-CoV-2-related viruses in bats outside China. This January a team isolated a coronavirus sequence showing a 92.6 percent match from two Shamel's horseshoe bats sampled in Cambodia in 2010. And in February a coronavirus named RacCS203 taken from acuminate horseshoe bats in Thailand's Chachoengsao Province showed 91.5 percent similarity in its genetic code.

Matches above 90 percent may sound high, but in genomic terms it's a wide evolutionary gap. After all, humans and bonobos are an 98.7 percent genetic match.

"The big problem is that bats are everywhere and there are so many species with a huge diversity of viruses, including coronaviruses," says Bart Haagmans, a virologist at the Erasmus Medical Center in the Netherlands. "It's difficult to find the bats with the virus that started the outbreak."

Why the lab-leak suspicion persists

Many scientists believe that SARS-CoV-2 originated in nature and is unlikely a product of laboratory engineering. In a March 2020 Nature Medicine study, for instance, Kristian Andersen, a virologist at the Scripps Research Institute in La Jolla, California, and his colleagues showed that some genetic features once considered unique to SARS-CoV-2—and thus potentially human-made—are found in nature. They found features like the furin cleavage site, which facilitates the virus's entry into human cells, and the receptor binding domain that allows the virus to anchor itself to human cells,also present in related viruses isolated from Malayan pangolins and bats.

But despite its likely natural origin, the theory that SARS-CoV-2 could have escaped from a laboratory continues to pique the interest of some scientists, several politicians, and many in the larger public sphere.

Part of the suspicion comes from the fact that the pandemic emerged very close to the Wuhan Institute of Virology, where researchers have been surveying bats for coronaviruses and maintaining a database of samples and virus sequences. "People look at the coincidence," Andersen says.

The institute's location doesn't surprise him, though. Wuhan is an extremely connected and populous city with several wet markets, and in the past, bat coronaviruses have been identified from the larger region.

“There are labs close to where outbreaks can happen, and where these outbreaks happen is where you want to study them,” Andersen says.

Still, experts and observers argue it’s possible members of the Wuhan Institute of Virology staff were infected due to safety lapses while working with the SARS-CoV-2 virus or during fieldwork, and then they inadvertently spread the disease.

> What’s frustrating is that with some transparency, it can all be cleared up.
>
> DARRYL FALZARANOVIROLOGIST

In a letter published in Science on May 14, some scientists suggested that the possibility of the virus escaping from the lab was not given due consideration during the WHO investigation. In a March 30 press briefing, WHO program manager Peter Ben Embarek, who led the COVID-19 fact-finding mission to China said: “Since [the lab leak theory] was not the key or main focus of the joint studies, it did not receive the same depth of attention and work as the other hypotheses.”

The Wuhan institute’s leading bat virologist Shi Zhengli said her laboratory records didn’t indicate any match between virus samples her team had collected from China’s bat caves and SARS-CoV-2 sequences. However, the WHO-China team couldn’t access those records.

Laboratory accidents aren’t unheard of. In Singapore, Taiwan, and China, four researchers in labs studying the SARS virus were accidently infected in the aftermath of the initial outbreak. In 2014, dozens of workers at the U.S. Centers for Disease Control and Prevention in Atlanta were potentially exposed to live anthrax bacteria resulting from a breach in safety procedures.

“Historically looking back, we can have lab leaks,” says Jesse Bloom, a virologist at the Fred Hutchinson Cancer Research Center and lead author of the Science letter. “To be confident about what happened, we need more investigation.”

Fresh controversy erupted when a May 23 Wall Street Journal story reported that an undisclosed U.S. intelligence report claimed three researchers at the Wuhan institute sought hospital care in November 2019 for “symptoms consistent with both COVID-19 and common seasonal illness.” The identity of those researchers or the exact illness they had still remains unknown.

The WHO report found no records of COVID-19-related illness or evidence of infection among the institute's staff prior to December 2019. However, the team didn't have access to raw patient data from 174 early COVID-19 cases identified in Wuhan, half of which weren't connected to the Huanan market. This information could aid the quest to trace the pandemic's origin.

"What's frustrating is that with some transparency, it can all be cleared up," says virologist Darryl Falzarano at the University of Saskatchewan. "This is all weaponized politically, which is unfortunate."

What happens next

Several molecular dating analyses have suggested that SARS-CoV-2 was potentially circulating as early as October 2019. The WHO report therefore recommends searching for SARS-CoV-2 antibodies in stored blood bank samples. This could help resolve the timeline for when the virus emerged, but the search for what started the pandemic may be a long and arduous one.

"You may have to spend the next 10 years sampling animals to find something that's really close," Falzarano says. "But you may not even find that perfect linkage."

The WHO team recommends searching for SARS-CoV-2-related viral sequences and antibodies in horseshoe bats mainly in southern China and in East and Southeast Asia. Similar surveys for potential intermediate host species could include pangolins, minks, rabbits, raccoon dogs, and domesticated cats, all of which have been infected by SARS-CoV-2 in the recent past.

Other projects include tracing wildlife farms that supplied markets in Wuhan and testing susceptible animals and people interacting with them, and analyzing the role of cold chains and frozen foods as a transmission source.

Recently, unpublished grant proposals and annual reports obtained by The Intercept gave insight into National Institutes of Health-funded coronavirus research in Wuhan in collaboration with New York-based non-profit EcoHealth Alliance.

In sophisticated, high-security facilities called Biosafety Level 3 labs, scientists tested the ability of new bat coronaviruses to infect humanized mice cells. These tests often used hybrid viruses created using a previously known SARS-like strain as the backbone and adding what's called a spike protein from a new virus that facilitates its entry into cells.

"It's standard virology research and it's addressing a really key question: What are the potential viruses that could emerge [as a potential threat to humans] and where are they found," says Andersen, who reviewed the documents on National Geographic's request. To him, the information doesn't indicate that SARS-CoV-2 was engineered in the Wuhan laboratory as the backbone strain used in their experiments is not the backbone of SARS-CoV-2.

Still, even before the grant documents came to light, some pundits were wondering if the laboratory will be investigated further for conducting any risky experiments or biosafety breaches.

"We don't know exactly what happened," Bloom says. "So, we can't rule out all possibilities"

Editor's Note: This story originally misspelled the name of the virologist at the Scripps Research Institute in La Jolla. It is Kristian Andersen.

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: Friday, September 10, 2021 4:33 PM
To: Peter Daszak b6; Gerald Keusch b6; Robert Kessler b6 Kristian Andersen b6; Eddie Holmes b6; Angie Rasmussen b6; Jason Gale <j.gale@bloomberg.net>
Subject: Fwd: origins of SARS-CoV-2

This lady totally misquotes me because she did't read her own notes and didn't let me go over the text as agreed to. The « waste of time » comment was about chasing lab leaks, not searching for viral origins

Grrrrr……. d

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

Begin forwarded message:

> **From:** Priyanka Runwal b6
> **Date:** September 10, 2021 at 16:24:14 EDT
> **To:** "Morens, David (NIH/NIAID) [E]" b6
> **Subject: Re: origins of SARS-CoV-2**
>
> Hi David,
> The story was finally published today: https://www.nationalgeographic.com/science/article/why-its-so-tricky-to-trace-the-origin-of-covid-19
> I really appreciate you taking the time to speak with me and sharing your insights.
>
> On Tue, Sep 7, 2021 at 12:52 PM Priyanka Runwal b6 wrote:
>
>> b6.
>>
>> On Tue, Sep 7, 2021 at 12:51 PM Priyanka Runwal b6 wrote:
>>
>>> Sounds good. Thank you.
>>> I'm at b6. Call me anytime.
>>>
>>> On Tue, Sep 7, 2021 at 12:45 PM Morens, David (NIH/NIAID) [E] b6 wrote:
>>>
>>>> No, but give me a number to call you. In a meeting now but should be free within the hour

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: Priyanka Runwal b6
Sent: Tuesday, September 7, 2021 12:37 PM
To: Morens, David (NIH/NIAID) [E] b6
Subject: Re: origins of SARS-CoV-2

Thank you for your reply. I can call you now or any other convenient time you prefer.

Is this the best number to reach you: b6 ?

On Tue, Sep 7, 2021 at 12:26 PM Morens, David (NIH/NIAID) [E] b6 wrote:

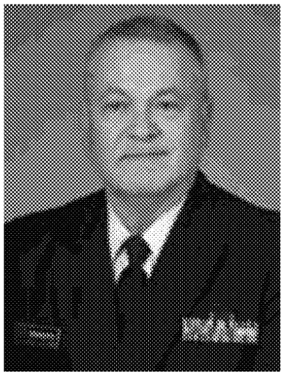
Sure, let me know…..

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: Priyanka Runwal b6
Sent: Tuesday, September 7, 2021 12:26 PM
To: Morens, David (NIH/NIAID) [E] b6
Subject: Re: origins of SARS-CoV-2

Dear David,

We spoke a while ago and my editor is looking to publish the story tomorrow.

I have, of course, included quotes from our earlier interview, but would you have any comment on the FOIA-ed grant proposals and suggestions of gain-of-function research The Intercept story cites:https://theintercept.com/2021/09/06/new-details-emerge-about-coronavirus-research-at-chinese-lab/

Your input would be helpful to our readers. I wouldn't take more than 10 minutes of your time. Let me know. Thank you.

On Fri, Jul 30, 2021 at 5:46 PM Priyanka Runwal b6 wrote:

> Thank you so much, David.
>
> On Fri, Jul 30, 2021 at 3:50 PM Morens, David (NIH/NIAID) [E] b6 wrote:
>
>> Hi Priyanka, attached is the article I mentioned that came out yesterday, expaining in part why legitimate scientists are afraid to speak out about the "origins" stories.
>>
>> David

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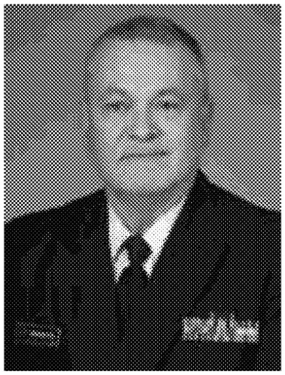

From: Priyanka Runwal b6
Sent: Thursday, July 29, 2021 6:36 PM
To: Morens, David (NIH/NIAID) [E] b6
Subject: Re: origins of SARS-CoV-2

Hi David,

Here are my questions:

1) Given past pandemics, what about the SARS-CoV-2 origin narrative/debate surprises you?

2) As an expert, what's the proof you're looking for to pin down the origin--either in nature or the much-debated lab leak/engineering?

Essentially, what evidence will convince you of the rightful SARS-CoV-2 origin.

3) In the same context, what are key data/pieces of evidence we should have had by now but are missing? This could touch on the early surveillance China did and the WHO team reviewed.

4) Are there any questions about the origin that we (media) aren't asking or science we aren't understanding/appreciating that we should?

Please let me know when and what number to call you tomorrow. Thanks

On Thu, Jul 29, 2021 at 10:47 AM Morens, David (NIH/NIAID) [E] b6 [redacted] wrote:

> Great, TY,
>
> 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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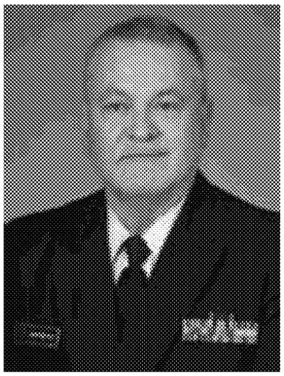

From: Priyanka Runwal b6
Sent: Thursday, July 29, 2021 10:15 AM
To: Morens, David (NIH/NIAID) [E] b6
Subject: Re: origins of SARS-CoV-2

Later tomorrow works for me.

I really appreciate you making the time.

I'll send some questions your way this afternoon. Thanks again.

On Thu, Jul 29, 2021 at 10:03 AM Morens, David (NIH/NIAID) [E] b6 wrote:

Possibly later tomorrow… My schedule is a bit messed up until next Tuesday as I am both working and have guests in town. My best times are typically late afternoons, like 4 or 5ish…. Also, it would be helpful if you could send me a few more sentences about specifically what you are looking for, so that I can perhaps pull out some of the key manuscripts, Ty,

David

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

Senior Advisor to the Director
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Building 31, Room 7A-03
31 Center Drive, MSC 2520
Bethesda, MD 20892-2520

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

From: Priyanka Runwal b6
Sent: Thursday, July 29, 2021 10:05 AM
To: Morens, David (NIH/NIAID) [E] b6
Subject: Re: origins of SARS-CoV-2

Hi David,

Thank you so much for your email.

I'm happy to work around your schedule to make this interview possible.

Would anytime this week work for you?

On Thu, Jul 29, 2021 at 9:56 AM Morens, David (NIH/NIAID) [E] b6 wrote:

> Hi Priyanka, our media office here suggested you may want to speak to me about the origins of SARS-CoV-2. Happy to do that, schedules permitting.
>
> David

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

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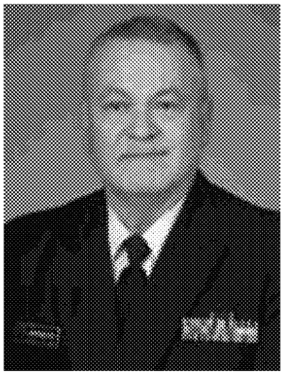

--

Best,

Priyanka Runwal

@priyanka_runwal

Science, environment & health journalist

Bylines: The New York Times, Scientific American, STAT, National Geographic, Audubon Magazine, Science News, Live Science, others

--

Best,

Priyanka Runwal

@priyanka_runwal

Science, environment & health journalist

Bylines: The New York Times, Scientific American, STAT, National Geographic, Audubon Magazine, Science News, Live Science, others

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--
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@priyanka_runwal
Science, environment & health journalist
Bylines: The New York Times, Scientific American, STAT, National Geographic, Audubon Magazine, Science News, Live Science, others

From: Morens, David (NIH/NIAID) [E] [b6 b6]
Sent: 7/30/2021 7:55:20 PM
To: Peter Daszak (b6) [b6]; Keusch, Jerry (b6) [b6]
Subject: FW: Fox: Fauci, top scientist called to brief House committees; phone call questioned

David

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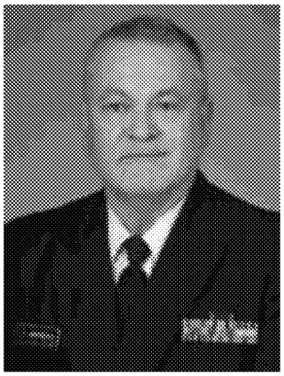

From: Folkers, Greg (NIH/NIAID) [E] b6
Sent: Friday, July 30, 2021 3:11 PM
To: NIAID COGCORE <COGCORE@mail.nih.gov>; NIAID OCGR Leg <NIAIDOCGRLeg@mail.nih.gov>; NIAID OD AM

<NIAIDODAM@niaid.nih.gov>
Subject: Fox: Fauci, top scientist called to brief House committees; phone call questioned

Fauci, top scientist called to brief House committees; phone call questioned

Edmund DeMarche
Fri, July 30, 2021, 1:37 AM·3 min read

A top scientist emailed Dr. Anthony Fauci during the early days of the COVID-19 outbreak that the virus seemed like it may have been engineered.

The following evening, the scientist joined other experts on a call with the top disease doctor and days later dismissed the idea of an engineered virus as a "crackpot" theory.

NYT WRITER HITS FAUCI IN SCATHING OP-ED

Two top House Republicans now want to know how a scientist can have such a dramatic change in opinion -- so quickly -- about a virus that continues to baffle top experts.

Rep. Jim Jordan, R-Ohio, said in a letter Thursday to Kristian Andersen, a virologist at California's Scripps Research Institute, that he's interested in learning what was discussed during the call that may have contributed to the change of opinion.

Andersen's email was released along with a trove of others back in June.

The email read, in part, "The unusual features of the virus make up a really small part of the genome (<0.1%) so one has to look really closely at all the sequences to see that some of the features (potentially) look engineered," he wrote. He admitted in the email that the research was in its early stages and his team needed more time to get a better grasp.

Jordan, the ranking member on the House Judiciary Committee, and Rep. James Comer, R-Ky., ranking member on the House Oversight and Reform Committee, pointed out in a letter to Andersen that the email was sent Jan. 31, 2020. The following evening, Andersen and "several other international virologists" were on a call with Fauci.

NYT'S BRET STEPHENS SLAMS MEDIA OVER LAB-LEAK THEORY: THOSE PANICKING ABOUT 'MISINFORMATION' 'PEDDLE IT' THEMSELVES

The Republicans said the contents of the call remain a mystery, but between the conversation and Feb. 4, 2020, Andersen sent Dr. Peter Daszak, CEO of EcoHealth Alliance, an email that called the man-made idea one of "the main crackpot theories going around at the moment."

"This is demonstrably not the case," Andersen wrote to Daszak, according to the statement.

Andersen, Fauci's National Institute of Allergy and Infectious Diseases and Daszak did not respond to after-hours emails from Fox News seeking comment.

"In three days, with no explanation as to why, you flipped your perspective entirely and began calling a theory you lent credence to only days earlier a 'crackpot theory,'" the representatives wrote. "It would appear the primary intervening event was the February 1 conference call with Dr. Fauci. We are very interested in understanding what happened on that call or what science came to light that caused such a dramatic change in your own hypothesis as to the engineering of COVID-19. Therefore, we request a staff level briefing as soon as possible but no later than August 5, 2021."

Andersen has been defended on social media by those who say it is common for scientists to have evolving theories about diseases.

A statement from the Republicans on the House Oversight Committee called on Fauci to join Andersen to discuss gain-of-function research conducted at the Wuhan lab.

From: Morens, David (NIH/NIAID) [E] [b6
b6]
Sent: 7/25/2021 11:32:19 PM
To: Peter Daszak [b6]
CC: Gerald Keusch [b6]
BCC: Morens, David (NIH/NIAID) [E] [b6
b6]
Subject: Re: Josh Rogin

…But, you are way too kind…. d

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

> On Jul 25, 2021, at 19:06, Peter Daszak b6 wrote:
>
> Amen - just read it. This guy is all-in for the US-China cold war, and is already making money out of it with his book that's used as his Twitter 'banner'. This is about his 10th Op Ed on exactly the same topic and using most of the same words. Can't take him more than an hour to bang one out and every time he does that he gets a quick $500 and a boost to his book readership. Add to that his paranoia about China and he just comes across
>
> b6
>
> One day I'm going to have the misfortune of meeting this person, or some others who've done me and our organization real harm (I'm thinking Francis Collins, Michael Lauer and many internet trolls out there). After a year and a half of swallowing my pride and controlling my anger, I wonder if I'll end up expressing myself to them in a similar Op Ed style diatribe,
> b6
>
> b6
>
> 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

-----Original Message-----
From: Morens, David (NIH/NIAID) [E] b6
Sent: Friday, July 23, 2021 8:07 AM
To: Peter Daszak b6; Gerald Keusch
b6
Subject:

another disgusting editorial by josh rogin in the post this morning.
when will the post stop this crap? d

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

From: Morens, David (NIH/NIAID) [E] [b6]
([b6])
Sent: 6/23/2021 4:53:42 PM
To: Peter Daszak [b6]; Keusch, Jerry [b6]; Rich Roberts [b6]
Subject: RE: Interview request: CNN / Jesse Bloom preprint

I discussed this very Q with Jeff T this morning, and he felt yes, deleting incomplete data in a larger dataset with complete data, in the context of having no reason to suspect some bias, is a normal approach. Certainly we do that in epi all the time, use only the "completely complete" data as the best and most honest way to present data.

David

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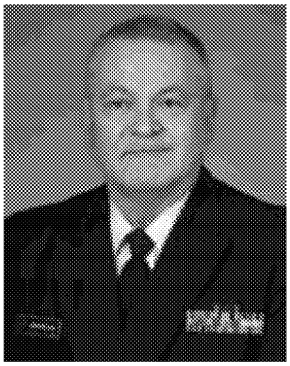

From: Peter Daszak b6
Sent: Wednesday, June 23, 2021 12:05 PM
To: Morens, David (NIH/NIAID) [E] b6; Keusch, Jerry b6; Rich Roberts b6
Subject: RE: Interview request: CNN / Jesse Bloom preprint

It's just sad that the press stories around this are not about how this adds to our information on origins (or not), but about how it looks to some people that Chinese scientists are corrupt and involved in a cover-up.

Of course, even scientists who don't regularly upload gene sequences (e.g. like me) don't really know whether what they did by removing them was normal or abnormal, and this is what these stories rely on – so complicated an issue that it just will continue a narrative that's already being amplified.

I'm trying to get others (b6) to comment on whether it would be normal to delete partial genomes because you think they might not be high quality. Maybe they already had a bunch of full genomes and didn't see great value in adding more partial sequences that could be incorrect, particularly when it didn't change the conclusions much. But, I just don't know …

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 11:17 AM
To: Peter Daszak (b6) b6; Keusch, Jerry (b6) b6 Rich Roberts (b6) b6
Subject: FW: Interview request: CNN / Jesse Bloom preprint

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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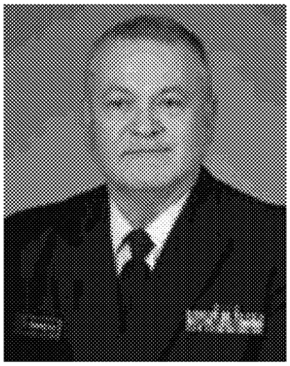

From: Routh, Jennifer (NIH/NIAID) [E] b6
Sent: Wednesday, June 23, 2021 11:11 AM
To: Leifman, Laura (NIH/NIAID) [E] b6 Conrad, Patricia (NIH/NIAID) [E] b6 ; NIAID FOG <fog@niaid.nih.gov>
Cc: NIAID COGCORE <COGCORE@mail.nih.gov>; NIAID Media Inquiries <mediainquiries@niaid.nih.gov>
Subject: RE: Interview request: CNN / Jesse Bloom preprint

& just to clarify (this is at the beginning of this thread), NIH prepared the statement below and sent to Maggie. So she already has this, but Maggie wanted someone to walk her through the findings themselves. (NSWB – we will work with OCPL on this topic – some inquiries will be satisfied by this statement alone, which OCPL will handle.)

NIH is aware of Dr. Bloom's preprint submission. Staff at the National Library of Medicine, which hosts the Sequence Read Archive (SRA), have reviewed the submitting investigator's request to withdraw the data. These SARS-CoV-2 sequences were submitted for posting in SRA in March 2020 and subsequently

requested to be withdrawn by the submitting investigator in June 2020. The requestor indicated the sequence information had been updated, was being submitted to another database, and wanted the data removed from SRA to avoid version control issues. The submitting investigator published relevant information about these sequences by preprint in March, 2020 and in a journal in June, 2020. Submitting investigators hold the rights to their data and can request withdrawal of the data.

Currently, the National Library of Medicine (NLM) has no plans to change the policy that recognizes submitters rights to their own data and the right to petition that their data be withdrawn from the Sequence Read Archive (SRA). The National Center for Biotechnology Information (NCBI), part of the NLM that manages the database, is the U.S. participating member of the International Nucleotide Sequence Database Collaboration, which provides guidelines for withdrawing data: http://www.insdc.org/documents/insdc-status-document. NLM/NCBI can't speculate on motive beyond a submitter's stated intentions.

Jennifer Routh [E]
News and Science Writing Branch
Office of Communications and Government Relations
National Institute of Allergy and Infectious Diseases (NIAID)
NIH/HHS
31 Center Drive Room 7A17C
Bethesda, MD 20892
Direct: b6
b6

From: Leifman, Laura (NIH/NIAID) [E] b6
Sent: Wednesday, June 23, 2021 9:52 AM
To: Conrad, Patricia (NIH/NIAID) [E] b6; NIAID FOG <fog@niaid.nih.gov>
Cc: NIAID COGCORE <COGCORE@mail.nih.gov>; NIAID Media Inquiries <mediainquiries@niaid.nih.gov>
Subject: Interview request: CNN / Jesse Bloom preprint
Importance: High

Maggie Fox
CNN
Maggie.Fox@cnn.com; b6
Topic: Jesse Bloom's analysis of early SARS-CoV-2 genetic data
Deadline: Today

Hi Patty,

Per the email string below, Maggie would like to interview someone who can help her unpack Jesse Bloom's analysis of the data (not about the deletion) that he posted in BioRx. Would ASF like to discuss this with her? She understands that NIAID didn't support the work.

Best,
Laura

From: Myles, Renate (NIH/OD) [E] b6
Sent: Wednesday, June 23, 2021 9:34 AM
To: NIAID OCGR NSWB <NIAIDOCGRNSWB@mail.nih.gov>
Cc: Fine, Amanda (NIH/OD) [E] b6; Wojtowicz, Emma (NIH/OD) [E] b6
Subject: FW: Jesse Bloom and missing SARS-Cov2-2 genetic sequences
Importance: High

Hi all:

I’m sure you’ve heard that Jesse Bloom of Fred Hutch posted a paper on BioRx that assigns motive to a Chinese investigators decision to withdraw early SARS-CoV-2 data from the NCBI Sequence Read Archive. Oure response is below. Maggie Fox is asking if someone can help her unpack the Bloom analysis of the data (not about the deletion). I told her NIAID didn’t support the work but that I would check. ASF and Alan Embry is aware of this>

Thanks,
Renate

From: Myles, Renate (NIH/OD) [E]
Sent: Wednesday, June 23, 2021 9:26 AM
To: Fox, Maggie <Maggie.Fox@cnn.com>
Cc: Fine, Amanda (NIH/OD) [E] b6; Burklow, John (NIH/OD) [E] b6; Wojtowicz, Emma (NIH/OD) [E] b6 Brodd, Lauren (NIH/OD) [E] b6
Subject: RE: Jesse Bloom and missing SARS-Cov2-2 genetic sequences

Hi Maggie:

We can check with NIAID to see if they have someone willing to speak to Dr. Bloom’s findings; NIAID didn’t support the work and this is a preprint publication that hasn’t been peer reviewed, so they may not be inclined to comment. Also NIAID can’t comment on the deletion of the data from SRA. We’ve provided the explanation below and Bloom’s assignment of motive beyond what the submitter stated is purely speculative.

Thanks,
Renate

From: Fox, Maggie <Maggie.Fox@cnn.com>
Sent: Wednesday, June 23, 2021 9:17 AM
To: Myles, Renate (NIH/OD) [E] b6
Cc: Fine, Amanda (NIH/OD) [E]; Burklow, John (NIH/OD) [E] b6
Wojtowicz, Emma (NIH/OD) [E] b6; Brodd, Lauren (NIH/OD) [E] b6
Subject: Re: Jesse Bloom and missing SARS-Cov2-2 genetic sequences

Thank you, Renate
Would it be possible to speak to someone else? This one is very complicated and we are going to have to report on it. I understand that no one is going to want to touch the politics of this, but I would very much like to talk to someone with genomics experience who can help me interpret Dr. Bloom’s findings.

I am pretty certain NIH is going back over what he has pointed out.

Can someone please help me, even on background? Thank you!

Maggie Fox
Senior Editor, Health
CNN

> On Jun 23, 2021, at 08:36, Myles, Renate (NIH/OD) [E] b6 wrote:

Hi Maggie:

Hope you're well. Dr. Collins is out on vacation this week, so isn't available. Here is a statement attributable to NIH generally.

NIH is aware of Dr. Bloom's preprint submission. Staff at the National Library of Medicine, which hosts the Sequence Read Archive (SRA), have reviewed the submitting investigator's request to withdraw the data. These SARS-CoV-2 sequences were submitted for posting in SRA in March 2020 and subsequently requested to be withdrawn by the submitting investigator in June 2020. The requestor indicated the sequence information had been updated, was being submitted to another database, and wanted the data removed from SRA to avoid version control issues. The submitting investigator published relevant information about these sequences by preprint in March, 2020 and in a journal in June, 2020. Submitting investigators hold the rights to their data and can request withdrawal of the data.

Currently, the National Library of Medicine (NLM) has no plans to change the policy that recognizes submitters rights to their own data and the right to petition that their data be withdrawn from the Sequence Read Archive (SRA). The National Center for Biotechnology Information (NCBI), part of the NLM that manages the database, is the U.S. participating member of the International Nucleotide Sequence Database Collaboration, which provides guidelines for withdrawing data: http://www.insdc.org/documents/insdc-status-document. NLM/NCBI can't speculate on motive beyond a submitter's stated intentions.

Thanks much,
Renate

From: Fox, Maggie <Maggie.Fox@cnn.com>
Sent: Wednesday, June 23, 2021 12:00 AM
To: Fine, Amanda (NIH/OD) [E] b6
Cc: Burklow, John (NIH/OD) [E] b6 Myles, Renate (NIH/OD) [E] b6 Wojtowicz, Emma (NIH/OD) [E] < b6
Subject: Jesse Bloom and missing SARS-Cov2-2 genetic sequences

Hi y'all-
Jesse Bloom, geneticist at Fred Hutchinson Cancer Center, published this preprint and has been all over Twitter tonight saying early sequences of coronavirus samples from Wuhan were somehow deleted from the NIH database. He says Dr Collins confirmed this and was helping him track it down?
https://www.biorxiv.org/content/10.1101/2021.06.18.449051v1.full.pdf

Can you all confirm this and may I speak to Dr. Collins about it?

Thank you so much!

Maggie Fox
Senior Editor, Health
CNN
b6

Disclaimer

From: Morens, David (NIH/NIAID) [E] [b6
(b6]
Sent: 7/26/2021 2:20:39 PM
To: Peter Daszak [b6]; Keusch, Jerry [b6]
Subject: RE: Science Speaks: Clues to COVID origins via Wuhan wet market study 2017-2019 of severe fever with thrombocytopenia syndrome

Every team meeds a professional clown

David

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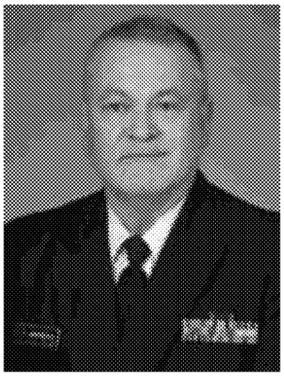

From: Peter Daszak b6
Sent: Monday, July 26, 2021 10:13 AM
To: Morens, David (NIH/NIAID) [E] b6; Keusch, Jerry b6

Subject: RE: Science Speaks: Clues to COVID origins via Wuhan wet market study 2017-2019 of severe fever with thrombocytopenia syndrome

Yes – thanks to him for ‘man-splaining’ how this work may or may not be possible to do!

No doubt this will form part of his application to join the WHO phase 2 team as US uber-investigator-General….

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

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From: Morens, David (NIH/NIAID) [E] b6
Sent: Monday, July 26, 2021 10:05 AM
To: Peter Daszak (b6) b6; Keusch, Jerry (b6)
b6
Subject: FW: Science Speaks: Clues to COVID origins via Wuhan wet market study 2017-2019 of severe fever with thrombocytopenia syndrome

From Uncle Dan Lucey…..

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

From: Folkers, Greg (NIH/NIAID) [E] b6
Sent: Sunday, July 25, 2021 6:13 PM
Subject: Science Speaks: Clues to COVID origins via Wuhan wet market study 2017-2019 of severe fever with thrombocytopenia syndrome

Science Speaks: Global ID News

Clues to COVID origins via Wuhan wet market study 2017-2019 of severe fever with thrombocytopenia syndrome

July 15, 2021.

By Daniel R. Lucey MD, MPH, FIDSA

Retrospective testing for SARS-CoV-2 virus and antibody could be (or has been) done using blood and other samples highly likely to have been obtained from the 18 mammalian species (including masked palm civet, racoon dogs, and mink) reported in the Wuhan wet markets, May 2017-November 2019, as part of a study on "Severe Fever with Thrombocytopenia (SFTS)" published not until June 7, 2021.

Photos from the Wuhan Huanan seafood market include racoon dogs, hedgehogs, bamboo rats, and badgers with the description of **"Poor welfare of animals on sale in Huanan seafood market."**

A tick found on a hedgehog is emphasized in the legend to Figure 2, given that ticks are thought to be the main transmission route from animals to humans of the bunyavirus first discovered in a 2009 outbreak in Hubei and Henan provinces of Severe Fever with Thrombocytopenia Syndrome. (An aerosol route is less commonly implicated in nosocomial, familial, and other cases of persons-to-person transmission of this bunyavirus causing SFTS).

Although *not explicitly stated* in this June 7 paper in *Nature*, it is highly likely that samples of blood and perhaps respiratory and other types of samples from the animals surveyed on a monthly basis in Wuhan wet markets from May 2017-November 2019 would have been obtained.

In addition, blood samples from humans working in these wet markets, including the Wuhan Huanan seafood market, would very likely have been obtained to test for bunyavirus and antibody to the bunyavirus that causes SFTS. (Less likely, even respiratory samples from humans may have been obtained).

Such samples from both animals and humans in the Wuhan wet markets could be tested for antibody to SARS-CoV-2, as well as any respiratory samples for SARS-CoV-2 itself, month-by-month over 30 months from May 2017-November 2019.

If antibody-negative results were demonstrated in 2017 and 2018, followed by some antibody (and perhaps virus)-positive results in 2019, **then a "look back" retrospective study of the supply chain of animals and the epidemiology of the humans could provide clues to the COVID origins in terms of emergence timeline, geography, animal species, and human infections.**

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From: Morens, David (NIH/NIAID) [E] [b6 b6]
Sent: 8/20/2021 2:48:25 PM
To: Wang Linfa [b6]; Jason Gale [j.gale@bloomberg.net]; b6; b6 Garry, Robert F [b6]; b6
CC: Taubenberger, Jeffery (NIH/NIAID) [E] (b6) [b6]; Memoli, Matthew (NIH/NIAID) [E] (b6) [b6]; Manning, Jessica (NIH/NIAID) [E] (b6) [b6 b6]
Subject: RE: (BN) SARS Survivors Offer Clues on Protecting Against Future Scourges

Dear Linfa, thanks and again, this is a potentially very important test for epidemiologic study, as well as, obviously, pointing a very promising way forward in vacine development.

I have taken the liberty of copying some of my NIH colleagues on this email, and sent several of them your NEJM paper yesterday, although I forgot to attach the supplementary data.

My NIH colleagues Jeff Taubenberger and Matt Memoli, and others, have been working on both influenza and SARS-CoV-2 vaccines designed to induce broad cross-protective immunity, including human challenges with flu but, at this point, only animal studies with SARS-CoV-2.

Our NIH colleague Jessica Manning has a field site in Cambodia and as I believe I mentioned to you last month, has identified a set of banked serums from folks in rural Cambodia that light up with SARS-CoV-2 in binding assays but not in Nt.

A multiplex assay would be a boon to field epidemiology by potentially specifying the viruses that positive individuals had been exposed to, in association with studying bats in those areas as well.

I think Peter D has mentioned that he has a paper coming out very soon that estimates a very large number of residents in the geographic area of interest, basically S and SW China plus the SEA countries… In other words, the ecosystem within which these viruses circulate and spill over to humaans/other mammals seems to be very broad and large.

Very exciting, and I hope your work will lead not only to better vaccines but also epidemiologic study relating to “origin” as well as characterizing the nature and extent of human exposures to sarbecoviruses.

David

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📠 301 496 4409
💻 b6

From: Wang Linfa b6
Sent: Thursday, August 19, 2021 10:55 AM
To: Morens, David (NIH/NIAID) [E] b6; Jason Gale <j.gale@bloomberg.net>; b6; Garry, Robert F b6
Subject: RE: (BN) SARS Survivors Offer Clues on Protecting Against Future Scourges

Thanks David.

We were able to make this discovery for a few reasons:

1) We had SARS survivors in Singapore who are willing to help
2) I was puzzled by the lack for cross-NAb in SARS patient sera against COVID, so wanted to know whether boosting with CVOID vaccine can make such antibodies more dominant
3) Last, but not the least, I had the multiplex sVNT which allowed accurate and reliable comparison of NAbs against different sarbecoviruses in a "drop of blood" literally. We did 10-plex, but we can go to all-sarbecovirus-in-one if we want

This same test platform will play a key role in our common interest: finding the origin and/or spillover events of sarbecoviruses, not just SARS-CoV-2.

So let me know if you have "high value" human or animal sera for testing.

Cheers,

LF

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: Morens, David (NIH/NIAID) [E] b6
Sent: Thursday, 19 August 2021 10:07 PM
To: Jason Gale <j.gale@bloomberg.net>; b6
b6; Wang Linfa b6; Garry, Robert F
b6
Subject: RE: (BN) SARS Survivors Offer Clues on Protecting Against Future Scourges

- External Email -

Yes, hugely important, congrats to Linfa! This was the paper you mentioned a couple weeks back and I've been keenly waiting to see it. Even better than expected. I think many wwill be surprised, which reminds us that assumptions we might make from other viruses like flu, flaviviruses, etc., might not be germane to sarbecoviruses....

David

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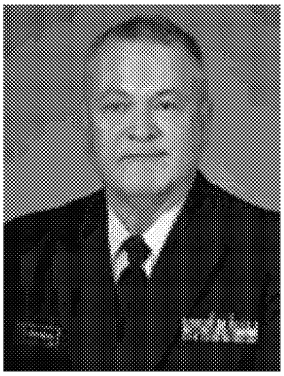

From: Jason Gale (BLOOMBERG/ NEWSROOM:) <j.gale@bloomberg.net>
Sent: Wednesday, August 18, 2021 7:43 PM
To: b6; Morens, David (NIH/NIAID) [E] <b6; Garry, Robert F b6
Subject: (BN) SARS Survivors Offer Clues on Protecting Against Future Scourges

Make sure you check out Linfa's cool paper in NEJM today
https://www.nejm.org/doi/full/10.1056/NEJMoa2108453?query=featured home

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SARS Survivors Offer Clues on Protecting Against Future Scourges
2021-08-18 21:00:00.0 GMT

By Jason Gale
(Bloomberg) -- A serendipitous discovery in survivors of the 2003 SARS outbreak offers important clues about how next-generation vaccines might counter dangerous coronavirus variants now and protect against future pandemics.

The signs were found in the blood of people who contracted the virus that causes severe acute respiratory syndrome, or SARS, almost 20 years ago. Survivors who recently received two shots of Pfizer Inc.'s Covid-19 vaccine developed antibodies that not only blocked the current virus and its variants, they countered related pathogens that could spawn future outbreaks.

"That was really, really unexpected, but an important discovery," said Linfa Wang, a professor of virology at Singapore's Duke-NUS Medical School and the lead author of the paper that compared the immune responses of different patient groups. The findings were published Thursday in the New England Journal of Medicine.

Wang is working on experimental vaccines based on SARS that could bolster the immunity generated by current Covid shots to protect against a broader array of SARS-CoV-2 variants and their virological cousins. That includes so-called sarbecoviruses

sometimes carried by bats, pangolins, civets and other wildlife
-- all potential vectors for novel infections in humans.
Read More: Delayed Wuhan Report Adds Crucial Detail to
Covid Origin Puzzle
“Based on our data, there is a glimpse of hope that now we can really develop an efficient pan-sarbecovirus vaccine,” which would protect against an array of infections, Wang said over Zoom. “For the first time, maybe we can do something in the context of pandemic preparedness.”

Prime Boost

More research is underway to understand how sequential vaccination is able to prime the immune system and then boost its response to defend against sarbecoviruses, Wang said. He hopes patient studies on the new shots will begin this year or next.
In addition, the potent infection-fighting antibodies produced by Covid-vaccinated SARS survivors may provide the basis for treatments known as monoclonal antibodies, Wang said. They will be studied further and, if successful, could be stockpiled to provide rapid treatment for patients infected with newly emerging sarbecoviruses, he said.
The research builds on technology developed by Wang and his colleagues that lets scientists identify the specific coronavirus strains that triggered production of their antibodies. In this way, a simple blood test could determine within an hour what variant a Covid-19 patient was infected with, Wang said. The antibody analysis technique could also be used to identify early cases of Covid-19 and potentially the progenitor of SARS-CoV-2, he said.
The study was supported by grants from the Singapore National Research Foundation and National Medical Research Council.

To contact the reporter on this story:
Jason Gale in Melbourne at j.gale@bloomberg.net
To contact the editors responsible for this story:
Brian Bremner at bbremner@bloomberg.net
Michelle Fay Cortez, Jason Gale

To view this story in Bloomberg click here:
https://blinks.bloomberg.com/news/stories/QY0NH0DWRGG1

From: Peter Daszak [b6]
Sent: 8/19/2021 2:37:31 PM
To: Morens, David (NIH/NIAID) [E] [b6] (b6); Robert Kessler [b6]; Keusch, Jerry [b6]
Subject: RE: Wpost: How Chinese pressure on coronavirus origins probe shocked the WHO - and led its director to push back

Texting with the WHO mission team this morning, I mentioned how this mysterious “WHO spokesperson” keeps slagging off the team’s work and making stories out of it that suit the DG’s politics as he lines up for re-election. I suggested it’s probably Gabby Stern, the WHO head of comms, who basically works for Tedros. b6 confirmed that. It’s a very successful political/communications strategy from the WHO DG that began as soon as Biden entered the WH. He undermined the report re. the lab leak publicly right after the Press conference from Wuhan. Despite this article he knew exactly what was in the report and no one “fell off their chair”. The DG then publicly criticized it re. the lab leak, got praises from the US State Dept because it helped with their goals of looking tough on China, and then launched his campaign for a second term, no doubt with US backing as opposed to his first campaign. Slick politician, awful public health guy.

By the way, at one point after we returned from Wuhan, the DG openly tried to get us to change the conclusions of our poll that we held in China re. the lab leak, so it would be more likely than “extremely unlikely”. Utterly shameless, and of course we refused to do that and pointed out we were reporting results of an actual poll that had already been openly reported on. This led to us (in particular myself and b6) arguing openly with the DG in a very ugly 2 hour zoom call.

Misinformation right from the top at WHO. Most of the senior staff around the DG are ashamed of his political maneuverings – b6 and others were very quiet on the zoom call when the DG announced to the team that he’d be setting up a new structure and we’d have to re-apply for membership for Phase 2 through our governments this time.

Cheers,

Peter

Peter Daszak
President

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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] b6
Sent: Thursday, August 19, 2021 9:52 AM
To: Peter Daszak (b6) b6; Kessler, Robert (b6) b6; Keusch, Jerry (b6) b6
Subject: FW: Wpost: How Chinese pressure on coronavirus origins probe shocked the WHO — and led its director to push back

David

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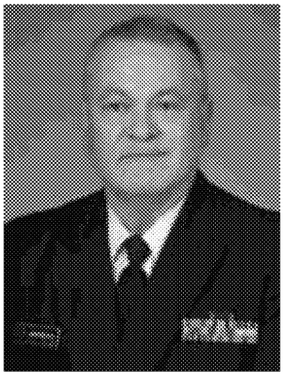

From: Folkers, Greg (NIH/NIAID) [E] b6
Sent: Thursday, August 19, 2021 8:41 AM

Subject: Wpost: How Chinese pressure on coronavirus origins probe shocked the WHO — and led its director to push back

How Chinese pressure on coronavirus origins probe shocked the WHO — and led its director to push back

By
Adam Taylor
Reporter
Today at 12:01 a.m. EDT

You're reading an excerpt from the Today's WorldView newsletter. Sign up to get the rest free, including news from around the globe, interesting ideas and opinions to know, sent to your inbox every weekday.

From the start of the coronavirus pandemic, the World Health Organization has been accused of being too soft on China. President Donald Trump last year accused the organization of pushing "China's misinformation about the virus" as he threatened to withdraw U.S. funding. At one point, Japan's deputy prime minister labeled it the "China Health Organization."

But a new book that details the relationship between the United States, China and the WHO during the pandemic offers a more nuanced and revealing story. It shows how WHO Director General Tedros Adhanom Ghebreyesus cautiously praised China in public while pressuring it in private. And it shows how the Trump administration undermined this tactic with open hostility toward China and the WHO.

"Aftershocks: Pandemic Politics and the End of the Old International Order," written by Thomas Wright and Colin Kahl and due to be published Tuesday, reveals how Tedros lost patience with China: When a WHO scientist on a coronavirus origins probe announced in February that the idea that the virus leaked from a lab was "extremely unlikely" and unworthy of further investigation, senior WHO staff in Geneva were shocked. "We fell off our chairs," one member told the authors.

The team in Wuhan appeared to have given in to Chinese pressure to dismiss the idea without a real investigation. Later, when the WHO-China team released a report that again dismissed that scenario, Tedros pushed back, saying that the research was not "extensive enough" and that there had not been "timely and comprehensive data-sharing."

Since then, relations between the WHO and China have nosedived. Chinese officials said in July that they would not accept any further investigation into the origin of the coronavirus in China and accused the United States of pressuring scientists. The WHO last week released a statement that resisted the idea that "the origins study has been politicized, or that WHO has acted due to political pressure."

Wright is a scholar at the Brookings Institution who focuses on America's global relationships, and Kahl was recently confirmed as undersecretary of defense for policy in the Biden administration. In an interview, Wright said researching for the book revealed how the WHO's cautious approach toward China was at odds with the Trump administration's brash style, though both were driven by legitimate concerns about China under President Xi Jinping.

The World Health Assembly, a representative body of WHO member states, approved an investigation into the pandemic's origins in May 2020. Soon an international team of experts led by WHO official Peter Ben Embarek was convened to travel to Wuhan, the virus's epicenter, to work with Chinese colleagues.

As the pandemic worsened, it became clear this path would be difficult. Trump had initially praised Xi's handling of the outbreak in Wuhan. But as the virus surged in the United States in spring 2020, Trump recognized the political peril it presented him and turned on China.

The virus's origins in Wuhan were particularly disputed. Though some scientists said the virus probably spread from bats to humans via an unknown third animal — zoonotic spread — influential members of the Trump administration pushed the idea that the virus could have inadvertently leaked from a laboratory in Wuhan, implying China was at fault.

WHO member states had authorized a probe that was specifically focused on zoonotic spread, but even this was difficult. The arrival of the team was delayed. After four weeks in Wuhan, including two in quarantine, Ben Embarek said in a Feb. 9 news conference that the group had ruled that indirect zoonotic spread was "likely" and a lab leak was "extremely unlikely" and not worthy of further investigation.

Wright and Kahl report that WHO leadership in Geneva were "stunned" by their colleague's statement. They did not believe the team that went to Wuhan had the access or data to rule out the lab-leak theory. Tedros told the investigative team this, the book reports, but the team was "defensive," describing pressure from Chinese officials that led to a compromise.

In a documentary released last week, Ben Embarek described how Chinese officials had wanted no mention of a lab leak at all. The scenario was only included "on the condition we didn't recommend any specific studies to further that hypothesis," he said.

Despite Tedros's criticism, when the probe's findings were released in a report in March, it repeated that the lab scenario was "extremely unlikely." Afterward, according to the book, the WHO director general told China's envoy in Geneva that he would tell the truth about the report "even if China did not like it."

Accounts of Tedros's belated shift on China may be unlikely to win over his critics. One senior Trump official told Wright and Kahl that the WHO only got tough on China after Trump left office because the impulsive Republican had provided Tedros the "cover" of a "pantomime villain."

But there's little evidence a U.S.-backed tough approach would have worked either. According to Wright, then-Secretary of State Mike Pompeo, a lab-leak theory proponent, "undermined it by taking it too far," diminishing support from allies. Though some Trump officials recognized the pandemic's gravity early on, they viewed it through the prism of a "China problem," rather than a public health emergency, Wright said.

"That U.S.-China rivalry really shaped everything else," he added.

As an international organization with limited powers, the WHO is beholden to its member states. "The U.S. has to engage with the WHO, work with China at the WHO, push for WHO reforms, but ultimately it has to recognize that these reforms are very unlikely to take root because China and maybe others as well won't commit to higher levels of transparency," Wright said.

A Trump-era plan for an alternative — dubbed "America's Response to Outbreaks" — faltered because of bureaucratic issues and the president's own uninterest. Wright and Kahl call for an alternative called the Global Alliance for Pandemic Preparedness, wherein like-minded nations could supplement the WHO's work.

As for the WHO-backed probe into the coronavirus's origins? Beijing told foreign diplomats last week that the March report calling a lab leak unlikely must be "respected," while U.S. intelligence is nearing the end of a 90-day deadline set by President Biden to reveal more about the virus's origin.

At a media briefing on Wednesday, WHO emergencies chief Mike Ryan said the organization was working behind the scenes to increase confidence in an investigation, and “we are making headway on that, but I have to admit, that has not been easy.”

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From: Peter Daszak [b6]
Sent: 8/11/2021 7:36:50 PM
To: Morens, David (NIH/NIAID) [E] [b6 b6]; Keusch, Jerry [b6]; Robert Kessler [b6]
Subject: RE: WaPo: Chinese state media has seized on a Swiss scientist critical of a covid origins probe. The one problem: He might not exist.

My God – talk about 'pop will eat itself'. The media doing hit job stories against other countries media because they've followed fake news stories. Meanwhile the WaPo is riddled with fake news for its coverage.

This is public health, meets politics, meets salacious entertainment…

Cheers,

Peter

Peter Daszak
President

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USA

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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, August 11, 2021 2:28 PM
To: Peter Daszak (b6) b6; Keusch, Jerry (b6) b6 Kessler, Robert (b6) b6
Subject: FW: WaPo: Chinese state media has seized on a Swiss scientist critical of a covid origins probe. The one problem: He might not exist.

David

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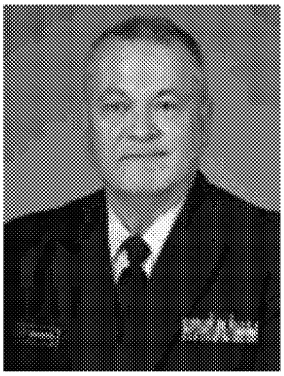

From: Folkers, Greg (NIH/NIAID) [E] b6
Sent: Tuesday, August 10, 2021 4:07 PM
Subject: WaPo: Chinese state media has seized on a Swiss scientist critical of a covid origins probe. The one problem: He might not exist.

Chinese state media has seized on a Swiss scientist critical of a covid origins probe. The one problem: He might not exist.

By Adam Taylor

Under the name Wilson Edwards, a Facebook user on July 24 penned a post critical of the U.S. position on the World Health Organization's investigation into the origins of the novel coronavirus. Claiming to be a Swiss biologist, Edwards argued that the probe had been politicized. The Biden administration had "spared no efforts in rebuilding U.S. influence in the organization," he wrote.

He was wading into hot water: China has rejected new efforts to learn more about how the coronavirus spread to humans, for which the United States and WHO have pushed. Few Western scientists have taken up Beijing's cause.

It was the United States, not China, that was seeking to influence the investigation into the origins of the coronavirus, Wilson argued, citing sources at the WHO who he claimed had told him: "The U.S. is so obsessed with attacking China on the origin-tracing issue that it is reluctant to open its eyes to the data and findings."

The post drew wide attention from Chinese state media, which used it to vindicate China's stance on the investigation. CGTN, China's state broadcaster, wrote that the post indicated "intimidation" on the part of a WHO advisory group tracing the origins of the coronavirus.

But on Tuesday, Swiss diplomats raised an inconvenient detail: Wilson Edwards does not actually appear to exist. Suggesting that the account was likely a source of "fake news," the Swiss Embassy in Beijing asked Chinese media companies to take down their stories. CGTN and other outlets appear to have quietly complied.

The dispute over the supposed Swiss biologist and his prominence in Chinese state media came amid continuing disputes about the origin of the coronavirus and a renewed push for the WHO to investigate further. More than a year and a half since the virus was first detected in Wuhan, China, before going on to kill millions around the world, the exact path it took remains unclear.

Though similar epidemics have started when a virus found in animals made the leap to humans, in what is known as zoonotic spread, scientists have not yet found an animal that appears to have directly infected humans. Internationally, some have argued that the virus could have inadvertently infected humans during research on bat coronaviruses in a Wuhan lab.

A joint WHO-China investigation into the origins published a report this year that concluded that zoonotic spread was most likely and dismissed the idea of a lab leak as unlikely and not worthy of further investigation. The report faced immediate criticism from WHO Director General Tedros Adhanom Ghebreyesus.

In May, President Biden gave the U.S. intelligence community 90 days for a renewed search for evidence about the origins of the coronavirus. Tedros also called for the WHO to continue its own probe, though Chinese officials suggested last month that it would be "impossible" for Beijing to accept a continuing China-focused probe.

The social media posts by the user going by Wilson Edwards played into this discourse. But even before the embassy stepped in, they came with some red flags. The account appeared to have been created recently and had only three friends. There was no identifying photograph or other information, other than a location set to Bern, Switzerland.

The account did not immediately respond to a message seeking comment.

Chinese state media outlets have been accused of using fake identities before. A French journalist named Laurène Beaumond contributed to CGTN's reporting on the Xinjiang Uyghur Autonomous Region, helping to portray a brighter image of events there in the face of allegations of mass repression of Uyghur people.

In March, Le Monde reported that there was no such French journalist to be found. The Chinese Foreign Ministry later argued that she existed, despite not being registered officially, but would not say whether she had used her real name.

Chinese state-backed media outlets have suggested without verified evidence that the United States could be where the coronavirus originated. An article in the English-language edition of the Global Times published Monday quoted an unnamed "insider" who said the United States was now considered "a major suspect responsible for leaking Covid-19."

By Adam Taylor

Adam Taylor writes about foreign affairs for The Washington Post. Originally from London, he studied at the University of Manchester and Columbia University.

From: Morens, David (NIH/NIAID) [E] [b6
(b6)]
Sent: 7/1/2021 4:21:40 PM
To: Peter Daszak (b6) [b6]; Keusch, Jerry (b6)
[b6]
Subject: FW: Fox News: Columbia professor who thanked Fauci for Wuhan lab messaging maintains close ties to China

David

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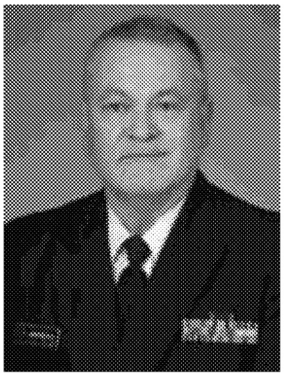


From: Folkers, Greg (NIH/NIAID) [E] b6
Sent: Thursday, July 1, 2021 12:17 PM
Subject: Fox News: Columbia professor who thanked Fauci for Wuhan lab messaging maintains close ties to China

Columbia professor who thanked Fauci for Wuhan lab messaging maintains close ties to China

Columbia professor Walter Ian Lipkin thanked Fauci for casting doubt on the lab leak theory

By Joe Schoffstall | Fox News
Published 37 mins ago

Reps. Fitzpatrick and Foxx discuss China's influence on U.S. universities

A Columbia University professor who expressed his gratitude to Dr. Anthony Fauci for downplaying the possibility that COVID-19 leaked from the Wuhan Institute of Virology maintains close ties to China, including Chinese Communist Party members.

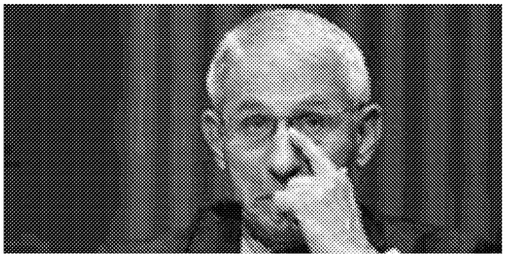
Walter Ian Lipkin, a professor of epidemiology at Columbia University, who is known as a "virus hunter," thanked Fauci last year for publicly dismissing notions that the virus could have originated and leaked from the Wuhan lab.

Fauci's coronavirus-related emails showed that he had worked behind the scenes to sow doubt about the virus leaking from the Wuhan Institute of Virology, the Washington Examiner noted in early June.

"We deeply appreciate your efforts in steering and messaging," Lipkin wrote to Fauci on May 5, 2020, a day after he cast doubt on the lab leak theory.

The "we" referenced in Lipkin's email to Fauci appears to include a Chinese government figure. As part of the message, Lipkin forwarded an email from Chen Zhu, China's former Minister of Health, who is currently a vice-chairperson of the Standing Committee of the National People's Congress of China. Li Zhanshu, a prominent figure in the Chinese Communist Party and a top advisor to China President Xi Jinping, chairs that governmental body.

The entire contents of Zhu's message are unknown due to redactions made before the email's release to Buzzfeed News, which obtained Fauci's coronavirus communications through a Freedom of Information Act request. The publication received and made public 3,200 pages of Fauci's email correspondence. (Lipkin's email begins on page 706).



Walter Ian Lipkin thanked Dr. Anthony Fauci for being publicly dismissive of the lab leak theory. (Jim Lo Scalzo/Pool via AP)

In addition to his government ties, Zhu also acts as president of the Red Cross Society of China, an entity that claims it is independent of state control. China's Red Cross, however, is funded and directed by the Chinese government. The honorary president of China's Red Cross, Wang Qishan, is also a member of the Chinese Communist Party and assists President Xi Jinping on foreign issues.

Lipkin and Zhu's relationship dates back to at least the early 2000s, when the pair had worked together on the SARS outbreak. At the time, Lipkin had served as an intermediary between the World Health Organization and the Chinese government.

In late January 2020, Lipkin traveled back to China to study the coronavirus outbreak. As part of the effort, he partnered with a Chinese research crew spearheaded by Lu Jiahai, a public health professor at Sun Yat-sen University. This institution is subordinate to China's Ministry of Education. Luo Jun, a Chinese Communist Party member, steers the university.

Lipkin shot down the lab leak theory just two weeks after reentering China. During an NPR segment in mid-February 2020, Lipkin said they had "examined the possibility that some have suggested that this virus might have originated in a biocontainment lab or might be some sort of biologically defined weapon." They had found "no evidence for that whatsoever," he said.

Before returning to China, Lipkin's extensive history with prominent Chinese researchers and government officials had earned him several accolades from the communist body.

In 2016, the Chinese government presented Lipkin with the International Science and Technology Cooperation Award, the country's highest honor to foreign scientists. The ceremony was presided by President Xinping.

"I am deeply honored by this award," Lipkin said at the time. "It solidifies my relationship with dear friends and colleagues in the Chinese Academy of Science, Ministry of Science and Technology and the Ministry of Health, and with the people of China."

In early January of this year, Lipkin was presented with a medal at the Chinese Consulate of New York. China's Central Government, Central Military Commission, and State Council provided the award.

Lipkin has also praised China's response and transparency early on in the coronavirus pandemic, despite indications that the Chinese government engaged in a cover-up.
Lipkin did not respond to a request for comment.

During the onset of the pandemic, Sen. Tom Cotton, R-Ark., raised measured questions about the Wuhan Institute of Virology, which ignited condemnation from Democrats and many media outlets, who chalked them up as "fringe conspiracy theories." Then-President Trump, likewise, consistently questioned whether the virus had leaked from the lab, further igniting left-wing media and political figures to paint the lab leak as a fringe theory.

However, the media and other skeptics have made an about-face and are now saying the lab leak theory deserves further investigation. Reports emerged stating that China had controlled an on-site World Health Organization inspection, including who the researchers spoke to at the lab.

Lipkin wasn't the only person to shower Fauci with praise for his messaging on the lab. Peter Daszak, a zoologist who leads EcoHealth Alliance, a nonprofit that directed nearly $600,000 in National Institutes of Health sub-awards to the Wuhan Institute of Virology to study bat coronaviruses, also thanked him for his public comments.

"I just wanted to say a personal thank you on behalf of our staff and collaborators, for publicly standing up and stating that the scientific evidence supports a natural origin for COVID-19 from a bat-to-human spillover, not a lab release from the Wuhan Institute of Virology," Daszak wrote to Fauci in April 2020.

"From my perspective, your comments are brave, and coming from your trusted voice, will help dispel the myths being spun around the virus's origins," Daszak said.

Daszak's nonprofit provided $1.3 million in funds to Lipkin's institution, Columbia University's Mailman School of Public Health, between July 1, 2018, and June 30, 2020, the group's tax forms show.

Columbia has received millions in foreign funding from China. According to the College Foreign Gift and Contract Report database, which relies on universities self-reporting their foreign cash, the university has raked in at least $17.7 million from China for research, facilities and professorships. Columbia did not provide a comment on the funding.
China conducts numerous influence campaigns within the United States, including targeting institutes of higher learning.

"China is in a league of their own; there's no question about it," Rep. Brian Fitzpatrick, R-Pa., told Fox News in a video interview (above). "I saw it as an FBI agent where I worked for 14 years, where we did counterintelligence, cybersecurity, counter-terrorism investigations. The one thing we learned about China – and I now sit on the Intelligence Committee, which is confirmed, everything I was getting briefed on as an agent – is that what China does – and other countries do the same – is they identify what they call the spheres of influence."

"China's identified five [spheres of influence] essentially in the United States," he added. "It's academia; it's the media, it's Big Tech, it's Hollywood and professional sports. They view those as the five influencers of human behavior in American culture. Essentially what they try to do is silent sabotage – soft influence old government approach – where they nestle in and engrain themselves in these institutions financially to make people economically dependent on them, and then they use that as a platform to get their message out - mainly in propaganda."

Rep. Virginia Foxx, R-N.C., echoed a similar sentiment concerning China and academia to Fox News.

"I would say it's been going on for a couple of years, very, very subtly with the Confucius Institutes that were widespread in the country," Foxx added. "Some of us have raised the issue many years ago – probably 10, 12 years ago – about our concern with the Confucius Institutes. It's taken a while for people to start paying attention to it, but we believe they are trying to change the way Americans think about China. They're very subversive. They've changed their name now to Chinese Cultural and Language Institutes and they claim they're teaching the Chinese language."

"One of the things we're concerned about is the Chinese trying to make American students believe that the communists in China are good people," Foxx said. "They want them to believe that the culture in China is good, and we know the culture of China is controlled by the Chinese Communist Party - and that is definitely not good for Americans."

Columbia University was the only Ivy League school to host a Confucius Institute, which it has since quietly dissolved.
But while the institute was in operation, the university had failed to disclose at least $1 million in Chinese government funding towards it, the Washington Free Beacon reported. Part of that money was used for professor Dedong Wei, an adviser to the Chinese regime's propaganda department, to lead the institute.

As China pours significant sums into universities across the United States to expand its influence, its actual cash totals remain unknown.

A Department of Education probe into universities last year found $6 billion in unreported funds from foreign countries, including China.

Joe Schoffstall is a Washington, D.C.-based reporter for Fox News.

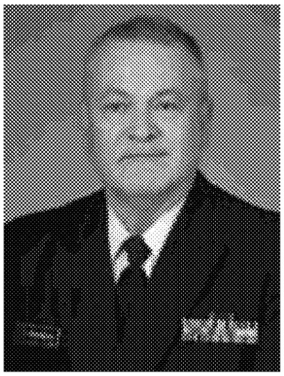
From: Morens, David (NIH/NIAID) [E] [b6
(b6]
Sent: 6/23/2021 5:39:26 PM
To: Peter Daszak [b6]; Keusch, Jerry [b6]; Rich Roberts [b6]
Subject: RE: Jesse Bloom preprint

I have heard similar comments from a different source....

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: Peter Daszak b6
Sent: Wednesday, June 23, 2021 1:34 PM
To: Morens, David (NIH/NIAID) [E] b6; Keusch, Jerry b6; Rich Roberts

b6

Subject: RE: Jesse Bloom preprint
Importance: High

Here are some (confidential) comments from a leading bioinformatician in a leading international virology group (not China):

“My conclusion is that the authors might have found some “obvious” sequencing errors and decided to withdraw them. You should know that:

> The authors are mostly doctors, not scientists, and seem to be unexperienced in this area of work
> They used Nanopore sequencing, which is not very reliable. We use it to get “draft” sequences
> Bloom did state the NCBI’s position is that withdrawal can’t be done by authors and has to be done by NCBI. My guess will be: NCBI thinks it is “nothing unusual”. This is not what Bloom wrote in this paper”

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

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From: Morens, David (NIH/NIAID) [E] b6
Sent: Wednesday, June 23, 2021 11:17 AM
To: Peter Daszak (b6) b6; Keusch, Jerry (b6) b6; Rich Roberts (b6) b6
Subject: FW: Interview request: CNN / Jesse Bloom preprint

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
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Bethesda, MD 20892-2520

☎ b6 (assistant: Whitney Robinson)
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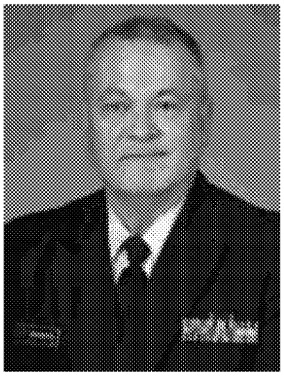
💻 b6



From: Routh, Jennifer (NIH/NIAID) [E] b6
Sent: Wednesday, June 23, 2021 11:11 AM
To: Leifman, Laura (NIH/NIAID) [E] b6; Conrad, Patricia (NIH/NIAID) [E] b6; NIAID FOG <fog@niaid.nih.gov>
Cc: NIAID COGCORE <COGCORE@mail.nih.gov>; NIAID Media Inquiries <mediainquiries@niaid.nih.gov>
Subject: RE: Interview request: CNN / Jesse Bloom preprint

& just to clarify (this is at the beginning of this thread), NIH prepared the statement below and sent to Maggie. So she already has this, but Maggie wanted someone to walk her through the findings themselves. (NSWB – we will work with OCPL on this topic – some inquiries will be satisfied by this statement alone, which OCPL will handle.)

NIH is aware of Dr. Bloom's preprint submission. Staff at the National Library of Medicine, which hosts the Sequence Read Archive (SRA), have reviewed the submitting investigator's request to withdraw the data. These SARS-CoV-2 sequences were submitted for posting in SRA in March 2020 and subsequently requested to be withdrawn by the submitting investigator in June 2020. The requestor indicated the

sequence information had been updated, was being submitted to another database, and wanted the data removed from SRA to avoid version control issues. The submitting investigator published relevant information about these sequences by preprint in March, 2020 and in a journal in June, 2020. Submitting investigators hold the rights to their data and can request withdrawal of the data.

Currently, the National Library of Medicine (NLM) has no plans to change the policy that recognizes submitters rights to their own data and the right to petition that their data be withdrawn from the Sequence Read Archive (SRA). The National Center for Biotechnology Information (NCBI), part of the NLM that manages the database, is the U.S. participating member of the International Nucleotide Sequence Database Collaboration, which provides guidelines for withdrawing data: http://www.insdc.org/documents/insdc-status-document. NLM/NCBI can't speculate on motive beyond a submitter's stated intentions.

Jennifer Routh [E]
News and Science Writing Branch
Office of Communications and Government Relations
National Institute of Allergy and Infectious Diseases (NIAID)
NIH/HHS
31 Center Drive Room 7A17C
Bethesda, MD 20892
Direct: b6
b6

From: Leifman, Laura (NIH/NIAID) [E] b6
Sent: Wednesday, June 23, 2021 9:52 AM
To: Conrad, Patricia (NIH/NIAID) [E] b6; NIAID FOG <fog@niaid.nih.gov>
Cc: NIAID COGCORE <COGCORE@mail.nih.gov>; NIAID Media Inquiries <mediainquiries@niaid.nih.gov>
Subject: Interview request: CNN / Jesse Bloom preprint
Importance: High

Maggie Fox
CNN
Maggie.Fox@cnn.com; b6
Topic: Jesse Bloom's analysis of early SARS-CoV-2 genetic data
Deadline: Today

Hi Patty,

Per the email string below, Maggie would like to interview someone who can help her unpack Jesse Bloom's analysis of the data (not about the deletion) that he posted in BioRx. Would ASF like to discuss this with her? She understands that NIAID didn't support the work.

Best,
Laura

From: Myles, Renate (NIH/OD) [E] b6
Sent: Wednesday, June 23, 2021 9:34 AM
To: NIAID OCGR NSWB <NIAIDOCGRNSWB@mail.nih.gov>
Cc: Fine, Amanda (NIH/OD) [E] b6; Wojtowicz, Emma (NIH/OD) [E] b6
Subject: FW: Jesse Bloom and missing SARS-Cov2-2 genetic sequences
Importance: High

Hi all:

I'm sure you've heard that Jesse Bloom of Fred Hutch posted a paper on BioRx that assigns motive to a Chinese investigators decision to withdraw early SARS-CoV-2 data from the NCBI Sequence Read Archive. Oure response is below. Maggie Fox is asking if someone can help her unpack the Bloom analysis of the data (not about the deletion). I told her NIAID didn't support the work but that I would check. ASF and Alan Embry is aware of this>

Thanks,
Renate

From: Myles, Renate (NIH/OD) [E]
Sent: Wednesday, June 23, 2021 9:26 AM
To: Fox, Maggie <Maggie.Fox@cnn.com>
Cc: Fine, Amanda (NIH/OD) [E] b6; Burklow, John (NIH/OD) [E] b6; Wojtowicz, Emma (NIH/OD) [E] b6; Brodd, Lauren (NIH/OD) [E] b6
Subject: RE: Jesse Bloom and missing SARS-Cov2-2 genetic sequences

Hi Maggie:

We can check with NIAID to see if they have someone willing to speak to Dr. Bloom's findings; NIAID didn't support the work and this is a preprint publication that hasn't been peer reviewed, so they may not be inclined to comment. Also NIAID can't comment on the deletion of the data from SRA. We've provided the explanation below and Bloom's assignment of motive beyond what the submitter stated is purely speculative.

Thanks,
Renate

From: Fox, Maggie <Maggie.Fox@cnn.com>
Sent: Wednesday, June 23, 2021 9:17 AM
To: Myles, Renate (NIH/OD) [E] b6
Cc: Fine, Amanda (NIH/OD) [E] <b6; Burklow, John (NIH/OD) [E] b6 Wojtowicz, Emma (NIH/OD) [E] b6; Brodd, Lauren (NIH/OD) [E] b6
Subject: Re: Jesse Bloom and missing SARS-Cov2-2 genetic sequences

Thank you, Renate
Would it be possible to speak to someone else? This one is very complicated and we are going to have to report on it. I understand that no one is going to want to touch the politics of this, but I would very much like to talk to someone with genomics experience who can help me interpret Dr. Bloom's findings.

I am pretty certain NIH is going back over what he has pointed out.

Can someone please help me, even on background? Thank you!

Maggie Fox
Senior Editor, Health
CNN

> On Jun 23, 2021, at 08:36, Myles, Renate (NIH/OD) [E] b6 wrote:
>
> Hi Maggie:

Hope you're well. Dr. Collins is out on vacation this week, so isn't available. Here is a statement attributable to NIH generally.

NIH is aware of Dr. Bloom's preprint submission. Staff at the National Library of Medicine, which hosts the Sequence Read Archive (SRA), have reviewed the submitting investigator's request to withdraw the data. These SARS-CoV-2 sequences were submitted for posting in SRA in March 2020 and subsequently requested to be withdrawn by the submitting investigator in June 2020. The requestor indicated the sequence information had been updated, was being submitted to another database, and wanted the data removed from SRA to avoid version control issues. The submitting investigator published relevant information about these sequences by preprint in March, 2020 and in a journal in June, 2020. Submitting investigators hold the rights to their data and can request withdrawal of the data.

Currently, the National Library of Medicine (NLM) has no plans to change the policy that recognizes submitters rights to their own data and the right to petition that their data be withdrawn from the Sequence Read Archive (SRA). The National Center for Biotechnology Information (NCBI), part of the NLM that manages the database, is the U.S. participating member of the International Nucleotide Sequence Database Collaboration, which provides guidelines for withdrawing data: http://www.insdc.org/documents/insdc-status-document. NLM/NCBI can't speculate on motive beyond a submitter's stated intentions.

Thanks much,
Renate

From: Fox, Maggie <Maggie.Fox@cnn.com>
Sent: Wednesday, June 23, 2021 12:00 AM
To: Fine, Amanda (NIH/OD) [E] b6
Cc: Burklow, John (NIH/OD) [E] b6; Myles, Renate (NIH/OD) [E] b6 Wojtowicz, Emma (NIH/OD) [E] < b6
Subject: Jesse Bloom and missing SARS-Cov2-2 genetic sequences

Hi y'all-
Jesse Bloom, geneticist at Fred Hutchinson Cancer Center, published this preprint and has been all over Twitter tonight saying early sequences of coronavirus samples from Wuhan were somehow deleted from the NIH database. He says Dr Collins confirmed this and was helping him track it down?
https://www.biorxiv.org/content/10.1101/2021.06.18.449051v1.full.pdf

Can you all confirm this and may I speak to Dr. Collins about it?

Thank you so much!

Maggie Fox
Senior Editor, Health
CNN
b6

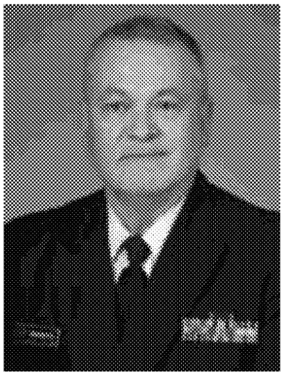
From: Morens, David (NIH/NIAID) [E] [b6 b6]
Sent: 10/5/2021 2:04:44 PM
To: Peter Daszak [b6]; Roberts, Rich [b6]; Taubenberger, Jeffery (NIH/NIAID) [E] [b6 b6]; Gerald Keusch [b6]
Subject: RE: Stepping Down as NIH Director

There will probably be no one really in charge for at least several months, and probably longer if the Republicans try to block any nominee…..

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: Peter Daszak b6
Sent: Tuesday, October 5, 2021 9:18 AM
To: Roberts, Rich b6; Morens, David (NIH/NIAID) [E] b6; Taubenberger, Jeffery (NIH/NIAID) [E] b6; Gerald Keusch b6
Subject: RE: Stepping Down as NIH Director

Bitter sweet news for me – good that he's going, but he's left our organization as a daily target for conspiracies, with death threats, media attacks, and legal actions against us. All this began the day he decided not to stand up to political interference in NIH funding, under Trump.

I hope the next Director has the mettle that a position like this requires.

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: Tuesday, October 5, 2021 9:04 AM
To: Morens, David (NIH/NIAID) [E] b6 Taubenberger, Jeffery (NIH/NIAID) [E] b6; Peter Daszak b6; Gerald Keusch b6
Subject: RE: Stepping Down as NIH Director

Best news I've heard in a long time.

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: Tuesday, October 5, 2021 7:45 AM
To: Taubenberger, Jeffery (NIH/NIAID) [E] b6 ; Peter Daszak
b6 ; Gerald Keusch b6 ; Roberts, Rich b6
Subject: Fwd: Stepping Down as NIH Director

EXTERNAL SENDER

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

Begin forwarded message:

> **From:** NIH Executive Secretariat <NIHExecSec@nih.gov>
> **Date:** October 5, 2021 at 07:40:24 EDT
> **To:** List NIH-ALL-STAFF <NIH-ALL-STAFF@list.nih.gov>
> **Subject: Stepping Down as NIH Director**
>
> Dear NIH Family:
>
> I write today with truly mixed emotions, including a lump in my throat, to tell you that I have decided to end my tenure as the Director of the National Institutes of Health by the end of this year. I love this agency, its mission, and its people so deeply that the decision to step down has been a difficult one, made in close counsel with my wife, Diane Baker, and my family. I fundamentally believe, however, that no single person should serve in the position too long, and that it's time to bring in a new scientist to lead NIH into the future. A decision on who will be stepping into the role of acting NIH director is expected to be made by the time I step down.
>
> It has been my greatest honor to lead this noble agency and to work with such a talented and dedicated workforce. Your extraordinary commitment to lifesaving research delivers hope to the American people and the world every day. That commitment has never been greater or more important than over the past 21 months. I feel remarkably fortunate to have stood at the helm of this great agency when science was called upon to provide rapid solutions to the COVID-19 pandemic. Together, we met that challenge with unprecedented speed, accuracy, and safety. Millions of lives will continue to be saved worldwide because of your work. I thank you for your unflagging support during this difficult period and throughout my tenure; it has meant the world to me.
>
> I also want to thank my wife, Diane Baker. I can't imagine having done this job without her. She is my teammate, my soulmate, and the person I'm most excited to spend more time with after I step down. I count my blessings every day for the gift of her presence in my life. I am also deeply indebted to the Institute and Center directors for their stellar scientific leadership, and to my staff in the Office of the Director for their wisdom, guidance, and tireless support. While I'm stepping down, I won't be far away. I will continue to lead my intramural research laboratory at the National Human Genome Research Institute.
>
> With sincere gratitude,
>
> Francis S. Collins, M.D., Ph.D.

NIH Director

Disclaimer

From: Morens, David (NIH/NIAID) [E] [b6 b6]
Sent: 6/23/2021 2:37:10 PM
To: Peter Daszak [b6]; Keusch, Jerry [b6]; Rich Roberts [b6]
Subject: RE: Hi David

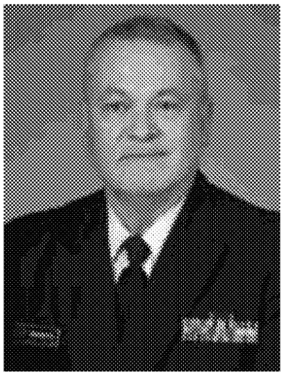
Yes, I think going forward the trick is to maintain insistence on working productively and openly and collaboratively with China and other countries, but not defending China's past behavior.

As I have said many times, having worked with MANY different authoritarian countries over the years, they ALL cover stuff up, it is built into their DNA, and the reasons why should be very well understood by diplomats and politicians. Rather than be faux-shocked we need deal realistically with our differences, find common ground, and go forward from there. This is not rocket science, but as you have said, we have done so much China bashing recently that we have hurt ourselves by throwing away important opportunities….

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: Peter Daszak b6
Sent: Wednesday, June 23, 2021 10:11 AM
To: Morens, David (NIH/NIAID) [E] b6; Keusch, Jerry b6; Rich Roberts b6
Subject: RE: Hi David

All your comments below are spot on David. In fact in the WHO report, we looked at only full genomes because they were the most reliable. We concluded that the amount of mutations suggests substantial transmission in December and that some of these mutations were also in Guangdong. This new paper takes some of the rejected partial genomes that we didn't look at, and comes basically to the same conclusion.

I've just seen some online chatter from an Economist reporter – Natasha Loder – of course, the headline is not the science, it's "why did China hide information on early cases" – that's the bloodlust for conspiracy that's out there in the public right now, including the educated public.

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 9:16 AM
To: Peter Daszak b6; Keusch, Jerry b6; Rich Roberts b6
Subject: RE: Hi David

For what it is worth, here is how an epidemiologist might look at it, based on the behavior of many different viruses in many different situations, especially influenza. The idea that one can and should find a "patient zero" is largely delusional. The initial host switch happens in obscurity long before an outbreak is recognized, allowing many serial generations in many different directions over moderately long periods of time, probably months in the case of SARS-COV-2. Outbreaks aren't detected early on because cases apear sporadically in large populations, severe and fatal disease is uncommon, the infecting agent is unknown and can't be tested for, and the signs and sympr oms are non-specific. In such a scenario, thousands of cases can occur over many months before anything unusual is detected, and particularly so in a geographically large country with a large and very mobile population.

In fact, to me, the diversity of the viruses early on is consistent with a virus that has been circulating, in humans, or animals, or both, long before the first detection. If that is true, some of these mysteries like viral diversity and inability to find a patient zero are not mysteries at all.

For example, the earliest 1918 flu sequneces from May 1918, before the pandemic was recognized anywhere (around 1 July 1918), are very clearly "bird virus-like" in all 8 genes, yet have many mutations that differ from the relatively conserved bird reservoir genes. Thus, host-switching not only takes place inside an obscure black box, but there may be a lot of viral evolution going on until such time as one or more of the evolved variants adapts sufficiently to become pandemically transmissible. At that point, evolution slows down and the virus evolves more gradually against the selection pressures imposed by large populations of humans.

Just some speculation. I fail to see what is so mysterious about COVID-19 emergence. That we don't yet no much about the origian isn't that surrpising to me. Nature does its business away from our gaze....

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)
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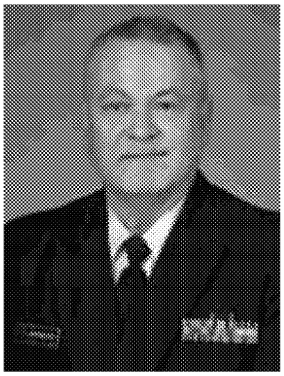
b6



From: Peter Daszak b6
Sent: Wednesday, June 23, 2021 8:48 AM
To: Morens, David (NIH/NIAID) [E] b6; Keusch, Jerry b6; Rich Roberts b6; Taubenberger, Jeffery (NIH/NIAID) [E] b6
Subject: RE: Hi David

Yes – I'm on an email chain with Bob Garry and people in China. The lead author of the China paper where the sequences come from says they deleted them because they were low quality, not full genomes and that they're not expert enough in bioinformatics to think that there was valid info in them. Bloom went into the NIH system and recovered deleted them from the cloud.

I read the paper last night – it doesn't really change any opinion about the origin – the WHO report shows that there was significant spread in Dec and that other cities were involved. This adds to that, and as you say provides further evidence that this is likely natural origin. All the 'detective' stuff and suspicions about ulterior motives is in my opinion totally unnecessary, at the least 'rude', and just sort of weird. Jesse Bloom has been on Twitter arguing for the lab leak for a good few months now, so I think he's got a general belief that Chinese scientists can't be trusted. I don't think that political stuff or suspicions of motives belongs in a paper.

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

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From: Morens, David (NIH/NIAID) [E] b6
Sent: Wednesday, June 23, 2021 7:22 AM
To: Peter Daszak (b6) b6; Keusch, Jerry (b6) b6; Rich Roberts (b6) b6; Taubenberger, Jeffery (NIH/NIAID) [E] b6
Subject: FW: Hi David

If you haven't seen this pre-print yet, have a strong cup of coffee first. I'd advise adding an ounce or two of Irish whiskey.

Jason Gale is a journalist with whom I have worked in the past, very smart and very honorable.

When I saw this I asked him to immediately contact b6 and b6, and he has already contacted b6, while I contacted b6 myself. They are both horrified, to use b6 word. If this gets picked up by the crazies there is no telling what will happen.

This is a good argument for banning pre-prints, since the damage will be done before the paper is retracted or shot down.

If there is an upside to this, legitimate scientists, even while hiding from the crazies, are starting to get really pissed off. b6 says he is planning to write a very geeky sciency review that covers the whole origin issue from a phylogeny basis, and without the politics. b6 is apparently upset, and Jason also contacted b6, who I don't know personally, and he had some really choice words to unload….

David

David M. Morens, M.D.
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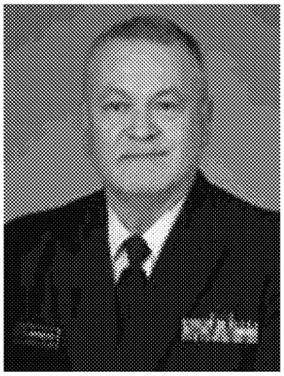
☎ b6 (assistant: Whitney Robinson)
📠 301 496 4409
💻 b6



From: Jason Gale (BLOOMBERG/ NEWSROOM:) <j.gale@bloomberg.net>
Sent: Tuesday, June 22, 2021 6:28 PM
To: Morens, David (NIH/NIAID) [E] b6
Subject: Hi David

Hi David,

I hope you're well.

I'm guessing y'all saw the Jesse Bloom pre-print paper.
https://www.biorxiv.org/content/10.1101/2021.06.18.449051v1.full.pdf

Interested to know what you make of it, even off the record.

Kindest regards,

Jason

Jason Gale, MHlthSec
Senior editor | 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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From: Morens, David (NIH/NIAID) [E] b6 (b6)
Sent: 8/27/2021 2:22:21 PM
To: Peter Daszak (b6) [b6]; Kessler, Robert (b6) [b6]; Keusch, Jerry (b6) [b6]
Subject: FW: Judicial Watch: New Fauci Agency COVID Emails Detail Discussions about Wuhan Institute; Describe Gates Foundation Placement of Chinese Representatives on 'Important International Counsels' https://bit.ly/3jqxbwR

David

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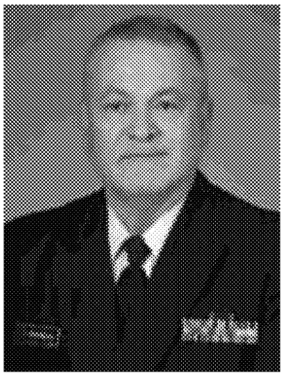
📠 301 496 4409
💻 b6

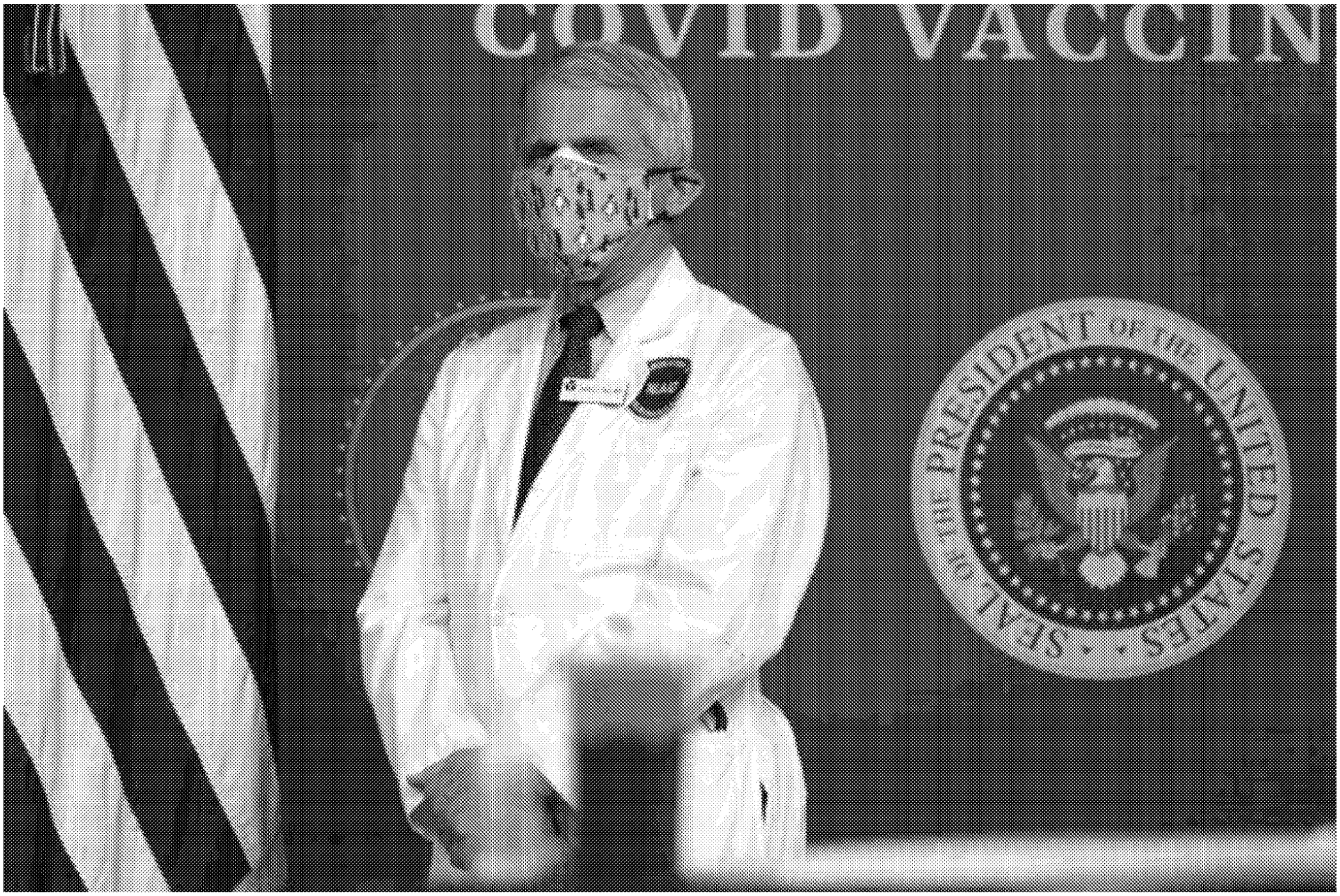


From: Folkers, Greg (NIH/NIAID) [E] b6
Sent: Thursday, August 26, 2021 5:54 PM

To: Handley, Gray (NIH/NIAID) [E]b6; NIAID COGCORE <COGCORE@mail.nih.gov>; NIAID OCGR Leg <NIAIDOCGRLeg@mail.nih.gov>; NIAID OD AM <NIAIDODAM@niaid.nih.gov>
Subject: Judicial Watch: New Fauci Agency COVID Emails Detail Discussions about Wuhan Institute; Describe Gates Foundation Placement of Chinese Representatives on 'Important International Counsels' https://bit.ly/3jqxbwR

August 25, 2021 | Judicial Watch

Judicial Watch: New Fauci Agency COVID Emails Detail Discussions about Wuhan Institute; Describe Gates Foundation Placement of Chinese Representatives on 'Important International Counsels'



(Washington, DC) – Judicial Watch announced today that it received 129 pages of records from the Department of Health and Human Services (HHS) which include "urgent for Dr. Fauci " email chain which cites ties between the Wuhan lab and the taxpayer-funded EcoHealth Alliance. The government emails also report that the foundation of U.S. billionaire Bill Gates worked closely with the Chinese government to pave the way for Chinese-produced medications to be sold outside China and help "raise China's voice of governance by placing representatives from China on important international counsels as high level commitment from China."

The new production of records also includes a January 6, 2020, "Wuhan Pneumonia Update" report which details how Peter Daszak, president of EcoHealth Alliance, was tied to the Wuhan lab and was "funded for work to understand how coronaviruses evolve and jump to human populations."

The documents were obtained by Judicial Watch through a Freedom of Information Act (FOIA) lawsuit for records of communications, contracts and agreements with the Wuhan Institute of Virology (*Judicial Watch, Inc. v. U.S. Department of Health and Human Services* (No. 1:21-cv-00696)). The lawsuit specifically seeks records about NIH grants that benefitted the Wuhan Institute of Virology. The agency is only processing 300 pages of records per month, which means it will take until the end of November for the records to be fully reviewed and released under FOIA.

The new emails include a report from Dr. Ping Chen, who had been the top Fauci agency official working in China:

You can ask [NIAID Human Coronavirus, Rhinovirus Research Program Officer] Erik Stemmy for the grant awarded to the Ecohealth in NYC who collaborates with Dr. Shi, Zhengli in Wuhan Institute of Virology (WIV), who has been doing coronavirus research in cave bats in China. Erik would know what exactly NIH funding supports.

I visited her and others at the Wuhan Ins Viro in 2018 and visited its BSL4 1ab. [Redacted]

Also in 1983 NIH and CAS [Chinese Academy of Sciences] (WIV is one of the research institutes under CAS) signed a MOU and it included sharing research materials. I know [sic] this a long time ago.

This email chain is part of a previously released January 23, 2020, exchange with the subject line "Urgent for Dr. Fauci: China's lab for studying SARS and Ebola is in Wuhan." It begins with Melinda Haskins, chief of legislative affairs for NIAID, writing to senior NIAID officials, and includes a link to a *Daily Mail* article, titled "China built a lab to study SARS and Ebola in Wuhan – and US biosafety experts warned in 2017 that a virus could 'escape' the facility that's become key in fighting the outbreak." She writes: "Dr. Fauci will be brief [sic] multiple Senators tomorrow on our novel coronavirus response … Would you please confirm the exact nature of our support to the Wuhan Institute of Virology/Biosafety Lab. You'll want to read the Daily Mail article above."

A January 6, 2020, email exchange on "coronavirus countermeasures," initiated by NIAID Chief Medical Officer Hilary Marston, includes a "Wuhan Pneumonia Update" report prepared by NIH/DMID.

The report was updated on January 8, 2020, and lists in its background information on "Wuhan Pneumonia:"

- In December 2019 the Wuhan Municipal Health Committee identified an outbreak of viral pneumonia cases of unknown cause.
- On December 31st the WHO China Country Office was notified of 44 patients with pneumonia of unknown etiology, 11 of which were severely ill.
- As of January 5th, 2020 there are 59 patients with a diagnosis of unknown viral pneumonia is Wuhan, 7 of which are severely ill. At least one patient is on ECMO … The earliest case was reported December 12th, and the latest onset was December 29th. All patients are isolated and receiving treatment in Wuhan medical institutions. 163 close contacts have been identified for ongoing medical observation.
- Case-patients in the outbreak are reported to have fever, difficulty breathing, and bilateral lung infiltrates on chest radiography (CDC, http://bit.ly/36GxY3y).
- Hong Kong has added Wuhan Pneumonia to the list of notifiable diseases. As of January 7th, 2020 the Hong Kong Center for Health Protection has reports of 30 cases under enhanced surveillance with recent travel history to Wuhan….
- Epidemiological investigation showed that some patients operated businesses in the Wuhan South China Seafood City. As of January 1st, 2020 the market has been closed for environmental sanitation and disinfection.
- There is currently no clear evidence of human-to-human transmission, however one family cluster has been identified. No nosocomial transmission has been seen …
- Fragments of coronavirus RNA with an 86% homology to SARS has been found in one patient…
- News reports on 1/8/2020 the virus is a novel coronavirus, sequenced in one patient and identified in others.

The report also details a NIH coronavirus grant "portfolio" that funded 13 basic science research grants, two treatment research grants and five vaccination research grants related to coronavirus:

Peter Daszak (R01A|110964-06) is funded for work to understand how coronaviruses evolve and jump to human populations, with an emphasis on bat CoVs and high-risk populations at the human-animal interface. Main foreign sites are in China (including co-investigators at the Wuhan Institute of Virology).

The report notes that one of the grants, made to Fang Li, "is funded to investigate the receptor recognition and cell entry in coronaviruses using structural approaches using spike proteins in complex with receptors. This award found the first evidence of a MERS-related CoV that uses the human receptor and provides evidence of a natural recombination event between bat CoVs." Another grant involves "a team of investigators using mouse models of SARS and MERS to investigate CoV pathogenesis and develop vaccines and therapeutics."

A section of the report on "Vaccines" details:

"The VRC [Vaccine Research Center] and collaborators have stabilized the MERS-CoV spike protein in its prefusion conformation. The stabilized spike protein is potently immunogenic and elicits protective antibodies to the receptor binding domain, n-terminal domain and other surfaces of the spike protein. The stabilized coronavirus spike protein, and mRNA expressing the spike protein through collaboration with Moderna Therapeutics, is currently being evaluated in the humanized DPP4 mouse model at UNC.

Another grant description indicates that NIH was funding research at Jefferson University using the rabies virus as a vector to deliver a potential vaccine. In an accompanying spreadsheet detailing the grants, one grant is listed as having gone to Dr. Ralph Baric of UNC-Chapel Hill to study "Mechanisms of MERV-CoV Entry, Cross Species Transmission and Pathogenesis." That grant had been funded from 2015-2020.

In a January 7, 2020, email exchange with the subject line "Wuhan Pneumonia" Stemmy asks Chen if she has any information about the "viral pneumonia outbreak in Wuhan." Chen replies: "Yes, I have been following the news. Here is what I know so far [redacted]. Chen also revealed that her tour in Beijing had ended three weeks earlier.

Stemmy asks, "Do you know if there is a replacement for you in embassy in Beijing? If so I'd love to connect with them." Chen replies, "No replacement for now <smiley face emoji>."

In a January 22, 2020, email exchange titled "Collecting info on N CoV [novel coronavirus]", NIAID "Senior Volunteer", Dr. Karl Western, informs Chen and other NIAID officials:

Two recent examples involving CAS Institute of Virology and BSL-4 facility include:

- University of Minnesota and CAS Institute of Virology review of the origin and evolution of pathogenic coronaviruses in *Nature Reviews: Microbiology.* Minnesota had a CEIRS award for one funding cycle.
- Columbia University School of Public Health, Eco-Health Alliance and CAS Institute of Virology published a few days ago on the results of surveillance of human animal interactions and bat coronavirus spillover potential in rural southern China. Columbia is a current CETR holder.

In a heavily redacted response email, Chen writes: "Thanks Dr. Western. Eco-health has NIAID grant which has collaboration with the Wuhan Institute of Virology, CAS, studying the coronaviruses in wild animals, focusing on bats, in China. One of the key Chinese collaborators is Dr. Zhengli Shi, who works on coronaviruses."

On February 6, 2020, Han Koo, an executive assistant to the Director of NIH who works in the Office of Grants Administration (OGA), emails Chen and Matthew Brown, then-Director of the NIH China Office: "We need POCs [points of contact] of the National Natural Science Foundation of China (NSFC) and The Chinese Academy of Science (CAS) ASAP."

Later in the chain Chen writes: "In 2018, NSF [the U.S. National Science Foundation] and NSFC [the National Science Foundation of China] had a joint initiative on Ecology and Evolution of infectious diseases. A workshop was held prior to the initiative (NIH is one of the participants to this initiative. Many participants of the workshop are from CAS institute including WIV [Wuhan Institute of Virology] scientists. NIAID grant to EcoHealth is studying coronaviruses in animals including bats. The grant has different countries as collaborators in addition to China." A colleague then responds: "Thanks! Do you recall who the US and Chinese PIs [principal investigators] are on that coronavirus vector/reservoir grant are?" Chen replies: "See the attachment I prepared previously. This grant is on bat [redacted]."

In an October 20, 2017, email exchange following Chen's submission of a situation report, NIAID official James Meegan tells Chen: "Jim LeDuc at U Texas Medical Branch, Director of the Galveston BSL4, works closely with them [Wuhan Institute of Virology]. In 1986 Jim and I spent the year on and off in Wuhan setting up a virology lab and studying Hantavirus infections and treating patients with ribavirin. We trained many, and some later came to the States. I think that helped it on its way to becoming a center for virology."

Further in the exchange, Chen writes, "The [Wuhan] lab will be operational soon. The visit has been arranged through one of our grantees. I know Jim LeDuc has been worked with WIV and had done some training. [Redacted.] Also, I was told only certain viruses can be worked in this lab. [Redacted]" Handley then tells Chen: "Please make a very careful and full report on what you learn during this visit. It will be a very important interaction and one that many are interested in. Please share your report with us before it goes into any other reporting. We will be glad to engage directly or via grantees in whatever will help ensure safe operations."

On March 4, 2020, Greg Folkers, Fauci's chief of staff, emails an academic paper titled "On the origin and continuing evolution of SARS-COV-2", published in *National Science Review* on March 3, 2020, to David Morens and other unidentified officials within NIAID, and asks in his cover note: "David, this may come up in ASF's [Anthony S. Fauci's] 10:00 hearing [likely referring to House Appropriations Committee hearings held on March 4, 2020, on NIH budget requests.] What do you make of this paper and the attendant press coverage?" Folkers highlights within the report two passages. One reads: "Our results suggest that the development of the new variations in functional sites in the receptor-binding domain (RBD) of the spike seen in SARS-COV-2 and viruses from pangolin SARS-CoVs are likely caused by mutations and natural selection besides recombination." The second highlighted passage reads: "Although the L type (~70%) is more prevalent than the S type (~30%), the S type was found to be the ancestral version. Whereas the L type was more prevalent in the early stages of the outbreak in Wuhan, the frequency of the L type decreased after early January 2020." Morens replied, but his response is entirely redacted.

Five years prior to the outbreak, in an October 30, 2014, report titled "Wuhan," Chen informs Ken Earhart that she had met with a Chinese official from Wuhan. Chen reports that his office "is similar to what I am doing here seeking, facilitating, and promoting international scientific collaborations for scientists in Wuhan." She continues that this official was asked by an organization put together in part by the Wuhan Institute of Virology "to help the members in the organization increase scientific exchanges between the members and international ID [infectious disease] experts."

In a September 5, 2017, situation report, Chen informs her colleagues that she had "attended a 'Belt and Road' High Level Meeting for Health Cooperation: towards a Health Silk Road." She also reported:

Last week USAID, CDC, ESTH [Environment, Science, Technology, and Health] and I met with Gates Foundation, initially planned to talk about global Malaria eradication efforts to see if there is any area we can work together. But we ended talking in general Chinese policies and the foundation's current strategies in China — capacity building to help China raise its national standards and leverage China's resource to help others. One of the examples for raising the national standards is to help China FDA for its reform. Gates foundation has managed to work out a mechanism with China FDA to provide fund[ing] to China FDA for placing experienced Chinese-Americans who had worked at US FDA for many years to work in China FDA as senior consultants....

On the approach for leveraging China's resource to help others, Gates Foundation is working with Chinese government on donations to its neighboring countries and African countries such as anti-malaria medicines, bed nest, diagnostics etc. More specifically, it helps Chinese companies to gain pre-qualification on medications so that Chinese company manufactured drugs can be sold outside China, helps the Chinese to establish bilateral collaboration with specific countries in Africa, teaches the Chinese how to do resource mobilization, and helps raise China's voice of governance by placing representatives from China on important international counsels as high level commitment from China.

Chen goes on to describe numerous other ways the Gates Foundation was helping the Chinese government by, for example, helping "Chinese companies gain pre-qualification on medications so that Chinese company manufactured drugs can be sold outside China." Chen continues: "Just met with a group from the Global Virome Project (GVP) which is funded partially by USAID. The head of the project, Peter Daszak of EcoHealth Alliance, is an NIAID funded PI. His collaborator at the Wuhan Institute of Virology in China has done excellent work on corona viruses in Chinese bat populations."

A heavily redacted October 26, 2017, email released to Judicial Watch in a previous production includes a newly released response from Handley. The email chain begins with Chen sending a trip report to her colleagues regarding her visit to the BSL4 Lab in Wuhan. She notes: "My contact who helped arrange the visit is Dr. Zhengli Shi, who is a Chinese collaborator on a NIAID grant to EcoHealth for SARS like corona virus project." She continues: "The P4 lab is located in a new developing zone about one hour car ride from the current institute location in central Wuhan city. The location will be the new campus for the entire institute in the near future (a lot of construction is going on right now). Since we are not allowed to take photos so only the photo from the outside is attached."

Newly released in this production of HHS documents is Handley's reply in the email chain: "This is a sensitive subject and will be of interest to others."

Later in the exchange, Handley tells Chen, "Please send us by e-mail your full report on the visit and then we can decide what to do with the information." After Chen emails Handley the report, he writes: "There is enough good information in your report that it needs to be shared in some form or another."

On July 18, 2016, Chen sends an "activity update" to top NIAID officials, summarizing her activities for the prior three weeks. In a discussion of the Chinese needing assistance with conducting clinical trials of new medicines, Chen notes: "GSK's [Glaxo Smith Kline's] Zhi Hong (the head of the GSK anti-infective program and led the GSK center for infectious diseases and public health in Beijing) met with Dr. Fauci on Monday, the 11th, asking for NIAID support for this clinical trial network in China. I know Dennis [presumably Dennis Dixon, Chief of NIAID Bacteriology and Mycology] and Carl [possibly Carl Dieffenbach, Director of NIAID AIDS Research] attended the meeting with Fauci. I don't know the outcome of the meeting." Further along, Chen writes: "I met with EcoHealth Alliance, a NY based non-profit organization on health. They have a R01 grant from DMID [Division of Microbiology and Infectious Diseases] on identifying SARS-like coronaviruses in China. They partner with Dr. Shi Zhengli at Wuhan Institute of Virology. I visited Dr. Shi over a year ago. She took bat samples in caves in certain regions of China, isolated and identified viruses and found some viruses are similar to SARS by sequencing. Now [redacted]. We are talking about close animal-human close contact in densely populated city." Chen also mentions an upcoming meeting of "Chinese NIH Alumni" and talks about NIH Director Francis Collins discussing with the head of Peking University Medical School "about the establishment of a Chinese NIH Alumni as there are so many Chinese researchers trained and worked at NIH in the past."

On October 12, 2016, Chen sends a "High" importance email to senior NIAID officials Handley, Bernabe and Dixon regarding an upcoming conference in China. Chen notes: "Another topic under session 1, Zoonotic Disease Characterization and Prevention, has some relevance to us. NIAID funded George Gao at CAS [Chinese Academy of Sciences] for avian flu (I think it was on avian flu genetics in birds) and we have grant from RDB funding coronavirus survey in bats. The Chinese collaborator is Wuhan Institute of Virology, a CAS institute too. The request for zoonotic diseases is from a Chinese agency I don't know, AQSIQ. [Redacted.]" Dixon replies: "Thanks Ping. I see the topic of 'prevention and control' by your name. While we have occasional projects in that realm, they are at the border of our mission area relative to CDC who list their name that way sometimes in reverse order."

In a January 20, 2017, situation report, Chen discusses the Global Virome Project "to identify viruses present in wildlife with potential crossing over to humans ... Following the identification of the viruses is the development of vaccines to protect human population. China has huge capacity for vaccine development (I think it has 7 national owned vaccine manufacturing facility and over 30 private vaccine making companies.) [Redacted] One of the partners in this project is EcoHealth Alliance. Peter Daszak from EcoHealth Alliance is one of the leaders of GVP and he has NIAID grant from RDB looking at the coronaviruses in bat populations in China in collaboration with Wuhan Institute of Virology. He came to visit me once in the Embassy. This grant has direct connection with the purpose of GVP."

In a July 7, 2017, situation report, Chen informs her colleagues: "RDB [NIAID's Respiratory Disease Branch] has a grant to EcoHealth which has a Chinese collaborator at WIV working on finding similar SARS viruses in bat populations and then look for human exposures to the viruses carried by the bats in the villagers near the caves. USAID funds the same organization and they do more virus seeking projects in China."

On May 27, 2018, Chen emails colleague Nancy Boyd, forwarding her an announcement sent to Chen by people at the Wuhan Institute of Virology, which Chen describes as "China's only publicly known P4 lab." Chen adds: "I copied Gayle [Bernabe] at OGR and she can forward to programs officers with the P4 pathogen portfolio."

"These emails provide extraordinary and troubling information about Fauci's agency partnership with China and its monitoring, concerns and funding for the Wuhan Institute," said Judicial Watch President Tom Fitton. "The Gates Foundation should also explain the government report about its assistance to and advocacy for China."

In July, Judicial Watch obtained records from NIAID officials in connection with the Wuhan Institute of Virology revealing significant collaborations and funding that began in 2014. The records revealed that NIAID gave nine China-related grants to EcoHealth Alliance to research coronavirus emergence in bats and was the NIH's top issuer of grants to the Wuhan lab itself.

In June, Judicial Watch announced that it filed Freedom of Information Act (FOIA) lawsuits against the Office of the Director of National Intelligence (ODNI) and the State Department for information on the Wuhan Institute of Virology and the origins of the SARS-CoV-2 virus.

Also in June, Judicial Watch obtained records from HHS revealing that from 2014 to 2019, $826,277 was given to the Wuhan Institute of Virology for bat coronavirus research by the NIAID.

In March, Judicial Watch publicly released emails and other records of Fauci and Dr. H. Clifford Lane from HHS showing that NIH officials tailored confidentiality forms to China's terms and that the WHO conducted an unreleased, "strictly confidential" COVID-19 epidemiological analysis in January 2020. Additionally, the emails reveal an independent journalist in China pointing out the inconsistent COVID numbers in China to NIH's National Institute of Allergy and Infectious Diseases' Deputy Director for Clinical Research and Special Projects Lane.

In October 2020, Judicial Watch uncovered emails showing a WHO entity pushing for a press release, approved by Fauci, "especially" supporting China's COVID-19 response.

###

From: Morens, David (NIH/NIAID) [E] [b6]
Sent: 10/4/2021 5:27:50 PM
To: Morens, David (NIH/NIAID) [E] [b6
b6]
Subject: Fwd: Molnupiravir was tested against the bat-CoVs discovered by our NIAID collaboration with Wuhan Institute of Virology

-------- Forwarded Message --------
Subject: RE: Molnupiravir was tested against the bat-CoVs discovered by our NIAID collaboration with Wuhan Institute of Virology
Date: Mon, 4 Oct 2021 03:13:06 +0000
From: Keusch, Gerald T b6
To: Peter Daszak b6, Hotez, Peter Jay b6, Roberts, Rich b6, David Morens b6
CC: Robert Kessler b6

This is of real importance for all of us, because it commonly comes up when GOF is discussed that there is considerable risk without much benefit. This is a useful way to counter that impression – and incidentally show how ignorant the proponents are (but that is a bit of editorializing).

And David should go ahead and contact b6. I could only talk off the record because of my commitment to b6 I would stay out of the public press until we resolve what happens to the now terminated COVID Task Force on Origins etc. But I am itching to openly say what I want to.

Jerry

From: Peter Daszak b6
Sent: Sunday, October 3, 2021 7:48 PM
To: Hotez, Peter Jay b6; Roberts, Rich b6; Keusch, Gerald T b6; David Morens b6
Cc: Robert Kessler b6
Subject: Molnupiravir was tested against the bat-CoVs discovered by our NIAID collaboration with Wuhan Institute of Virology
Importance: High

This is mainly for David Morens to let people know at NIAID, but may be of interest to you all.

The latest therapeutic to make headline news – Molnupiravir from Merck and Ridgeback Biotherapeutics (AKA EIDD-2801), was tested against the exact same bat-origin CoVs discovered in our terminated, now-suspended R01 from NIAID.

Here's an article on the drug: https://www.reuters.com/business/healthcare-pharmaceuticals/mercks-covid-19-pill-cuts-risk-death-hospitalization-by-50-study-2021-10-01/

..and here are a couple of papers that tested it against the bat-CoVs: https://stm.sciencemag.org/content/12/541/eabb5883 "Here, we show that the ribonucleoside analog β-D-N^4-hydroxycytidine (NHC; EIDD-1931) has broad-spectrum antiviral activity against SARS-CoV-2, MERS-

CoV, SARS-CoV, and related zoonotic group 2b or 2c bat-CoVs, as well as increased potency against a CoV bearing resistance mutations to the nucleoside analog inhibitor remdesivir". .

And here: https://www.nature.com/articles/s41586-021-03312-w "Collectively, our results demonstrate the utility of LoM as a single in vivo platform to evaluate and compare the replication and pathogenesis of past, present and future pre-emergent, epidemic and pandemic coronaviruses, which will allow for accelerating the development and testing of therapeutic and pre-exposure prophylaxis agents such as EIDD-2801".

Here's a full list from the information I have on the drugs/therapeutics that were tested against our viruses:

Vaccines, therapeutics tested against the bat-CoVs discovered by EHA/WIV in China

Remdesivir: Formerly known as GS-5734 https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5567817/ Now in use via FDA EUA: https://www.cnn.com/2020/04/29/health/gilead-sciences-remdesivir-covid-19-treatment/index.html

Molnupiravir: NHC; EIDD-1931 & prodrug EIDD-2801: tested against range of CoVs here https://stm.sciencemag.org/content/12/541/eabb5883. Shown to effectively block SARS-CoV-2 here https://www.nature.com/articles/s41586-021-03312-w. Currently in Phase II/III clinical trials, showing good efficacy to all variants in preliminary results (Oct 2021): https://www.reuters.com/business/healthcare-pharmaceuticals/mercks-covid-19-pill-cuts-risk-death-hospitalization-by-50-study-2021-10-01/

Adagio ADG20 (refined from ADG2): https://science.sciencemag.org/content/371/6531/823. Now in Phase II/III clinical trials https://www.clinicaltrialsarena.com/news/adagio-trial-covid-19-prevention/

Broadly-neutralizing RBD-specific antibody DH1047: Martinez *et al.* https://www.biorxiv.org/content/10.1101/2021.04.27.441655v1

Chimeric NTD/RBD spike mRNA vaccines: Martinez *et al.* https://www.biorxiv.org/content/10.1101/2021.03.11.434872v1

Neutralizing Ab vaccine for pandemic and pre-emergent coronaviruses. https://www.nature.com/articles/s41586-021-03594-0 Cited as 'proof-of-concept' for Universal CoV vaccine initiative announced by Dr. Fauci on CNN 5/13/21

Cheers,

Peter

Peter Daszak
President

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

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

From: Hotez, Peter Jay b6
Sent: Sunday, October 3, 2021 1:18 PM
To: Roberts, Rich b6; Keusch, Gerald T b6; Peter Daszak b6; David Morens b6
Cc: Robert Kessler b6
Subject: Re: Good LA Times article.

FYI b6 contacted me and asked if we could speak, I gave him my cell

Peter Hotez, MD, PhD, DSc (hon), FASTMH, FAAP

Dean, National School of Tropical Medicine
Professor, Departments of Pediatrics, Molecular Virology & Microbiology
Health Policy Scholar

Baylor College of Medicine

Texas Children's Hospital Endowed Chair of Tropical Pediatrics
Co-Director, Texas Children's Hospital Center for Vaccine Development

University Professor, Baylor University

Faculty Fellow, Hagler Institute for Advanced Study

Senior Fellow, Scowcroft Institute of International Affairs

Texas A&M University

Baker Institute Fellow in Disease & Poverty and Adjunct Professor of Bioengineering, Rice University

Adjunct Professor, University of Texas, School of Public Health

Donate to our COVID-19 Vaccine Development

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Daily Beast Contributor https://www.thedailybeast.com/author/peter-j-hotez

Like us on Facebook https://www.facebook.com/BCMNationalSchoolOfTropicalMedicine/

Senior Coordinator / Executive Support: Douglas Soriano

b6

Phone: b6

Fax: 713-798-2299

From: Roberts, Rich b6
Sent: Sunday, October 3, 2021 11:09 AM
To: Keusch, Gerald T b6; Peter Daszak b6; David Morens b6
Cc: Robert Kessler b6; Hotez, Peter Jay b6
Subject: RE: Good LA Times article.

*****CAUTION:*** This email is not from a BCM Source. Only click links or open attachments you know are safe.**

Jerry:

I did get an answer from b6 and anticipate a direct conversation soon.
The contact I have was passed from b6 in confidence so let me see if he would agree to converse with you directly after I have spoken with him.

I spoke with b6 yesterday and found him to be quite reasonable. He did agree to pass any quotes he might use past me before publishing. I specifically mentioned that it would be greatly appreciated if he could write something in direct support of Peter within the article.

Rich

Richard J. Roberts
New England Biolabs
240 County Road
Ipswich, MA 01938-2723
USA
Tel: b6

Fax: (978) 412 9910
email: b6

From: Keusch, Gerald T b6
Sent: Saturday, October 2, 2021 6:20 PM
To: Roberts, Rich b6 ; Peter Daszak b6 ; David Morens b6
Cc: Robert Kessler b6 ; peter hotez b6
Subject: RE: Good LA Times article.

EXTERNAL SENDER

I talk to him regularly, most recently about the attacks on b6 and the task force we were on under the Lancet COVID Commission which b6 has unilaterally terminated. I couldn't really allow him insights into where we are or to use anything I said (all off the record) because we are negotiating with Lancet for a different way to continue our work.

I think he is a decent guy. I know b6 has concerns so if you do speak to b6 be careful about what you say and how you say it, and require him to run any quotes he plans to use by you. That's his general modus operandi.

What we need is to get the amendment out of the appropriations bill, and while the senators are important it may be somebody like b6 who is a cabinet member to get them to pay attention. The administration is mightily distracted.

Rich, if you are able to share your entre to b6 I would happily follow up. I have contacted them, b6 and my representation and all I get back is the auto thank you reply.

Jerry

From: Roberts, Rich b6
Sent: Saturday, October 2, 2021 3:47 PM
To: Peter Daszak b6 ; Keusch, Gerald T b6 ; David Morens b6
Cc: Robert Kessler b6 ; peter hotez b6
Subject: RE: Good LA Times article.

Peter:

I just spoke with b6 from b6 . I mentioned that you were being attacked completely unfairly and that it would be good if he could find some encouraging words to help you. I am wondering if one of you would also be prepared to talk to b6

Rich

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

From: Peter Daszak b6
Sent: Tuesday, September 28, 2021 11:47 PM
To: Roberts, Rich b6; Keusch, Gerald T b6; David Morens b6
Cc: Robert Kessler b6
Subject: Good LA Times article.

Just saw a piece in the LA Times that sums up the state of the origins “debate” pretty clearly:

https://www.latimes.com/business/story/2021-09-28/evidence-against-a-lab-leak-as-covid-source

It’s firewalled so here’s the article:

Column: New evidence undermines the COVID lab-leak theory — but the press keeps pushing it

BY MICHAEL HILTZIKBUSINESS COLUMNIST
SEPT. 28, 2021 6 AM PT

When it comes to the pandemic, pseudoscience has outweighed real science at almost every turn. One of the best examples of that is the unsupported assertion that the virus causing COVID-19 escaped from a Chinese laboratory.

Despite mounting evidence that the virus reached humans through natural pathways — from infected animals such as bats — the lab-leak hypothesis recently jumped back into the news, thanks to CNN, the investigative news site the Intercept, and the Atlantic.

All treat the idea that the virus escaped from a lab credulously. They downplay or entirely ignore the latest scientific findings that support the theory that the virus’ origin can be found in the animal kingdom — the view accepted by a preponderance of experts in virology.

> *It’s a likely probability that this one originated from animals as well. But the possibility also remains that the virus leaked from a lab.*
> CNN’S SANJAY GUPTA OVERSTATES THE LAB LEAK THEORY

This is known as the zoonotic theory, from the term for a disease that can be transmitted from animals to humans.

We’ve reported before on the near absence of evidence for a lab leak, whether or not it’s the product of a deliberate act.

Ever since the lab-leak claim first emerged during the Trump administration, where it was part of a White House information campaign demonizing China, one of the arguments in its favor has been that evidence for a zoonotic origin has also been spotty.

That argument has never been quite true — virologists know that animals have been the source of most of the viral diseases afflicting humanity — but it has become weaker than ever over the last year.

The question of the origin of COVID-19 isn't of merely academic interest. The answer could guide the world's preparation for future pandemics; if the virus emerged from a laboratory, then improving lab safety measures will be prioritized. If scientific opinion continues to coalesce around animal-to-human transmission, that will underscore the importance of regulating contact between humans and wildlife.

To put it another way, if we focus on the wrong answer, the right measures won't be taken. In a real sense, humankind's future depends on not being distracted by an unsupported, politically motivated claim about Chinese labs.

Before examining the flaws in the CNN, Intercept and Atlantic treatments, let's look at what's been published recently about the zoonotic path.

For context, keep in mind that the earliest cluster of COVID-19 cases, in late 2019, was identified in the environs of the Huanan seafood market in the Chinese metropolis of Wuhan. Lab-leak theorists find this significant, because it's 7.5 miles from the Wuhan Institute of Virology, which does research on bat viruses.

A paper posted online earlier this month chiefly by researchers at France's Institut Pasteur and under consideration for publication in a Nature journal, however, reports that three viruses were found in bats living in caves in northern Laos with features very similar to SARS-CoV-2, the virus responsible for COVID-19.

As Nature reported, those viruses are "more similar to SARS-CoV-2 than any known viruses."

Another paper, posted in late August by researchers from the Wuhan lab, reports on viruses found in rats also with features similar to those that make SARS-CoV-2 infectious in humans. Two other papers published on the discussion forum virological.org present evidence that the virus jumped from animals to humans at more than one animal market in Wuhan, not just the Huanan seafood market.

Given that these so-called wet markets have long been suspected as transmission points of viruses from animals to humans because they sell potentially infected animals, that makes the laboratory origin vastly less likely, according to a co-author of one of the papers.

"That a laboratory leak would find its way to the very place where you would expect to find a zoonotic transmission is quite unlikely," Joel Wertheim, an associate professor at UC San Diego's medical school, told me. "To have it find its way to multiple markets, the exact place where you would expect to see the introduction, is unbelievably unlikely."

As virologist Robert F. Garry of Tulane, one of Wertheim's co-authors, told Nature, the finding is "a dagger into the heart" of the lab-leak hypothesis.

Garry and Wertheim are among the 21 expert co-authors of a "critical review" of virological findings on the origins of COVID-19. The review concludes, "There is currently no evidence that SARS-CoV-2 has a laboratory origin."

Now let's look at the recent reporting in support of the lab-leak theory.

On Sept. 19, CNN aired an hourlong documentary entitled "The Origins of COVID-19: Searching for the Source." Hosted by the channel's star science anchor, Sanjay Gupta, the program carries the veneer of an evenhanded approach.

Proponents of the zoonotic origin theory are given airtime, including Kristian Andersen of the Scripps Research Institute in La Jolla and Peter Daszak, a prominent grant maker in the virology field.

But so are proponents of the lab-leak theory. They include Alina Chan, a researcher at the Broad Institute, a biomedical research center, and Josh Rogin, a Washington Post columnist. Neither has any experience in virology. Chan is co-writing a book about COVID's origins that is expected to feature the lab-leak theory prominently, a fact not mentioned by CNN.

Yet at the top of the hour, referring to the common pattern of viruses jumping from animals to humans, Gupta says, "It's a likely probability that this one originated from animals as well. But the possibility also remains that the virus leaked from a lab."

By posing these two theories as simply two equally plausible solutions to a mystery, CNN glosses over the fact that the virological community regards the animal origin as vastly more likely than a lab leak. In fact, the two hypotheses are miles apart in credibility.

One of the program's chief targets is a report by a World Health Organization team issued in early 2021 that found spillover from an animal host to be "likely to very likely" and a laboratory incident an "extremely unlikely pathway."

Gupta calls the WHO report "the only scientific study of COVID's origins to date." That's not remotely accurate. There have been countless scientific studies, both before the WHO report and since. Indeed, Gupta mentions one of them, a seminal paper by Andersen and colleagues, published in March 2020. That paper termed the lab-leak theory "a speculative incomplete hypothesis with no credible evidence."

Much of the rest of the CNN program is filled with speculation about the Wuhan Institute, typically presented with portentous music on the soundtrack, suggesting subliminally that something sinister is going on there. The absence of information from the institute or the Chinese government is generally taken as tantamount to an admission of guilt.

"Over the course of 2020," Gupta declares, "more and more revelations emerged related to the Wuhan Institute of Virology."

One of these revelations concerned three staff members who reportedly sought hospital treatment for a flu-like illness in November 2019, before the COVID pandemic emerged.

Nothing has ever transpired to suggest these workers had COVID — November is flu season, after all. That they sought treatment at a hospital is immaterial, since it is well-known that people in China often go to hospitals for primary care, which residents of other countries would tend to receive in a doctor's office.

A CNN reporter appearing on air overstated the case, saying the patients were "hospitalized with an unknown illness." There has been no evidence that they were admitted to the hospital or that their illness was "unknown."

CNN doesn't bring its audience up to date on any of the latest research supporting the zoonotic theory, though it was published well before the air date and superseded what Gupta described as "the only scientific study" of COVID origins.

More recently, the Intercept trumpeted a purported scoop based on a leaked document — a grant proposal submitted in 2018 by Daszak's organization, the EcoHealth Alliance, to the Pentagon's Defense Advanced Research Projects Agency, or DARPA.

The proposal, for a laboratory manipulation of a virus related to SARS, the viral disease that caused an outbreak of pulmonary disease in China in 2003. DARPA rejected the proposal, however, and there's no evidence that it was submitted to, much less approved by, any other funding body.

"Many questions remain about the proposal, including whether any of the research described in it was completed," the Intercept acknowledged.

Commentators on the Intercept's disclosure have displayed, perhaps in spite of themselves, that they lack the courage of their own convictions. In an article published Sept. 24, the Atlantic, unable or unwilling to delve into what the Intercept's document actually meant, if anything, settled for declaring that it made the lab-leak debate "even messier."

The magazine's Daniel Engber and Adam Federman wrote: "Does the SARS-CoV-2 pandemic have an unnatural origin? The answer hasn't changed: probably not. But we have learned something quite disturbing in the past few days, simply from how and when this information came to light."

By pretending that the debate itself is important, as if both sides have something to offer, they manage to report on a claim that has no substance. The approach also protects journalists from their persistent fear of landing on the wrong side of things — the authors preserve an out in case the lab-leak hypothesis turns out to be true, as unlikely as that is. If that happens, they can point to their lily-livered observations and say, "See, we knew it all along."

In this debate, however, the zoonotic camp has evidence and the lab-leak camp nothing to offer but innuendo.

Here's the true state of the discussion. There is no evidence that the virus leaked from the Wuhan laboratory or any other lab. There is no evidence that the Wuhan lab was working with a bat virus that had anything but a very distant resemblance to SARS-CoV-2. Viruses that resemble it much more closely have been found in natural settings a thousand miles from Wuhan, as the crow, or bat, flies.

Evidence that artificial manipulation of a virus gave rise to SARS-CoV-2 has faded, as scientists find more evidence that features of SARS-CoV-2 thought to be unnatural occur in nature. Meanwhile, evidence for zoonotic transmission is constantly accumulating. No one who reports on the issue without acknowledging these two trends should be trusted.

Los Angeles Times columnist Michael Hiltzik writes a daily blog appearing on latimes.com. His seventh book, "Iron Empires: Robber Barons, Railroads, and the Making of Modern America," has just been published by Houghton Mifflin Harcourt. Follow him on Twitter at twitter.com/hiltzikm and on Facebook at facebook.com/hiltzik.

Cheers,

Peter

Peter Daszak
President

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USA

Tel.: [redacted] 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]
Sent: Tue, 5 May 2020 17:25:10 +0000
To: Babcock Sarah [(b)(6)] ((b)(6)); Ellen Carlin
Subject: FW: Bloomberg: A Vet Detective Squad Is Preparing For the Next Pandemic

David

David M. Morens, M.D.
CAPT, United States Public Health Service
Senior Advisor to the Director
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☎ (b)(6) (assistants: Kimberly Barasch; Whitney Robinson)
📠 301 496 4409
💻 (b)(6)

From: Folkers, Greg (NIH/NIAID) [E] (b)(6)
Sent: Tuesday, May 5, 2020 11:40 AM
Subject: Bloomberg: A Vet Detective Squad Is Preparing For the Next Pandemic

A Vet Detective Squad Is Preparing For the Next Pandemic

May 5, 2020, 10:01 AM

- Most infectious diseases in humans come from animals
- Australia to fund training for over 200 vets in Asia Pacific

As the coronavirus death toll surpasses 250,000 and the world scrambles to find a vaccine, a new scientific taskforce is headed to the wilderness to try and stop the next pandemic.

After decades of patchy global investment into researching the linkages between animal and human health, more than 40 scientists will embark on an Australian government-funded program that will teach veterinarians in southeast Asia and the Pacific how to detect infectious diseases - before they make the leap into the human population.

“The majority of infectious diseases are zoonotic, which means they are transmittable from animals to humans,” said Navneet Dhand, associate professor of veterinary biostatistics and epidemiology at the University of Sydney.

Detecting diseases early in the animal population would help prevent future outbreaks among humans, said Dhand, who helms the effort. To that end, the Australian government has pledged A$4.3 million ($2.8 million) to the three-year project that covers 11 countries across the region. It’s part of an existing A$300 million Indo-Pacific program that pushes for a more proactive approach to fighting pandemics and strengthening health security.

There is broad scientific consensus that the new coronavirus came from animals, although it’s still unknown how and when it made the leap to humans. While researchers are calling for earlier mitigation in the spread of disease as the best defense against future outbreaks, government investment into such strategies hasn’t been nearly consistent enough.

READ MORE: Deadly Virus Finds a Breeding Ground in China’s Food Markets

Not enough

Famous for its unique wildlife and A$48 billion agricultural industry that drives much of the economy, Australian scientists say they’re in a position to pass on unique knowledge to less-developed regions.

Dhand’s team will train more than 200 veterinarian and para-veterinarians in Southeast Asia to collect and track data from sick animals, both on nature’s front line and on farms.

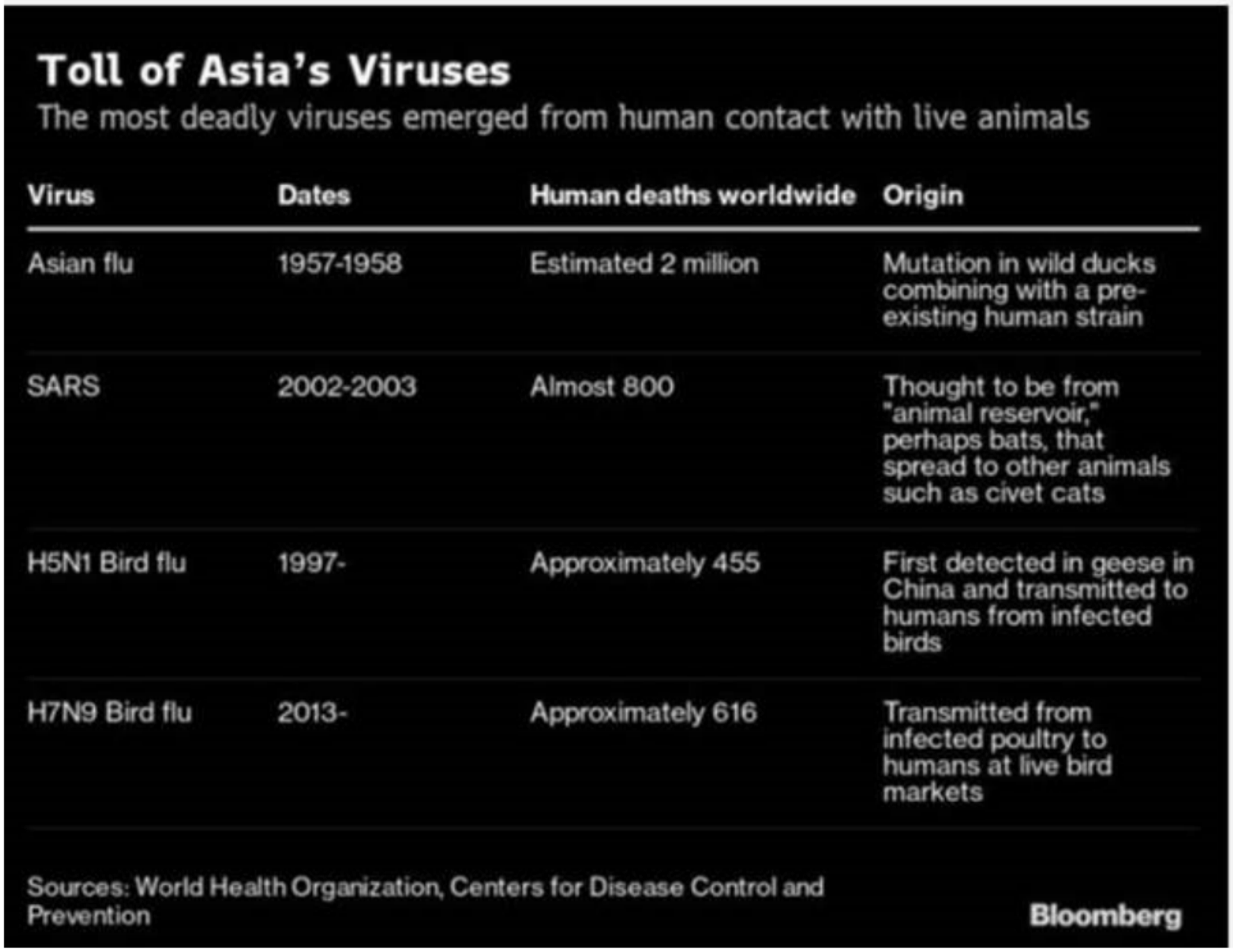
Participants will be taught skills like how to examine a sick animal for more than just the prevailing illness apparent when they’re called to farms or animal sites, as well as check for signs of spread among other animals they’ve been in contact with.

They will also learn how to collect animal samples to build out a database that, over time, can pick up on particular ecological trends and animal behavior patterns. These could show where outbreaks are more likely to occur and how they might spread, thus giving scientists clues on how the disease is transmitted.

In the long run, these efforts can help stop a disease’s spread before it reaches the stage of being able to jump to humans.

READ MORE: To Stop the Next Pandemic, Start Protecting Wildlife Habitats

Opportunities for animal diseases to transmit to humans have increased with accelerated urbanization and population growth. People now live in closer proximity to, and have more frequent contact with, wildlife, said Dhand.



Toll of Asia's Viruses

The most deadly viruses emerged from human contact with live animals

Virus	Dates	Human deaths worldwide	Origin
Asian flu	1957-1958	Estimated 2 million	Mutation in wild ducks combining with a pre-existing human strain
SARS	2002-2003	Almost 800	Thought to be from "animal reservoir," perhaps bats, that spread to other animals such as civet cats
H5N1 Bird flu	1997-	Approximately 455	First detected in geese in China and transmitted to humans from infected birds
H7N9 Bird flu	2013-	Approximately 616	Transmitted from infected poultry to humans at live bird markets

Sources: World Health Organization, Centers for Disease Control and Prevention

Bloomberg

There have been at least six large-scale zoonotic disease outbreaks in four decades, including the H1N1 flu, SARS and HIV, collectively resulting in the deaths of millions and impacting the world economy.

But after those outbreaks faded, there's been relatively little effort to prevent the next one.

"We've suffered from a siloed approach, historically, and had a big emphasis on responding to health in emergencies but less of an emphasis on preventing those emergencies," Mark Schipp, president of the World Organization for Animal Health said. "Diseases in animals spill over into humans on a regular occurrence."

True Economic Impact

Zoonotic pathogens that infect humans are only part of the threat. Even if the disease never transfers to a human host, outbreaks of sickness among animal populations impacts food security and international trade.

The 2018 African swine disease outbreak decimated pork supplies, affecting the diets of millions in China, where it is the major source of protein. It also dealt a major economic blow to a myriad of agricultural sectors, including pig farmers.

"The impact of not controlling non-zoonotic vaccine-preventable disease in animals is much larger than the zoonotic impact, if it's properly calculated," said Robyn Alders, senior technical advisor with the Centre for Global Health Security at Chatham House. But data relating to food security "isn't there to show the true impact on the economy."

As the coronavirus pandemic starts to come under control in many countries through social-distancing measures, there's a chance that public attention may turn elsewhere and governments once again neglect investment in preventive strategies.

“The problem here with animal health is that when that perceived human threat is controlled or significantly reduced, the money dries up,” said Alders.

From: Jon Epstein
Sent: Mon, 19 Oct 2020 13:21:26 -0400
To: Morens, David (NIH/NIAID) [E]
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] (b)(6) 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.

(b)(6) and (b)(6) are ACAV members and (b)(6) 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.

(b)(6) and (b)(6) are running a corona symposium this year, and (b)(6) (b)(6) 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.
CAPT, United States Public Health Service

Senior Advisor to the Director
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☎ (b)(6) (assistants: Kimberly Barasch; Whitney Robinson)
📠 301 496 4409
💻 (b)(6)

From: Jon Epstein (b)(6)
Sent: Saturday, October 17, 2020 9:43 PM
To: Morens, David (NIH/NIAID) [E] (b)(6)
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] (b)(6) 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

David M. Morens, M.D.
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From: Jon Epstein (b)(6)
Sent: Wednesday, October 14, 2020 2:51 PM
To: Morens, David (NIH/NIAID) [E] (b)(6)
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] (b)(6) wrote:

Wow!

David

David M. Morens, M.D.
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From: Robert Tesh (b)(6)
Sent: Friday, October 9, 2020 3:45 AM
To: Garcia-Blanco, Mariano A. (b)(6); Murphy, Frederick A. (b)(6); Charles H Calisher (b)(6); Weaver, Scott Morens, David (NIH/NIAID) [E] (b)(6)
Subject: Fwd: Bennett et al Nature s41586-020-2812-9.pdf

---------- Forwarded message ---------
From: **Ksiazek, Thomas G.** (b)(6)
Date: Fri, Oct 9, 2020, 12:15 AM
Subject: Bennett et al Nature s41586-020-2812-9.pdf
To: Amman Brian (b)(6), Towner Jonathan (CDC/CCID/NCZVED) (b)(6), Nichol Stuart (b)(6), Rollin Pierre (b)(6), Tesh Robert (b)(6), Bob Swanepoel (b)(6)

One of the papers

--

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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

From: Morens, David (NIH/NIAID) [E]
Sent: Tue, 23 Nov 2021 02:25:42 +0000
To: Daniel Mira-Salama
Cc: Karesh,William Bamberger; (b)(6)
Bcc: Morens, David (NIH/NIAID) [E]
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 (b)(6) 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] (b)(6)
Sent: Tuesday, November 23, 2021 12:24 AM
To: Karesh,William Bamberger (b)(6)
Cc: (b)(6) ; Daniel Mira-Salama (b)(6)
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

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301 496 4409
(b)(6)

From: William B. Karesh (b)(6)
Sent: Monday, November 22, 2021 7:27 AM
To: Morens, David (NIH/NIAID) [E] (b)(6)
Cc: Catherine Machalaba (b)(6); Daniel Mira-Salama (b)(6)
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] (b)(6) 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 (b)(6) 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.

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

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From: Alison Andre
Sent: Thu, 20 Feb 2020 16:07:02 +0000
To: Taubenberger, Jeffery (NIH/NIAID) [E]
Cc: Peter Daszak; Morens, David (NIH/NIAID) [E]
Subject: Re: New England Journal of Medicine 20-02106
Attachments: NEJM CTA-2017.pdf, ICMJE Disclosure Form.pdf, Change of Authorship Form_daszak.doc

Hi Jeff,

Attached forms here. For the change in authorship form, I was unsure if the order mattered but I changed it to what you had in your previous email. Peter's delighted to be a co-author and the author order of Morens, Daszak, Taubenberger is great.

Happy to send these straight to Maria at NEJM if easier – just let me know.

Thanks,
Alison

Alison Andre
Executive Assistant to the President

EcoHealth Alliance
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New York, NY 10001

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

From: "Taubenberger, Jeffery (NIH/NIAID) [E]" (b)(6)
Date: Thursday, February 20, 2020 at 10:44 AM
To: Alison Andre (b)(6)
Cc: Peter Daszak , "Morens, David (NIH/NIAID) [E]" (b)(6)
Subject: FW: New England Journal of Medicine 20-02106

Hi Alison,

I was given your name by Peter about this upcoming NEJM perspectives article for which Peter will be a coauthor. Cc'ing you in hopes that you can coordinate with Peter to get all the needed author information in their system as soon as possible.

Thanks

Jeff

Jeffery K. Taubenberger, M.D., Ph.D.,
Chief, Viral Pathogenesis and Evolution Section
Deputy Chief, Laboratory of Infectious Diseases
National Institute of Allergy and Infectious Diseases
National Institutes of Health
33 North Drive, Room 3E19A.2 MSC 3203
Bethesda, MD 20892-3203 USA

Tel. (b)(6) ; Fax. 1-301-480-1696
email: (b)(6)

From: Morens, David (NIH/NIAID) [E] (b)(6)
Sent: Thursday, February 20, 2020 10:34 AM
To: Peter Daszak (b)(6) ; Peter Daszak (b)(6)
Cc: Taubenberger, Jeffery (NIH/NIAID) [E] (b)(6)
Subject: Fwd: New England Journal of Medicine 20-02106

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

Begin forwarded message:

From: "Sedjo, Maria" (b)(6)
Date: February 20, 2020 at 10:17:52 EST
To: "Taubenberger, Jeffery (NIH/NIAID) [E]" (b)(6)
Cc: "Morens, David (NIH/NIAID) [E]" (b)(6)
Subject: RE: New England Journal of Medicine 20-02106

Dear Dr. Taubenberger,

The editors have approved your request to add Dr. Daszak as a co-author. As we have already accepted your piece, and it is flying through our production process to go online quickly, time is of the essence. I will need the following ASAP to make this a possibility:

-an email address for Daszak
-his completed CTA and ICMJE forms
-a change of authorship form - each of you please sign a form and return to me
-an updated title page with his information

Forms are attached. All forms can be returned to me at (b)(6).

Thanks!

Maria Sedjo
Executive Assistant to the Editor-in Chief

New England Journal of Medicine
10 Shattuck Street
Boston, MA 02115
(b)(6)
http://www.nejm.org

-----Original Message-----
From: Taubenberger, Jeffery (NIH/NIAID) [E] (b)(6)
Sent: Wednesday, February 19, 2020 10:12 AM
To: NEJM Editorial <editorial@nejm.org>
Cc: Morrissey, Stephen (b)(6) Morens, David (NIH/NIAID) [E]
(b)(6); Taubenberger, Jeffery (NIH/NIAID) [E] (b)(6)
Subject: RE: New England Journal of Medicine 20-02106

Dear Debbie,

Thank you for the opportunity to submit a revision to our coronavirus perspectives manuscript. I have submitted a revision online this morning. I am attaching a tracked version here.

As you consider this revision, We would like to ask you and Dr. Baden, who emailed with co-author David Morens about this manuscript before we submitted it, if we can get a special dispensation to add a third co-author, Dr. Peter Daszak. The three of us had originally planned to write this, not recalling that you had a two author limit, but when we were asked to submit quickly we could not reach Dr. Daszak to approve the final draft (it turned out he was at WHO Geneva dealing with the coronavirus epidemic), so we submitted without his name, but assuming he would approve it when we reached him. If it is not possible to add him, then we would at least like to acknowledge him for helpful discussion.

With best wishes,

Jeff Taubenberger

Jeffery K. Taubenberger, M.D., Ph.D.,
Chief, Viral Pathogenesis and Evolution Section Deputy Chief, Laboratory of Infectious Diseases National Institute of Allergy and Infectious Diseases National Institutes of Health
33 North Drive, Room 3E19A.2 MSC 3203
Bethesda, MD 20892-3203 USA

Tel. (b)(6) ; Fax. 1-301-480-1696
email: (b)(6)

==

-----Original Message-----
From: New England Journal of Medicine <onbehalfof@manuscriptcentral.com>
Sent: Tuesday, February 18, 2020 8:17 PM
To: Taubenberger, Jeffery (NIH/NIAID) [E] (b)(6)
Subject: New England Journal of Medicine 20-02106

Dear Jeff,

Thank you for submitting your Perspective manuscript about the new coronavirus. We plan to move forward with it quickly (always pending acceptance of a final version by the editor-in-chief), so I am attaching an edited version for your review, revisions, and responses. Although I've saved a copy with all the changes tracked, this version has the edits tentatively accepted and a number of queries embedded in it as "comments"; if you can't locate these, please let me know.

Feel free to e-mail me directly ((b)(6)) if you have questions or concerns. Otherwise, please go ahead and work on this version, tracking your changes, and upload a revision when you're done.

To upload your revision, log into https://nam12.safelinks.protection.outlook.com/?url=http%3A%2F%2Fmc05.manuscriptcentral.com%2Fnejm&data=02%7C01%7Cmsedjo%40nejm.org%7Ccaccc42e9c2748740c4008d7b5849df9%7C458a53272e354039ab37680f1f49c047%7C0%7C0%7C637177453505730137&sdata=e59AaPyFEEjr7yzTGFmCO%2FRpktyou%2BV%2BW4fhwbPSENA%3D&reserved=0 and enter For Authors, where you will find your title listed under "Manuscripts with Decisions." Under "Actions," click on "Create a Revision." Your manuscript number has been appended to denote a revision. So that it will convert properly, please select "Manuscript text - clean" from the menu.

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Please send completed forms to Maria Sedjo at (b)(6) (preferred), or upload them to your Author Dashboard of ScholarOne Manuscripts along with your revision.

Thank you.

Best,

Debbie Malina

Debra Malina, Ph.D.
Perspective Edigtor
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(b)(6)
Fax: (617) 739-9864
http://www.nejm.org

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THE NEW ENGLAND JOURNAL OF MEDICINE
10 SHATTUCK STREET, BOSTON, MA 02115 U.S.A.
(781) 207-6529 FAX

Contribution/Manuscript Number (required): NEJM 20-02106

Short Title or description of Contribution: Another Novel Coronavirus Escapes Pandora's Box

Corresponding Author: Jeffrey Taubenberger

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If author was a U.S. Government employee at the time the Work was written, please check below.

[___]

PRINTED NAME Peter Daszak

SIGNATURE (b)(6)

DATE SIGNED: February 20, 2020

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SAVE

ICMJE Form for Disclosure of Potential Conflicts of Interest

Instructions

The purpose of this form is to provide readers of your manuscript with information about your other interests that could influence how they receive and understand your work. The form is designed to be completed electronically and stored electronically. It contains programming that allows appropriate data display. Each author should submit a separate form and is responsible for the accuracy and completeness of the submitted information. The form is in six parts.

1. Identifying information.

2. The work under consideration for publication.

This section asks for information about the work that you have submitted for publication. The time frame for this reporting is that of the work itself, from the initial conception and planning to the present. The requested information is about resources that you received, either directly or indirectly (via your institution), to enable you to complete the work. Checking "No" means that you did the work without receiving any financial support from any third party -- that is, the work was supported by funds from the same institution that pays your salary and that institution did not receive third-party funds with which to pay you. If you or your institution received funds from a third party to support the work, such as a government granting agency, charitable foundation or commercial sponsor, check "Yes"

3. Relevant financial activities outside the submitted work.

This section asks about your financial relationships with entities in the bio-medical arena that could be perceived to influence, or that give the appearance of potentially influencing, what you wrote in the submitted work. You should disclose interactions with ANY entity that could be considered broadly relevant to the work. For example, if your article is about testing an epidermal growth factor receptor (EGFR) antagonist in lung cancer, you should report all associations with entities pursuing diagnostic or therapeutic strategies in cancer in general, not just in the area of EGFR or lung cancer.

Report all sources of revenue paid (or promised to be paid) directly to you or your institution on your behalf over the 36 months prior to submission of the work. This should include all monies from sources with relevance to the submitted work, not just monies from the entity that sponsored the research. Please note that your interactions with the work's sponsor that are outside the submitted work should also be listed here. If there is any question, it is usually better to disclose a relationship than not to do so.

For grants you have received for work outside the submitted work, you should disclose support ONLY from entities that could be perceived to be affected financially by the published work, such as drug companies, or foundations supported by entities that could be perceived to have a financial stake in the outcome. Public funding sources, such as government agencies, charitable foundations or academic institutions, need not be disclosed. For example, if a government agency sponsored a study in which you have been involved and drugs were provided by a pharmaceutical company, you need only list the pharmaceutical company.

4. Intellectual Property.

This section asks about patents and copyrights, whether pending, issued, licensed and/or receiving royalties.

5. Relationships not covered above.

Use this section to report other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work.

Definitions.

Entity: government agency, foundation, commercial sponsor, academic institution, etc.

Grant: A grant from an entity, generally [but not always] paid to your organization

Personal Fees: Monies paid to you for services rendered, generally honoraria, royalties, or fees for consulting , lectures, speakers bureaus, expert testimony, employment, or other affiliations

Non-Financial Support: Examples include drugs/equipment supplied by the entity, travel paid by the entity, writing assistance, administrative support, etc.

Other: Anything not covered under the previous three boxes

Pending: The patent has been filed but not issued

Issued: The patent has been issued by the agency

Licensed: The patent has been licensed to an entity, whether earning royalties or not

Royalties: Funds are coming in to you or your institution due to your patent

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ICMJE Form for Disclosure of Potential Conflicts of Interest

Section 1. Identifying Information

1. Given Name (First Name)
Peter

2. Surname (Last Name)
Daszak

3. Date
2/20/2020

4. Are you the corresponding author? ☐ Yes ☑ No

5. Manuscript Title
Another Novel Coronavirus Escapes Pandora's Box

6. Manuscript Identifying Number (if you know it)
NEJM 20-02106

Section 2. The Work Under Consideration for Publication

Did you or your institution **at any time** receive payment or services from a third party (government, commercial, private foundation, etc.) for any aspect of the submitted work (including but not limited to grants, data monitoring board, study design, manuscript preparation, statistical analysis, etc.)?

Are there any relevant conflicts of interest? ☐ Yes ☑ No

If yes, please fill out the appropriate information below. If you have more than one entity press the "ADD" button to add a row. Excess rows can be removed by pressing the "X" button.

Name of Institution/Company	Grant?	Personal Fees?	Non-Financial Support?	Other?	Comments	
	☐	☐	☐	☐		× ADD

Section 3. Relevant financial activities outside the submitted work.

Place a check in the appropriate boxes in the table to indicate whether you have financial relationships (regardless of amount of compensation) with entities as described in the instructions. Use one line for each entity; add as many lines as you need by clicking the "Add +" box. You should report relationships that were **present during the 36 months prior to publication**.

Are there any relevant conflicts of interest? ☐ Yes ☑ No

If yes, please fill out the appropriate information below.

Name of Entity	Grant?	Personal Fees?	Non-Financial Support?	Other?	Comments	
	☐	☐	☐	☐		× ADD

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Section 4. Intellectual Property -- Patents & Copyrights

Do you have any patents, whether planned, pending or issued, broadly relevant to the work? ☐ Yes ☑ No

If yes, please fill out the appropriate information below. If you have more than one entity press the "ADD" button to add a row. Excess rows can be removed by pressing the "X" button.

Patent?	Pending?	Issued?	Licensed?	Royalties?	Licensee?	Comments	
	☐	☐	☐	☐			✕

ADD

Section 5. Relationships not covered above

Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

☐ Yes, the following relationships/conditions/circumstances are present (explain below):

☑ No other relationships/conditions/circumstances that present a potential conflict of interest

At the time of manuscript acceptance, journals will ask authors to confirm and, if necessary, update their disclosure statements. On occasion, journals may ask authors to disclose further information about reported relationships.

Section 6. Disclosure Statement

Based on the above disclosures, this form will automatically generate a disclosure statement, which will appear in the box below.

Generate Disclosure Statement

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ICMJE Form for Disclosure of Potential Conflicts of Interest

Evaluation and Feedback

Please visit http://www.icmje.org/cgi-bin/feedback to provide feedback on your experience with completing this form.

RE: NEJM 20-02106

STATEMENT OF AUTHORSHIP CHANGE

Eric J. Rubin, MD, PhD
Editor-in-Chief
New England Journal of Medicine
10 Shattuck Street
Boston, MA 02115
USA

We hereby allow a change in authorship for "" from:

David Morens, Jeffery Taubenberger

To:

David Morens, Peter Daszak, Jeffery Taubenberger

Sincerely,

Date: **February 20, 2020**

Printed Name: **Peter Daszak**

Signature: (b)(6)

From: Morens, David (NIH/NIAID) [E]
Sent: Fri, 3 Dec 2021 20:44:17 +0000
To: Kevin Olival
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
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National Institutes of Health
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31 Center Drive, MSC 2520
Bethesda, MD 20892-2520
☎ (b)(6) (assistant: Whitney Robinson)
📠 301 496 4409
💻 (b)(6)

From: Kevin Olival (b)(6)
Sent: Thursday, December 2, 2021 4:47 PM
To: Morens, David (NIH/NIAID) [E] (b)(6)
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] (b)(6) wrote:

<Branswell-2021-Some experts suggest Omicron va.pdf>

From: Morens, David (NIH/NIAID) [E]
Sent: Wed, 3 Nov 2021 18:00:43 +0000
To: Kevin Olival
Subject: RE: bioRxiv: Multiple spillovers and onward transmission of SARS-Cov-2 in free-living and captive White-tailed deer (Odocoileus virginianus)

Maybe you guys should study this long-range, as it has been found I think several times around the country. The high PCR positivity is surprising so following deer prospectively is important.

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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☎ (b)(6) (assistants: Kimberly Barasch; Whitney Robinson)
📠 301 496 4409
💻 (b)(6)

From: Kevin Olival (b)(6)
Sent: Wednesday, November 3, 2021 12:53 PM

To: Morens, David (NIH/NIAID) [E] (b)(6)
Subject: Re: bioRxiv: Multiple spillovers and onward transmission of SARS-Cov-2 in free-living and captive White-tailed deer (Odocoileus virginianus)

Thanks David, yes, spotted that paper earlier today! Interesting stuff, and you were correct to flag this early on w the promed post.

Kevin J. Olival, PhD
Vice President for Research

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New York, NY 10018

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

On Nov 3, 2021, at 12:51 PM, Morens, David (NIH/NIAID) [E] (b)(6) 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
☎ (b)(6) (assistants: Kimberly Barasch; Whitney Robinson)
📠 301 496 4409
💻 (b)(6)

<image002.jpg>

From: Folkers, Greg (NIH/NIAID) [E] (b)(6)
Sent: Tuesday, November 2, 2021 2:52 PM
Subject: bioRxiv: Multiple spillovers and onward transmission of SARS-Cov-2 in free-living and captive White-tailed deer (Odocoileus virginianus)

Multiple spillovers and onward transmission of SARS-Cov-2 in free-living and captive White-tailed deer (Odocoileus virginianus)

View ORCID ProfileSuresh V Kuchipudi, Meera Surendran-Nair, Rachel M Ruden, Michele Yon, Ruth H Nissly, Rahul K Nelli, Lingling Li, Bhushan M Jayarao, Kurt Vandegrift, Costas D Maranas, Nicole Levine, Katriina Willgert, View ORCID ProfileAndrew J.K Conlan, Randall J Olsen, James Davis, James M. Musser, Peter J Hudson, Vivek Kapur

doi: https://doi.org/10.1101/2021.10.31.466677

00000308

- Abstract
- Info/History
- Metrics
-
- Preview PDF

Abstract

Many animal species are susceptible to SARS-CoV-2 and could potentially act as reservoirs, yet transmission in non-human free-living animals has not been documented. White-tailed deer (Odocoileus virginianus), the predominant cervid in North America, are susceptible to SARS-CoV-2 infection, and experimentally infected fawns transmit the virus to other captive deer. To test the hypothesis that SARS-CoV-2 may be circulating in deer, we evaluated 283 retropharyngeal lymph node (RPLN) samples collected from 151 free-living and 132 captive deer in Iowa from April 2020 through December of 2020 for the presence of SARS-CoV-2 RNA. Ninety-four of the 283 deer (33.2%; 95% CI: 28, 38.9) samples were positive for SARS-CoV-2 RNA as assessed by RT-PCR. Notably, between Nov 23, 2020, and January 10, 2021, 80 of 97 (82.5%; 95% CI 73.7, 88.8) RPLN samples had detectable SARS-CoV-2 RNA by RT-PCR. Whole genome sequencing of the 94 positive RPLN samples identified 12 SARS-CoV-2 lineages, with B.1.2 (n = 51; 54.5%), and B.1.311 (n = 19; 20%) accounting for ~75% of all samples. The geographic distribution and nesting of clusters of deer and human lineages strongly suggest multiple zooanthroponotic spillover events and deer-to-deer transmission. The discovery of sylvatic and enzootic SARS-CoV-2 transmission in deer has important implications for the ecology and long-term persistence, as well as the potential for spillover to other animals and spillback into humans. These findings highlight an urgent need for a robust and proactive One Health approach to obtaining a better understanding of the ecology and evolution of SARS-CoV-2.

Competing Interest Statement

The authors have declared no competing interest.

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From: Ellen Carlin
Sent: Mon, 11 May 2020 21:07:52 -0400
To: Morens, David (NIH/NIAID) [E]
Cc: Sarah Babcock
Subject: Re: Bloomberg: A Vet Detective Squad Is Preparing For the Next Pandemic

Thanks, David—sounds a little bit like a cross between PREDICT x FETPv x One Health Workforce.

Hope you are hanging in there. It's not like NIAID has been in the news much lately…

On May 5, 2020, at 1:25 PM, Morens, David (NIH/NIAID) [E] (b)(6) wrote:

<image002.gif>

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

<image003.jpg>

From: Folkers, Greg (NIH/NIAID) [E] (b)(6)
Sent: Tuesday, May 5, 2020 11:40 AM
Subject: Bloomberg: A Vet Detective Squad Is Preparing For the Next Pandemic

A Vet Detective Squad Is Preparing For the Next Pandemic

May 5, 2020, 10:01 AM

- Most infectious diseases in humans come from animals
- Australia to fund training for over 200 vets in Asia Pacific

As the coronavirus death toll surpasses 250,000 and the world scrambles to find a vaccine, a new scientific taskforce is headed to the wilderness to try and stop the next pandemic.

After decades of patchy global investment into researching the linkages between animal and human health, more than 40 scientists will embark on an Australian government-funded program that will teach veterinarians in southeast Asia and the Pacific how to detect infectious diseases - before they make the leap into the human population.

“The majority of infectious diseases are zoonotic, which means they are transmittable from animals to humans,” said Navneet Dhand, associate professor of veterinary biostatistics and epidemiology at the University of Sydney.

Detecting diseases early in the animal population would help prevent future outbreaks among humans, said Dhand, who helms the effort. To that end, the Australian government has pledged A$4.3 million ($2.8 million) to the three-year project that covers 11 countries across the region. It’s part of an existing A$300 million Indo-Pacific program that pushes for a more proactive approach to fighting pandemics and strengthening health security.

There is broad scientific consensus that the new coronavirus came from animals, although it’s still unknown how and when it made the leap to humans. While researchers are calling for earlier mitigation in the spread of disease as the best defense against future outbreaks, government investment into such strategies hasn’t been nearly consistent enough.

READ MORE: Deadly Virus Finds a Breeding Ground in China’s Food Markets

Not enough

Famous for its unique wildlife and A$48 billion agricultural industry that drives much of the economy, Australian scientists say they’re in a position to pass on unique knowledge to less-developed regions.

Dhand’s team will train more than 200 veterinarian and para-veterinarians in Southeast Asia to collect and track data from sick animals, both on nature’s front line and on farms.

Participants will be taught skills like how to examine a sick animal for more than just the prevailing illness apparent when they’re called to farms or animal sites, as well as check for signs of spread among other animals they’ve been in contact with.

They will also learn how to collect animal samples to build out a database that, over time, can pick up on particular ecological trends and animal behavior patterns. These could show where outbreaks are more likely to occur and how they might spread, thus giving scientists clues on how the disease is transmitted. In the long run, these efforts can help stop a disease’s spread before it reaches the stage of being able to jump to humans.

READ MORE: To Stop the Next Pandemic, Start Protecting Wildlife Habitats

Opportunities for animal diseases to transmit to humans have increased with accelerated urbanization and population growth. People now live in closer proximity to, and have more frequent contact with, wildlife, said Dhand.

<image001.jpg>

There have been at least six large-scale zoonotic disease outbreaks in four decades, including the H1N1 flu, SARS and HIV, collectively resulting in the deaths of millions and impacting the world economy.

But after those outbreaks faded, there's been relatively little effort to prevent the next one.

"We've suffered from a siloed approach, historically, and had a big emphasis on responding to health in emergencies but less of an emphasis on preventing those emergencies," Mark Schipp, president of the World Organization for Animal Health said. "Diseases in animals spill over into humans on a regular occurrence."

True Economic Impact

Zoonotic pathogens that infect humans are only part of the threat. Even if the disease never transfers to a human host, outbreaks of sickness among animal populations impacts food security and international trade.

The 2018 African swine disease outbreak decimated pork supplies, affecting the diets of millions in China, where it is the major source of protein. It also dealt a major economic blow to a myriad of agricultural sectors, including pig farmers.

"The impact of not controlling non-zoonotic vaccine-preventable disease in animals is much larger than the zoonotic impact, if it's properly calculated," said Robyn Alders, senior technical advisor with the Centre for Global Health Security at Chatham House. But data relating to food security "isn't there to show the true impact on the economy."

As the coronavirus pandemic starts to come under control in many countries through social-distancing measures, there's a chance that public attention may turn elsewhere and governments once again neglect investment in preventive strategies.

"The problem here with animal health is that when that perceived human threat is controlled or significantly reduced, the money dries up," said Alders.

From: Morens, David (NIH/NIAID) [E]
Sent: Mon, 22 Nov 2021 16:56:10 +0000
To: William B. Karesh
Cc: Catherine Machalaba; Daniel Mira-Salama
Subject: RE: figure for World Bank report

Yes, that would work, thanks

David

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

BK

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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

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<Figure 1 11-22-2021.tif>

Disclaimer

From: Morens, David (NIH/NIAID) [E]
Sent: Thu, 2 Dec 2021 18:46:31 +0000
To: Kevin Olival ((b)(6))
Subject: FW: Branswell 2021 reference from my EndNote library -- Some experts suggest Omicron variant may have evolved in an animal host
Attachments: Branswell-2021-Some experts suggest Omicron va.pdf

Kevin, any thoughts?

David

David M. Morens, M.D.
CAPT, United States Public Health Service
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💻 (b)(6)

From: Ksiazek, Thomas G. (b)(6)
Sent: Thursday, December 2, 2021 1:35 PM
To: Ksiazek, Thomas (Galveston National Labortory-UT) (b)(6)
Subject: Branswell 2021 reference from my EndNote library -- Some experts suggest Omicron variant may have evolved in an animal host

Branswell H. (2021, 20211202). **Some experts suggest Omicron variant may have evolved in an animal host.** Stat Retrieved 1202, 2021,

https://www.statnews.com/2021/12/02/some-experts-suggest-omicron-variant-may-have-evolved-in-an-animal-host/

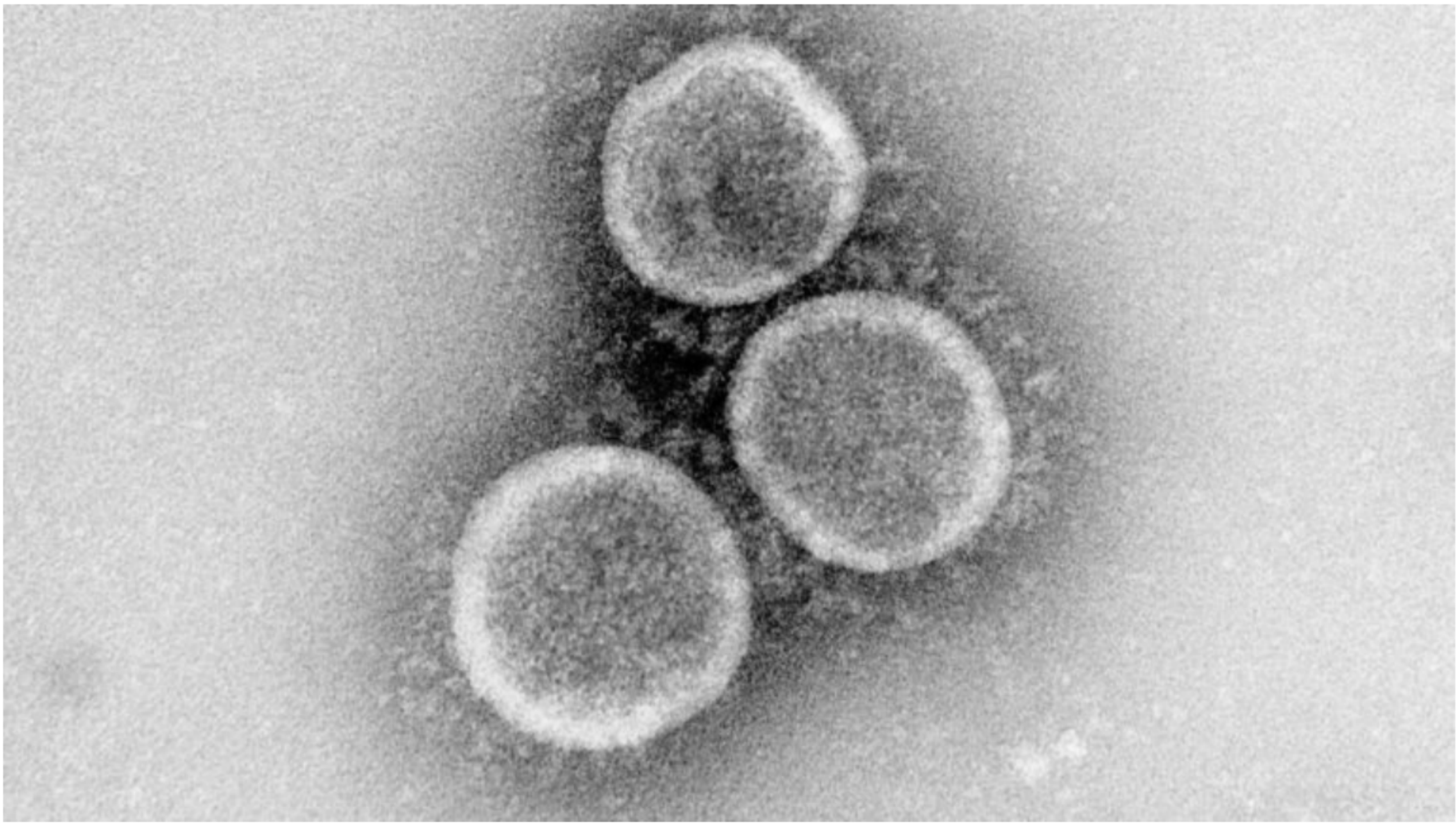
Skip to Main Content

STAT

Some experts suggest Omicron variant may have evolved in an animal host

- 

By Helen Branswell[1 2] Dec. 2, 2021



Transmission electron micrograph of SARS-CoV-2 virus particles. *NIAID/NIH*

When Covid-19 variants arise, the accepted wisdom is that the constellation of mutations they contain developed in an immunocompromised person who contracted the virus and couldn't shake the infection. But some scientists have an alternative theory for where the latest variant of concern, Omicron, may have acquired the unusual mutations that stud its spike protein.

They speculate the virus could have evolved in another animal species.

The theory goes that some type of animal, potentially rodents, was infected with the SARS-CoV-2 virus sometime in mid-2020. In this new species, the virus evolved, accumulating roughly 50 mutations on the spike protein before spilling back over into people.

Kristian Andersen, an immunologist at the Scripps Research Institute, is among those who has been raising the idea that Omicron may have emerged from a reverse zoonotic event.

(A zoonotic event is when an animal pathogen starts to infect and spread among people. A reverse zoonosis is when such a virus passes back into an animal species.)

"I know that most people think that these [come from] immunocompromised individuals, and I do think that that's plausible, but to be perfectly honest, I actually think this reverse zoonosis followed by new zoonosis seems more likely to me given just the available evidence of the really deep branch, and then the mutations themselves, because some of them are quite unusual," Andersen told STAT.

"I don't think we should dismiss that possibility, because I think it's definitely on the table."

A number of other scientists who study the evolution of viruses have told STAT they think the idea isn't out of the question. Some place more weight on the theory that variants develop in immunocompromised people, while others feel there isn't enough evidence at this point to favor one option over the other.

"Personally, I think it's probably more likely it was circulating undetected, in an immunocompromised individual," Emma Hodcroft, a molecular epidemiologist at the Institute of Social and Preventive Medicine in Bern, Switzerland, said via email. Having said that, though, Hodcroft insisted that it is important to explore the hypothesis.

“I would certainly consider it a plausible alternative hypothesis to the evolution during a persistent infection in a human,” said Andrew Rambaut, a professor of molecular evolution at the Institute of Evolutionary Biology in Edinburgh. He cautioned that coming up with a definitive answer won’t be quick.

“I am not sure we will be in a position to say for sure for a while,” Rambaut wrote in an email.

One of the peculiar traits of SARS-2 underpins this thinking. It is what virologists describe as a promiscuous virus; it is capable of infecting a number of species[5]. Dogs and house cats. Large cats. Mink[6]. White-tailed deer[7]. Given how easily the virus seems to jump from species to species, people studying it assume this list will grow.

The original virus that came out of Wuhan, China, in early 2020 did not infect rodents. But as variants — Alpha, Beta, Delta — started to emerge, those viruses could infect rodents.

Robert Garry, a professor of microbiology and immunology at Tulane Medical School, has been tracking the SARS-2 mutations that have arisen. Seven are associated with rodent adaptation — the changes that seemed to allow the virus to infect mice, rats, and related species. All seven of those mutations are in Omicron, Garry noted. He believes it’s a toss-up whether the variant developed in an animal or a human host, but if it’s the former, his bet would be on rodents.

Getting a firm answer might require enormous luck. Scientists are looking at various animal species to see if they can be infected with SARS-2; were they to find viruses like Omicron in any, that would swing the needle.

But Michael Worobey, a professor of evolutionary biology at the University of Arizona, thinks one could do some experiments on selected species of wild animals to see if they can be infected and if, when infected, similar patterns of viral evolution occur.

Studying the molecular clock of viruses that spread in animals — looking at the speed at which they evolve and comparing it to SARS-2 evolution in humans — could also provide some clues, said Worobey, who initially thought Andersen's idea was not impossible, but not the likeliest of explanations for Omicron. After hearing details of the explosive outbreak in white-tailed deer, he's rethinking the idea.

For Worobey, the question is whether any animal species can become chronically infected with SARS-2 — in effect, whether there are animal species in which SARS-2 lingers in the way it does in immunocompromised people. That could put positive selective pressure on the virus — in other words give it an incentive to mutate to stay ahead of the animal's immune response.

"It does move my thinking in terms of Omicron possibly having come from a reservoir, if there are [animal] reservoirs that do chronic infections," he said.

Part of what leads Andersen to wonder about an animal source is the fact that the variant traces back to viruses that were spreading over a year ago. "That in itself you need to be able to explain," he said.

Angela Rasmussen, a coronavirus virologist at the University of Saskatchewan's Vaccine and Infectious Disease Organization, agreed.

"I think it's pretty obvious to everybody … that this virus has been on an independent evolutionary track for quite some time and it's very surprising, which to me just kind of goes back to say well, the idea that this could be … plausible," she said.

Regardless of whether this variant emerged in another species or not, given SARS-2's ability to jump species, it is possible the world will face animal-derived variants in the future, Garry warned. The upshot of that? "We're going to have to keep tweaking the vaccines."

About the Author

Helen Branswell[1]

Senior Writer, Infectious Disease

Helen covers issues broadly related to infectious diseases, including outbreaks, preparedness, research, and vaccine development.

@HelenBranswell [2]
7 Comments

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10. https://www.statnews.com/topic/coronavirus/
11. https://www.statnews.com/topic/infectious-disease/

From: Ellen Carlin
Sent: Tue, 18 Feb 2020 14:15:29 -0500
To: Morens, David (NIH/NIAID) [E]
Cc: Sarah Babcock
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] (b)(6) 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?
(b)(6) 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 (b)(6), 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 (b)(6). 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: William B. Karesh
Sent: Mon, 22 Nov 2021 12:02:13 -0500
To: Morens, David (NIH/NIAID) [E]
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<Figure 1 11-22-2021.tif>

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From: William B. Karesh
Sent: Mon, 22 Nov 2021 08:45:20 -0500
To: Morens, David (NIH/NIAID) [E]
Cc: Catherine Machalaba; Daniel Mira-Salama
Subject: Re: figure for World Bank report

Thank you sir.

BK

On Nov 22, 2021, at 8:16 AM, Morens, David (NIH/NIAID) [E] (b)(6) [redacted] wrote:

OK, will do. I am on the road at the moment so it might take a couple days, but will connect with our graphics folks now. David

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

On Nov 22, 2021, at 07:26, William B. Karesh (b)(6) [redacted] wrote:

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] (b)(6) [redacted] 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 (b)(6) 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

(b)(6) (direct)
+1.212.380.4465 (fax)
www.ecohealthalliance.org

President, OIE Working Group on Wildlife

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

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

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

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From: Morens, David (NIH/NIAID) [E]
Sent: Sat, 18 Sep 2021 15:43:35 +0000
To: Peter Daszak; Wang Linfa; Edward Holmes; Jason Gale
Cc: Stephen Goldstein; (b)(6) ; Garry, Robert F; (b)(6) Robert Kessler; David Morens;
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
31 Center Drive, MSC 2520
Bethesda, MD 20892-2520
☎ (b)(6) (assistant: Whitney Robinson)
📠 301 496 4409
💻 (b)(6)

From: Peter Daszak (b)(6)
Sent: Saturday, September 18, 2021 10:09 AM
To: Wang Linfa (b)(6) ; Edward Holmes (b)(6) ;
Jason Gale <j.gale@bloomberg.net>
Cc: Stephen Goldstein (b)(6) ; Garry, Robert F
(b)(6) ; Morens, David
(NIH/NIAID) [E] (b)(6) ; Robert Kessler (b)(6) ; David
Morens (b)(6)
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.: (b)(6)
Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

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

---

From: Wang Linfa (b)(6)
Sent: Friday, September 17, 2021 10:56 PM
To: Edward Holmes (b)(6); Jason Gale <j.gale@bloomberg.net>
Cc: Stephen Goldstein (b)(6);
(b)(6); Peter Daszak (b)(6);

(b)(6)
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: (b)(6)

From: Edward Holmes (b)(6)
Sent: Thursday, 16 September 2021 3:31 PM
To: Jason Gale <j.gale@bloomberg.net>
Cc: Stephen Goldstein (b)(6);
(b)(6); Peter Daszak (b)(6);
(b)(6) Wang Linfa (b)(6)
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 (b)(6)
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: (b)(6) At: 09/16/21 14:24:33 UTC+10:00
To: Jason Gale (BLOOMBERG/ NEWSROOM:)
Cc: (b)(6),
(b)(6),
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 (b)(6)
@jwgale | Linkedin: http://www.linkedin.com/pub/jason-gale/6/249/a56

From: Peter Daszak
Sent: Sat, 18 Sep 2021 09:44:43 -0400
To: Edward Holmes; Wang Linfa
Cc: Jason Gale; Stephen Goldstein; (b)(6) ; Garry, Robert F; (b)(6) ; Morens, David (NIH/NIAID) [E]; Robert Kessler
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

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To: Wang Linfa (b)(6)
Cc: Jason Gale <j.gale@bloomberg.net>; Stephen Goldstein (b)(6) ; (b)(6) ; Peter Daszak (b)(6)
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.

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(b)(6) ; Peter Daszak
(b)(6) ; Wang Linfa

(b)(6)

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

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Jason Gale, MHlthSec
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Tel. (landline) +61-3-9228-8783 | Mobile (b)(6)
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<210918-preprint-Lao-RBD very close to SARS-CoV-2.pdf>

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(b)(6)

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

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@jwgale | Linkedin: http://www.linkedin.com/pub/jason-gale/6/249/a56

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

Yuri Deigin
@ydeigin

Wow. On a nucleotide level the new Laotian RBD/RBM is MUCH closer to SARS2 than that of the pangolin CoV. A VERY important piece of the puzzle that essentially proves the RBM "itself" was not engineered but actually came from a bat CoV. Doesn't rule out a lab leak/passaging etc.

2:26 PM · Sep 19, 2021 · Twitter Web App

11 Retweets 5 Quote Tweets 59 Likes

From: Morens, David (NIH/NIAID) [E]
Sent: Sun, 19 Sep 2021 19:59:43 -0400
To: Edward Holmes
Cc: Jason Gale; Peter Daszak; (b)(6); (b)(6) Wang Linfa; Garry, Robert F; (b)(6); Taubenberger, Jeffery (NIH/NIAID) [E]
Bcc: Morens, David (NIH/NIAID) [E]
Subject: Re: Study from 2007 shows SARS-infected civets on farms in Hubei
Attachments: Screenshot from 2021-09-19 17-04-25.png

Agree totally except your certainty that China is the ultimate source. Admittedly much data point in that direction but how can you be sure? d

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

On Sep 19, 2021, at 19:28, Edward Holmes (b)(6) wrote:

It's not phylogenetics.

One thing is ascertainment bias which could be huge.

Second thing is to distinguish the long-term ecology of these viruses from the short-term emergence of the virus. These Laos viruses are the former. Clearly these viruses are commonplace in SE Asia. And I don't just think that bats and pangolins will be the only animals with SC2-like viruses. Virus ecology does not work like that. But this is not the same as determining the events that happened in Wuhan. To me, China still looks like the most likely source.

Third, I'm pretty certain that groups in China are sitting on more SC2-like viruses. If you sample bats you find them. It is striking to me that CCDC have published so little on this yet have supposedly sampled so many animals. That doesn't add up. Never discount the politics.

Professor Edward C. Holmes FAA FRS
The University of Sydney

On 20 Sep 2021, at 9:00 am, Morens, David (NIH/NIAID) [E] (b)(6) wrote:

Eddie, please clarify, i don't « get » all the phylogenetic asumptions you guys understand, but can you put it in lsyman's terms? As you know, i have said repeatedly to look past Yunnan to all of SE Asia, as i have bennunconconvinced of the Yunnan centrality of all this, suspecting thAt the universe of these viruses crosses borders to include not only SW and S China but all of SEA.

If that is so, the implications ate huge: this is annintetnational problem demanding international cooperation. d

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

On Sep 19, 2021, at 18:33, Edward Holmes (b)(6) wrote:

Yes, good idea.

The receptor binding domain of some of these Laotian bats is so close to that of SARS-CoV-2 even some of the die-hard leakers are beginning to see the light…

This also effectively excludes that virus-receptor relationship was generated through lab passage, that the pangolin sequences were faked, and that this outbreak had anything to do with the Mojiang mine as a virus from a different country is now closer. That mine will go down in history as the reddest of herrings.

That said, I am a little worried about confirmation bias for the origin being bats from Yunnan/Laos/Cambodia. The more they find there, the more they sequence. But no doubt these Laotian samples are of huge significance. As are the Hubei civets.

<Screenshot from 2021-09-19 17-04-25.png>

--

PROFESSOR EDWARD C. HOLMES FAA FRS

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School of Life & Environmental Sciences and School of Medical Sciences,
The University of Sydney | Sydney | NSW | 2006 | Australia
T (b)(6)
E

On 20 Sep 2021, at 7:52 am, Morens, David (NIH/NIAID) [E] (b)(6) wrote:

Yes, do it! This is important and i say modestly, game changing. The whole « origin » controversy needs to be rethought from the ground up

We have been too micro-focusing (as i have long said to hard push back) but the sarobecovirus and merbecovirus problems are geographically and virologically complex and require us to drop back and study the viral-host universe. Thst universe is huge, complicated , and holds surprises, in my view. d

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

On Sep 19, 2021, at 17:36, Jason Gale (BLOOMBERG/ NEWSROOM:) <j.gale@bloomberg.net> wrote:

I'm planning to pull the threads Peter has so eloquently laid out into a story. Bob, Stephen, Joel (and Kristian), if you have time/interest to get on Zoom today, let me know. Thanks a lot. Jason

From:
(b)(6) At: 09/20/21 07:31:51 UTC+10:00

To:
(b)(6)

Cc:
Jason Gale (BLOOMBERG/ NEWSROOM:) ,
(b)(6) ,

(b)(6)

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

nPeter, as i am perennially swamped with work that has nothing to do with COVID issues of importance, i am always catching up on reading the important stuff

Just now i poured a martini and-read word for word your “A strategy…” paper with first author Sánchez. Also Kevin and Lin-fa were coauthors. Wow!!!

This is dynamite and also beautifully written. I mean, Hemingway, Conrad, Nin, couldn’t have written it better. Beautiful job and so important.

I think you need to promote this work, and emphasize that the conclusions are far reaching and a sort of call to arms.

Let us all keep pushing,
and keep our eyes on the
prize of getting to the bottom of it all
david

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

On Sep 18, 2021, at 12:05, Peter Daszak (b)(6) wrote:

I put it all in a twitter thread while drinking coffee in my local diner (Saturday is “full English breakfast” day for me).

https://twitter.com/peterdaszak/status/1439236376776658945?s=21

No doubt ill be attacked by multiple lab leak aficionados but so be it - at least eddie,
Garry and Kristian won’t see. The horrors of that…

Cheers,

Peter

Peter Daszak
(Sent from my iPhone)

President
EcoHealth Alliance

460 West 34th Street, New York, NY10001, USA

www.EcoHealthAlliance.org

On Sep 18, 2021, at 10:26 AM, Garry, Robert F (b)(6) wrote:

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.

Yuri Deigin
@ydeigin

Wow. On a nucleotide level the new Laotian RBD/RBM is MUCH closer to SARS2 than that of the pangolin CoV. A VERY important piece of the puzzle that essentially proves the RBM *itself* was not engineered but actually came from a bat CoV. Doesn't rule out a lab leak/passaging etc.

2:26 PM · Sep 19, 2021 · Twitter Web App

11 Retweets 5 Quote Tweets 59 Likes

From: Kevin Olival
Sent: Sun, 19 Sep 2021 21:55:27 -0400
To: Morens, David (NIH/NIAID) [E]
Subject: Re: Study from 2007 shows SARS-infected civets on farms in Hubei

Thanks David, means a lot to read your encouraging words! Let's keep on keeping on!

Kevin

Kevin J. Olival, PhD
Vice President for Research

EcoHealth Alliance
520 Eighth Avenue, Suite 1201
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 Sep 19, 2021, at 5:33 PM, Morens, David (NIH/NIAID) [E] (b)(6) wrote:

Kevin, for some reason i could not fix, outlook would not copy your email on this, so i sm sending sepatately. Great work!!!! david

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

Begin forwarded message:

From: "Morens, David (NIH/NIAID) [E]" (b)(6)
Date: September 19, 2021 at 17:31:50 EDT
To: Peter Daszak (b)(6)
Cc: "Garry, Robert F" (b)(6), Wang Linfa (b)(6), Edward Holmes (b)(6), Jason Gale (b)(6), Stephen Goldstein (b)(6), (b)(6), Robert Kessler (b)(6), David Morens (b)(6),

HRSA OL <OL@hrsa.gov>
Subject: Re: Study from 2007 shows SARS-infected civets on farms in Hubei

nPeter, as i am perennially swamped with work that has nothing to do with COVID issues of importance, i am always catching up on reading the important stuff

Just now i poured a martini and-read word for word your “A strategy…” paper with first author Sánchez. Also Kevin and Lin-fa were coauthors. Wow!!!

This is dynamite and also beautifully written. I mean, Hemingway, Conrad, Nin, couldn’t have written it better. Beautiful job and so important.

I think you need to promote this work, and emphasize that the conclusions are far reaching and a sort of call to arms.

Let us all keep pushing,
and keep our eyes on the
prize of getting to the bottom of it all
david

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

On Sep 18, 2021, at 12:05, Peter Daszak (b)(6) wrote:

I put it all in a twitter thread while drinking coffee in my local diner (Saturday is “full English breakfast” day for me).

https://twitter.com/peterdaszak/status/1439236376776658945?s=21

No doubt ill be attacked by multiple lab leak aficionados but so be it - at least eddie, Garry and Kristian won’t see. The horrors of that…

Cheers,

Peter

Peter Daszak
(Sent from my iPhone)

President

EcoHealth Alliance

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