
From: Morens, David (NIH/NIAID) [E] [b6]
Sent: 3/12/2021 4:37:21 PM
To: Morens, David (NIH/NIAID) [E] [b6]
Subject: Fwd: Fwd: Your article has been published at <http://www.bmj.com>

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Subject: Re: Fwd: Your article has been published at <http://www.bmj.com>

Date: Fri, 12 Mar 2021 11:14:49 -0500

From: Dennis Carroll [b6]
To: Morens, David (NIH/NIAID) [E] [b6]
CC: BRIAND, Sylvie [b6], Christine Kreuder Johnson [b6],
Oyewale Tomori [b6], S Wacharapluesadee [b6],
Subhash Morzaria [b6], Sumption, Keith (CJW)
[b6]

Thanks David. I've talked with Jono Quick at RF about this, not sure with much success. I've also been able to connect with Francis Desouza, Illumina CEO as part of a Milken Institute effort to promote such a system. Much support there. Also in discussion with Victor Dzou at NAM about co-hosting a series of workshop (with Illumina) to drill down into some of the details required for such a network (ie. what specific genetic and metadata needs to be collected). David Cameron is also using his position to get this topic on the G7 agenda. So agree, lots of movement- now for meaningful action

d

On Fri, Mar 12, 2021 at 10:12 AM Morens, David (NIH/NIAID) [E] [b6] wrote:

Dennis, great news, thanks for doing this!!! Over the past couple weeks many others have been weighing in with similar ideas. Among those I have been in touch with are the academicians Jim Musser at Houston and Scott Layne at UCLA, and a small think tank team put together by former Sec of State Madeleine Albright with Dr. Tedros, the WHO Director -General, and top folks from BMGF, Rockefeller, including Raj Shah and Rick Bright (who just joined RU), several health ministers of major countries, the CEO of Illumina, who has recently been writing and speaking about this, and separately there is also also Nickie Lurie and Jerry Keusch, who you know, also of course Peter and the EcoHealth folks. Thus these sorts of ideas are in play, but without an obvious mechanism to establish it. It might need some simultaneous networking both from the bottom and from the top down. david

On 3/12/2021 8:07 AM, Dennis Carroll wrote:

All, see link below for our article in the BMJ. Thanks for all your patience. Now, we need to make a global viral surveillance network a reality

Best to all and stay safe

d

On Fri, Mar 12, 2021 at 7:40 AM <bmj-mailer@highwire.stanford.edu> wrote:

We are delighted to tell you that your article

Preventing the next pandemic: the power of a global viral surveillance network

has now been published online by BMJ.

Access your article at: <http://bmj.com/cgi/content/full/bmj.n485>

Toll-free link:

<http://bmj.com/cgi/content/full/bmj.n485?ijkey=ZIx099cFiAbmNno&keytype=ref>

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From: Peter Daszak
Sent: Mon, 23 Aug 2021 20:40:19 -0400
To: Morens, David (NIH/NIAID) [E]; Keusch, Jerry; Robert Kessler; Roberts, Rich; Hotez, Peter Jay
Subject: Under Embargo - Commentary in Nature Wednesday morning
Attachments: Koopmans et al. Comment Covid Origins Nature 2021.pdf
Importance: High

I'm attaching a commentary that will come out on Wednesday in Nature. It was originally written as a response to the WHO DG deciding to bail on the WHO team and call for a new structure and a focus on the lab leak/audit. We've watered it down so it's not too political, and focuses on the fact that this has stalled the process. The key messages from our point of view are that:

1. the search for the origins is important and needs to continue
2. since our report, we feel that most attention has gone to debates regarding likelihood of a lab leak, at the cost of progress in other areas
3. we should all be concerned that time passing - in part owing to these discussions – and this could close the window of opportunity for some critical studies
4. there are critical issues to deal with that are laid out in the report as recommendations for Phase 2: tracking back from the market, following new leads from the recent paper on mammals in the market, representative wild animal and farmed wild animal surveys, and comparative serosurveys in all regions where there has been evidence of early circulation.
5. the lab audit - as added- will need to be developed to define questions. The smallpox audit example cited by WHO in their press addresses biosafety and biosecurity for that pathogen, but would not necessarily help identify evidence for a lab leak. Developing those studies, and agreeing them with China may take of lot of time and that these should not lead to further delays for the other recommended studies

I'm still trying to stay out of publicity as much as possible, so will be avoiding reporters on this one.

Cheers,

Peter

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

From: Peter Daszak (b)(6)
Sent: Monday, August 23, 2021 8:35 PM
To: 'Morens, David (NIH/NIAID) [E]' (b)(6); 'Keusch, Jerry (b)(6)'; (b)(6); Robert Kessler (b)(6); 'Roberts, Rich' (b)(6)
Subject: Francis Collins on CNBC today

Hello everyone - Not looking forward to the publicity this week with the Intel report coming out sometime soon, but wanted to share a couple of things.

First – here’s an interview by Francis Collins on Squawkbox CNBC that makes him come over like a wet lettuce. He goes one way then the other, making sure he sounds somewhat anti-China (they could have been doing mysterious things), but makes it clear NIH didn’t fund Gain of Function there.

It’s the definition of flip-flopping I guess. Maybe he genuinely believes China were up to something. In any case, it feels like he basically couldn’t care less about the organization in the middle (EcoHealth) that’s being batted around like a table tennis ball...

The URL is here: <https://www.cnbc.com/2021/08/23/covid-origin-nih-director-doesnt-rule-out-that-virus-could-have-leaked-from-lab.html>

NIH director says Covid likely came from nature, but doesn’t rule out it could have escaped from lab

PUBLISHED MON, AUG 23 2021 12:53 PM EDT UPDATED MON, AUG 23 2021 11:08 PM EDT
Rich.Mendez@RICHMENDEZCNBC

KEY POINTS

- President Joe Biden gave the U.S. intelligence community 90 days to investigate Covid's origins and report the findings, which are due Tuesday.
- Through a grant to non-profit EcoHealth Alliance, the NIH funded research at the Wuhan Institute of Virology to study how bat viruses could infect humans.
- Collins said the research didn't meet the technical definition of so-called gain-of-function research.

The director of the National Institutes of Health said Monday it appears Covid-19 originated from an animal, but he didn't rule out the possibility that scientists at the Wuhan Institute of Virology were secretly studying it and that it could have leaked out from there.

It's still unknown if the virus leaked out of a Wuhan lab, NIH director Dr. Francis Collins said Monday in an interview on CNBC's "Squawk Box," adding that the World Health Organization's investigation into the origin of the coronavirus has gone "backwards."

"The vast evidence from other perspectives says no, this was a naturally occurring virus," Collins said. "Not to say that it could not have been under study secretly at the Wuhan Institute of Virology and got out of there, we don't know about that. But the virus itself does not have the earmarks of having been created intentionally by human work."

The WHO investigation has been made harder by China's refusal to participate, says Collins.

"I think China basically refused to consider another WHO investigation and just said 'nope not interested'," Collins told CNBC's Squawk Box.

"Wouldn't it be good if they'd actually open up their lab books and let us know what they were actually doing there and find out more about those cases of people who got sick in November of 2019 about which we really don't know enough," Collins said.

U.S. intelligence reports first reported by the Wall Street Journal indicated that in November 2019, three workers at the Wuhan Institute of Virology fell ill with symptoms similar to those seen in Covid-19 infections, a report that China said was "completely untrue."

About three months ago, President Joe Biden [initiated an investigation](#) of his own and gave his intelligence community 90 days to further the investigation the virus' origins and report the findings. The deadline is Tuesday.

“It will be an interesting week because tomorrow is the day of the 90-day deadline that President Biden set for the intelligence community to do all their poking around that they could to see if they could come up with anymore insight as to how this virus got started in China,” Collins said.

Most of the information gathered will likely remain classified, but some information from the report will be released, according to Collins.

“We don't know what they're going to come up with either, but we're intensely interested,” Collins said.

Collins also weighed in on the debate over whether or not the U.S. funded so-called gain-of-function research at the Wuhan lab, a debate that Republican Sen. Rand Paul of Kentucky and medical advisor to the president, Dr. Anthony Fauci, [have engaged in](#) time and time again. Gain-of-function research is when scientists take a pathogen and make it more contagious, deadly or both to study how to combat it.

“The kind of gain-of-function research that's under very careful scrutiny is when you take a pathogen for humans, and you do something with it that would enhance its virulence or its transmissibility,” Collins said. “They were not studying a pathogen that was a pathogen for humans, these are bat viruses.”

Some of the research at the Wuhan Institute of Virology that was funded, in part, by the NIH through a grant to non-profit EcoHealth Alliance studied how bat viruses could infect humans.

“So by the strict definition, and this was look at exquisitely carefully by all the reviewers of that research in anticipation that this might come up, was that this did not meet the official description of what's called gain-of-function research that requires oversight,” Collins said. “I know this has gotten lots of attention, but I think it's way out of place.”

Cheers,

Peter

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

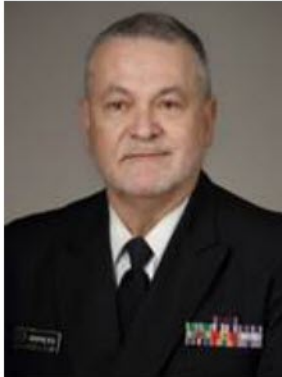
From: Morens, David (NIH/NIAID) [E] (b)(6)
Sent: Monday, August 23, 2021 5:33 PM
To: Peter Daszak ((b)(6)); (b)(6); Keusch, Jerry ((b)(6)); (b)(6); Kessler, Robert ((b)(6)); (b)(6)
Subject: FW: Vice: Why China Is Struggling to Make the Lab Leak Theory Go Away

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From: Folkers, Greg (NIH/NIAID) [E] (b)(6)
Sent: Sunday, August 22, 2021 12:29 AM
Subject: Vice: Why China Is Struggling to Make the Lab Leak Theory Go Away

Why China Is Struggling to Make the Lab Leak Theory Go Away

U.S. spy agencies are about to report on COVID-19's origins, but don't hold your breath.

by [Alan Wong](#)

by [Viola Zhou](#)

August 20, 2021, 9:38am

Robert Redfield has a lot of questions. The virologist and former director of the U.S. Centers for Disease Control and Prevention wants to know what happened at the Wuhan Institute of Virology, especially in the months before the emergence of COVID-19 in the same city. But China's answers didn't satisfy him. "On Sept. 12, 2019, coronavirus bat sequences were deleted from the institute's database. Why? It changed the security protocols for the lab. Why? It put out requests for more than \$600 million for a new ventilation system. What prompted this new need?"

Redfield, who [believes](#) that the coronavirus escaped from the lab in Wuhan, asked those questions in the *Wall Street Journal* on Sunday, alluding to the possibility that something bad happened at the facility as early as September that year and caused a pandemic that has killed more than 4 million people worldwide. To bolster this view, he said a Harvard study of satellite images revealed a shutdown of traffic around the Wuhan lab around that time and that hospital parking lots in the city were filling up—signs, perhaps, of a lab accident and a subsequent surge in sick people.

But almost all of those insinuations are disputed, inaccurate, or just plain wrong.

The opinion article offers a stark illustration of the limits of circumstantial evidence as the search for the origins of COVID-19 enters a contentious new phase.

U.S. spy agencies are preparing to release a report on their findings on whether the pandemic started from human contact with an infected animal or a laboratory accident in China. The report is expected no later than next week, after President Joe Biden in May gave the U.S. intelligence community a 90-day deadline to further collect and analyze information that could “bring us closer to a definitive conclusion” on the origins of COVID-19.

But China is not keen to cooperate. Further muddling the search is Beijing’s renewed push of an unsubstantiated, alternative theory that the virus could have originated in a U.S. army lab at Fort Detrick, Maryland. The move has only fueled suspicions that the Chinese government is hiding something.

Unless U.S. spies uncovered substantial evidence—such as proof that the Wuhan lab possessed the virus that caused COVID-19 or evidence that it created the virus—the [debate on the pathogen’s origins](#) is likely to persist.

Redfield co-authored the *Journal* article with Marc Siegel, a physician and *Fox News* contributor who last March said the coronavirus was [no worse than the flu](#). It was riddled with mistakes.

For example, the planned ventilation system upgrade at the Wuhan Institute of Virology cost about \$600,000, not \$600 million as the authors stated. The figure was [corrected](#) on Friday, a day after VICE World News emailed questions to the *Journal*’s opinion desk. That number came from a report by Republicans that [exaggerated the amounts of several other projects by orders of magnitude](#) and has been cited in several other [prominent news outlets](#).

The Trump-appointed former director of the CDC apparently also misattributed the findings of a military contractor’s report to Harvard. The [Harvard study](#) he links to analyzed satellite images of hospital parking lots in Wuhan, but it did not once mention the Wuhan Institute of Virology. It was also criticized for its [poor dataset, abuse of statistical methods, and mistranslation](#).

The analysis of traffic outside the Wuhan institute used commercial satellite imagery and phone location data to conclude that traffic was unusually thin around the Wuhan institute and was the result of containment efforts following a hazardous event. But the report’s key assertions were [found to be false](#) as early as June last year.

These are just a few examples, from one article, showing the challenges of investigating the origins of the coronavirus without being in China and without the country’s full cooperation.

The closest thing to a field study the world has seen was the World Health Organization (WHO) trip to China early this year, but the global health body has complained about not being able to access the complete raw data from the early COVID-19 patients that could give researchers insights into how the virus emerged.

Last month, the WHO chief urged Beijing to share the data, but Chinese officials said the information could not be disclosed due to patients’ privacy. Some scientists are not convinced by the argument, citing the possibility of disclosing the data while keeping the patients’ anonymous.

Beijing’s obsession with a theory that the coronavirus could have been brought into China through frozen food imports has also raised doubts. Officials have kept calling for more research into such potential [cold-chain transmission](#), although few scientists abroad have found it credible enough to justify further investigation.

“In my opinion, it’s even less likely than lab origin,” Angela Rasmussen, a virologist at the University of Saskatchewan in Canada, told VICE World News. Rasmussen, who has argued in favor of a natural origin of the coronavirus, said the Chinese government might be trying to distract people from the [wildlife trade](#) that could have led to a virus zoonotic spillover.

Scientists say only greater transparency will help Chinese authorities fend off all these suspicions. “We are being asked to take their words for it, without seeing any data,” said Alina Chan, a biologist at the Broad Institute in Cambridge, Massachusetts, who has promoted the lab leak hypothesis. Chan told VICE World News she would like to see all of the sequences of the pathogens that were processed at the

Wuhan lab. If the data could not be made public, she said, they should at least be reviewed by an international team of scientists.

“This situation is setting precedents for how future outbreaks are tracked,” she said. “If every single country does this, and refuses to let international investigators check where the virus came from, we would just be facing a future where viruses are just exploding everywhere, and we are just getting a new pandemic every five or ten years.”

Some other scientists still maintain that the lab leak theory is unlikely, in contrast with what they have called a “substantial body of scientific evidence” supporting a natural origin for the coronavirus, according to a [peer-reviewed paper](#) published in *Cell* this week.

Still, with few new data points to inform the origins probe, scientists on both sides of the debate have called for greater transparency.

WHO Director-General Tedros Adhanom Ghebreyesus in July said the lack of raw data on the early days of the outbreak was hampering the investigations into the origin of the virus and urged China to be more transparent. Tedros suggested further studies into Chinese laboratories in the next phase of studies.

But the Chinese government would not feel comfortable with this degree of transparency. The Communist Party leadership is used to conducting investigations and making decisions behind closed doors, and sees the call for openness as a political threat.

“That is not atypical in China’s crisis management,” Yanzhong Huang, a senior fellow for global health at the Council on Foreign Relations, told VICE World News. “The U.S. could push for more transparency, but they fail to recognize that the lack of transparency itself is part of the authoritarian governance in the country.”

This mindset could hurt China’s reputation—the pandemic is not a small crisis but one that has upended almost everyone’s life. “Even if the virus is caused by a natural spillover event,” Huang said, “when you don’t show transparency, when you are perceived as unwilling to share the data, people naturally will think you have something to hide.”

The Chinese government has remained intransigent to the mounting calls for more transparency.

At the press conference last month, Chinese officials said they were “shocked” to hear about WHO’s proposal for fresh audits into Chinese labs, adding the suggestion indicated “disrespect for common sense and an arrogant attitude toward science.”

The same month, state media quoted a Facebook post by a self-claimed Swiss biologist named Wilson Edwards as saying that researchers faced intimidation from the U.S. for supporting the WHO-China origin-tracing study. The Swiss embassy said [no such person exists](#).

It’s unclear whether the U.S. intelligence probe, which was condemned by Chinese state media as a “political witch-hunt,” would yield anything more than circumstantial evidence.

By the time a preliminary report was drafted, the intelligence community was still divided over the lab leak theory and the natural origin one, CNN reported this month. The outlet cited a source as saying that the draft contained “[nothing too earth shattering](#).”

In September 2019, the Wuhan Institute of Virology shut off public access to its database, which holds thousands of genetic sequences of bat coronaviruses it studied.

Shi Zhengli, director of the Center for Emerging Infectious Diseases at the institute, said the online database was shut down after cyberattacks—believe it or not, that’s the answer to ex-CDC director Robert Redfield’s first question. But almost two years later, the database remains offline. It’s no wonder that people are asking questions.

Follow [Alan Wong](#) and [Viola Zhou](#) on Twitter.

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Comment



ALY SONG/REUTERS/ALAMY

The World Health Organization assembled a team of staff and independent experts tasked with understanding the origins of SARS-CoV-2.

Origins of SARS-CoV-2: window is closing for key scientific studies

Marion Koopmans, Peter Daszak, Vladimir G. Dedkov, Dominic E. Dwyer, Elmoubasher Farag, Thea K. Fischer, David T. S. Hayman, Fabian Leendertz, Ken Maeda, Hung Nguyen-Viet & John Watson

Authors of the March WHO report into how COVID-19 emerged warn that further delay makes crucial inquiry biologically difficult.

Our group was convened by the World Health Organization (WHO) in October 2020. We have been the designated independent international members of a joint WHO–China team tasked with understanding the origins of SARS-CoV-2. Our report was published this March¹. It was meant to be the first step in a process that has stalled. Here we summarize the scientific process so far, and call for action to fast-track the follow-up scientific work required to identify how COVID-19

emerged, which we set out in this article.

The window of opportunity for conducting this crucial inquiry is closing fast: any delay will render some of the studies biologically impossible. Understanding the origins of a devastating pandemic is a global priority, grounded in science.

The mandate

We, all the members of the international expert team, each submitted detailed, confidential statements to the WHO on potential

conflicts of interest, including funding, collaborative studies, public statements and other issues around the origins of COVID-19 that could be perceived as conflicts. After the WHO had reviewed these, team members were appointed in their individual capacity, not as representatives of their employers.

So far, our mission has been guided by terms of reference agreed between the WHO and China in 2020, before our involvement¹. These terms tasked us with making a detailed reconstruction of the early phase of the pandemic, beginning in Wuhan, China, where the first known cases were reported. Our mandate was to conduct a collaborative study with leading scientists in China to review data they had generated on the basis of initial questions from the WHO. We refined the generic list of questions described in the mandate into a detailed workplan described in the mission report¹ (see also Annex A; go.nature.com/3k26jzx).

The workplan specified eight items: specific retrospective studies detailing the profile of respiratory illness in the general community and hospitalized people in Wuhan and Hubei in the second half of 2019; a review of patient files for 76,000 cases in the same time period that had been notified by 233 Wuhan health centres; a review of death certificates and analysis of those data for possible clusters; and a detailed reconstruction of the investigation into the early outbreak, combining all data and findings from the various groups involved in human, animal and environmental studies (a One Health approach; see go.nature.com/3jy7ekh). The other four items were: extensive mapping and traceback of the supply chain of products sold at the Huanan seafood market in Wuhan; testing of a wide range of livestock, wildlife, pets and zoo animals for evidence of infection with SARS-CoV-2; analysis of published and unpublished viral genomic data and linking them with metadata for reconstruction of initial clusters; and a review of relevant literature related to the origins mission.

The possibility of a laboratory origin for the virus's introduction into the local human population – what has come to be called the lab-leak hypothesis – was not part of the WHO's original terms of reference for the team.

The mission

This January, we undertook a 28-day mission to Wuhan to interview clinical, laboratory and public-health professionals and visit institutions involved in the early epidemic response and subsequent investigations. Our work was supported by a team of staff from the WHO



Officials collect COVID-19 test samples in a fresh market in China's Shanxi province in January.

China office and from WHO headquarters in Geneva, Switzerland; staff from the Food and Agriculture Organization of the United Nations (FAO) and the World Organisation for Animal Health (OIE); and a WHO-appointed team leader¹. The huge burden of preparatory work was shouldered by the team in China, including more than 1,000 health-care professionals who collected, analysed, presented and discussed data and study outcomes during our joint mission.

Scientific discussions between the international and Chinese teams during this mission

“We had limited time on the ground in Wuhan and a limited mandate.”

were lively. Large amounts of information were exchanged on the basis of the work carried out. It took days of discussion to develop recommendations on essential further work and ongoing data sharing. We drafted a model of the potential ‘pathways of emergence’ to structure our thoughts. We listed current evidence for and against these pathways (see Fig. 1 of ref. 1).

We found the laboratory origin hypothesis too important to ignore, so brought it into the discussions with our Chinese counterparts. And we included it as one of the hypotheses for SARS-CoV-2 origin in our report.

We had limited time on the ground in Wuhan

and a limited mandate. So we prioritized understanding the role of labs in the early days of the epidemic, the overall lab biosafety procedures and potential staff illness or absenteeism owing to respiratory disease in the late part of 2019. We spoke to the leadership and staff at the three Wuhan labs handling coronaviruses: the Wuhan Institute of Virology, the Chinese Center for Disease Control and Prevention (CDC) in Wuhan, and the Hubei provincial CDC. We reviewed published work from these labs to assess their scientific history of working with coronaviruses related to severe acute respiratory syndrome (SARS).

The Chinese team was and still is reluctant to share raw data (for instance, on the 174 cases identified in December 2019), citing concerns over patient confidentiality. Access to data on these cases was not specified in the mandate, although the WHO had demanded it during the investigation, and has done so since. The legal and possible other barriers could not be addressed in the short time frame of our visit. Also, by then, it was clear that the 174 cases were not likely to be the earliest ones, so we considered them less urgent for understanding origins.

It was therefore agreed that a second phase of studies would address these concerns and review these data.

The report

In our joint report¹, members of both teams concluded unanimously that there was clear evidence of widespread SARS-CoV-2



A woman pushes a cart at the closed wholesale seafood market in Wuhan, China, last January.

circulation in Wuhan during December 2019. We reported evidence for earlier emergence but reached no resolution on when, where and how that occurred. We concluded that the Huanan seafood market had a significant role in the early part of the pandemic, and that there were credible links to wild-animal markets to follow up. We agreed that the earliest cases of COVID-19 had probably been missed, as is common for outbreaks of new diseases².

Our joint report summarized the evidence base that was generated during this first phase of origin tracing. It concluded that there was no definitive proof for or against any of the four proposed pathways: direct zoonotic introduction (through a spillover from wild animals) and three indirect routes of introduction (see Fig. 1 of ref. 1). These three are: zoonotic infection from handling infected farmed animals; zoonotic introduction through the consumption of contaminated food or food from infected animals; or introduction through escape from a laboratory working with animal viruses. The report noted that we considered direct introduction

or indirect zoonotic introduction through an intermediate host the most plausible.

As laid out in our terms of reference, this initial study was not expected to provide definitive answers to the origin of SARS-CoV-2. Rather, phase 1 was always intended to form the foundation of a longer process of scientific investigation that could last for months or years. Therefore, the report put forward recommendations for phase 2 studies that would follow the evidence and trace back further along the most likely pathways. As a joint WHO–China study report, these recommendations were agreed on by members of both the international and the Chinese team. The report also stated that this assessment could be revised if new evidence became available.

The response

Before the report was released, formal statements to the WHO from some governments were circulated in February, with three contentions: that China had not shared data adequately; that we had paid insufficient attention

to the lab-leak hypothesis; and that our scientific conclusions were influenced by China's political stance regarding transmission through the food chain.

Since its release, our report has received extensive coverage in the popular and scientific press and on social media. Much of this has focused on how we conducted the work, and has critiqued us, our methods and results. Five months on, criticisms of the WHO–China joint study continue to emerge.

When asked, our team has emphasized that much new information was shared by the Chinese team as a result of the agreed studies, and that even more was shared as part of the iterative process between the international and Chinese teams.

Our critics have also suggested that the report dismisses the possibility of a lab leak. A laboratory origin hypothesis is presented in the pathway model in Figure 5 on page 119 of the report; we explicitly state in the report that it is possible. We held frank discussions with key scientists in the relevant Wuhan institutions – a line of inquiry that exceeded our original mandate. When we reviewed the responses to our questions on this issue, and all other available data, we found no evidence for leads to follow up; we reported this fact.

In our report, we state that if evidence supporting any of the hypotheses becomes known following publication, phase 2 studies should carefully examine this. For instance, we described that there was evidence of the presence of live animals in the market at the end of December 2019, but that the data presented to the team did not show definitive evidence of live mammals. This evidence came to light after publication³ (as we discuss in more detail later in this article).

Another criticism was that the potential for introduction of SARS-CoV-2 through frozen food was included owing to pressure from China. The report addressed this hypothesis for three reasons: analysis showed that frozen food imported from all over the world was sold at the Wuhan market, including frozen wild-animal meat; foodborne viral-disease outbreaks are widely documented, including occasionally from frozen foods; and SARS-CoV-2 can remain infectious when frozen⁴. Therefore, the team felt it could not rule out introduction from undercooked meat from infected animals.

Some of the public discourse around the report probably originates from miscommunication and misunderstanding about the nature of the work. Although the published report correctly calls it a joint study to reflect what was laid out in the World Health Assembly resolution and terms of reference, it was publicly called an investigation by journalists, by representatives from some member states and, on occasion, by representatives of the WHO. This might have led to expectations that

the report would provide watertight evidence based on formal audits of the institutes involved in the studies.

New data

There have been calls from scientists for further investigation of the lab-leak hypothesis⁵. And there has been a wave of media items that give equivalence to the weight of evidence for a lab leak and for emergence through an intermediate host – an equivalence that the currently available data do not support, in our view.

The arguments and data for a zoonotic spillover event were summarized in a review published as a July preprint by a group of scientists who were not part of the international team⁶. That review includes new data released since the report, on SARS-CoV-2-related coronaviruses in bats in China's Yunnan province^{7,8} and an inventory of live mammals for sale in Wuhan markets up until November 2019, some of which could have theoretically been able to harbour SARS-related coronaviruses³. This inventory, compiled by scientists from the United Kingdom, Canada and China, would have been welcomed by the team had it been available earlier; it needs to be taken up in the phase 2 studies.

In June, a preprint⁹ was published analysing genomic data that had been deleted after March 2020 from the database of the US National Center for Biotechnology Information at the request of the scientists from China who generated the information (that team had published its findings based on the raw data in June 2020; ref. 10). Our colleagues in China contacted the authors of the June 2020 paper, retrieved the data and added them to the SARS-CoV-2 genome phylogenetic data published in our report. The data were from people who had an onset of illness in January, so they did not contribute any new information to the origins question.

In the report, and since, we have publicly called for any data supporting the lab-leak hypothesis to be published and submitted to the WHO. None has, so far.

Six priorities

To keep up the momentum for phase 2 studies, our team has met weekly since the publication of the joint report. We have continued collaboration with our Chinese co-authors, including work on a list of connections to the phase 1 report. Both the international team and the Chinese team have now put forward to the WHO priorities for phase 2 studies, developed from the recommendations in the joint report.

The international team listed the following priorities:

Further trace-back studies. On the basis of disease reporting, look for early COVID-19 cases in all regions inside and outside China that have

the earliest evidence for SARS-CoV-2 circulation.

Antibody surveys. Use standardized methods in the regions that have the earliest evidence for SARS-CoV-2 circulation (inside and outside China) to identify any places where infections occurred that were not observed through disease reporting.

Trace-back and community surveys. These will need to be conducted at sites of wildlife farms that supplied animals to markets in Wuhan in the months before human cases were recognized (inside and outside China, depending on supply-chain analysis).

Risk-targeted surveys of possible hosts. Assess wild bats and other potential reservoirs or intermediate hosts in China and neighbouring countries, and selected high-risk farmed animals (including those farmed for fur), for evidence of exposure.

Detailed risk-factor analysis. Analyse pockets of earlier cases evidenced from the antibody surveys or other studies, and conduct an assessment of all possible exposures.

Follow-up. Investigate any credible new leads.

Time's up

The search for the origins of SARS-CoV-2 is at a critical juncture. There is willingness to move forward from both the WHO international team and the Chinese team.

Crucially, the window is rapidly closing on the biological feasibility of conducting the critical trace-back of people and animals inside and outside China. SARS-CoV-2 antibodies wane, so collecting further samples and testing people who might have been exposed before December 2019 will yield diminishing returns. Chinese wildlife farms employ mil-

“The search for the origins of SARS-CoV-2 is at a critical juncture.”

lions of people (14 million, according to a 2016 census¹¹) and supplied live mammals to cities across China, including Wuhan³. In response to the SARS-CoV-2 pandemic, many of these farms are now closed and the animals have been culled, making any evidence of early coronavirus spillover increasingly difficult to find.

In July, four months after the full report and five months after our debriefing, the WHO informed member states of plans to create a committee that will oversee future origins studies. We are pleased to see both this and its implication that outbreak investigations will be conducted routinely, rather than in an ad hoc manner that could be perceived as politically motivated or with potentially punitive goals.

However, applying this new process to the continuing SARS-CoV-2 origins mission runs

the risk of adding several months of delay. Member-state representatives would need to negotiate detailed terms around the sensitive issue of investigating laboratory practices, then nominate and select team members, who would then have to develop a work plan.

Therefore, we call on the scientific community and country leaders to join forces to expedite the phase 2 studies detailed here, while there is still time.

The authors

Marion Koopmans is head of the Department of Viroscience at Erasmus Medical Center, Rotterdam, the Netherlands. **Peter Daszak** is president of EcoHealth Alliance, New York City, New York, USA. **Vladimir G. Dedkov** is deputy director-general for research at the Pasteur Institute, St Petersburg, Russia. **Dominic E. Dwyer** is director of New South Wales Health Pathology's Institute of Clinical Pathology and Medical Research, Westmead Hospital, Sydney, Australia. **Elmoubasher Farag** is acting head of communicable-disease control programmes in the Public Health Department, Ministry of Public Health, Doha, Qatar. **Thea K. Fischer** is director of clinical research at Nordsjællands University Hospital, Hillerød, Denmark. **David T. S. Hayman** is co-director of the Molecular Epidemiology and Public Health Laboratory, Massey University, Palmerston North, New Zealand. **Fabian Leendertz** is head of the Epidemiology of Highly Pathogenic Microorganisms group at the Robert Koch Institute, Berlin, Germany. **Ken Maeda** is director of the Department of Veterinary Science at the National Institute of Infectious Diseases, Tokyo, Japan. **Hung Nguyen-Viet** is co-leader of the Animal and Human Health Programme at the International Livestock Research Institute, Nairobi, Kenya. **John Watson** is the former senior medical adviser for Public Health England, UK. e-mail: m.koopmans@erasmusmc.nl

1. World Health Organization. *WHO-Convened Global Study of Origins of SARS-CoV-2: China Part. Joint WHO–China Study* (WHO, 2021).
2. Anderson, R. M. et al. *Phil. Trans. R. Soc. Lond. B* **359**, 1091–1105 (2004).
3. Xiao, X., Newman, C., Buesching, C. D., Macdonald, D. W. & Zhou, Z.-M. *Sci. Rep.* **11**, 11898 (2021).
4. Huang, S. Y. et al. *mSphere* **6**, e00104-21 (2021).
5. Bloom, J. D. et al. *Science* **372**, 694–694 (2021).
6. Holmes, E. C. et al. Preprint at Zenodo <https://doi.org/10.5281/zenodo.5075888> (2021).
7. Li, L.-L. et al. Preprint at bioRxiv <https://doi.org/10.1101/2021.03.17.435823> (2021).
8. Zhou, H. et al. *Cell* <https://doi.org/10.1016/j.cell.2021.06.008> (2021).
9. Bloom, J. D. Preprint at bioRxiv <https://doi.org/10.1101/2021.06.18.449051> (2021).
10. Wang, M. et al. *Small* **16**, 2002169 (2020).
11. Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services. *IPBES Workshop on Biodiversity and Pandemics: Workshop Report*. (IPBES, 2020).

The authors declare competing interests, see go.nature.com/3d2rmx6.

From: (b)(6)
Sent: Mon, 23 Aug 2021 20:40:02 -0400
To: Peter Daszak
Cc: Keusch, Jerry; Robert Kessler; Roberts, Rich
Bcc: Morens, David (NIH/NIAID) [E]
Subject: Re: Francis Collins on CNBC today

u got it exactly right, sorry to say. d

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

On Aug 23, 2021, at 20:35, Peter Daszak (b)(6) wrote:

Hello everyone - Not looking forward to the publicity this week with the Intel report coming out sometime soon, but wanted to share a couple of things.

First – here’s an interview by Francis Collins on Squawkbox CNBC that makes him come over like a wet lettuce. He goes one way then the other, making sure he sounds somewhat anti-China (they could have been doing mysterious things), but makes it clear NIH didn’t fund Gain of Function there.

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The URL is here: <https://www.cnbc.com/2021/08/23/covid-origin-nih-director-doesnt-rule-out-that-virus-could-have-leaked-from-lab.html>

NIH director says Covid likely came from nature, but doesn’t rule out it

could have escaped from lab

PUBLISHED MON, AUG 23 2021 12:53 PM EDT UPDATED MON, AUG 23 2021 11:08 PM EDT

[Rich Mendez@RICHMENDEZCNBC](mailto:Rich.Mendez@RICHMENDEZCNBC)

KEY POINTS

- President Joe Biden gave the U.S. intelligence community 90 days to investigate Covid's origins and report the findings, which are due Tuesday.
- Through a grant to non-profit EcoHealth Alliance, the NIH funded research at the Wuhan Institute of Virology to study how bat viruses could infect humans.
- Collins said the research didn't meet the technical definition of so-called gain-of-function research.

The director of the National Institutes of Health said Monday it appears Covid-19 originated from an animal, but he didn't rule out the possibility that scientists at the Wuhan Institute of Virology were secretly studying it and that it could have leaked out from there.

It's still unknown if the virus leaked out of a Wuhan lab, NIH director Dr. Francis Collins said Monday in an interview on CNBC's "Squawk Box," adding that the World Health Organization's investigation into the origin of the coronavirus has gone "backwards."

"The vast evidence from other perspectives says no, this was a naturally occurring virus," Collins said. "Not to say that it could not have been under study secretly at the Wuhan Institute of Virology and got out of there, we don't know about that. But the virus itself does not have the earmarks of having been created intentionally by human work."

The WHO investigation has been made harder by China's refusal to participate, says Collins.

"I think China basically refused to consider another WHO investigation and just said 'nope not interested'," Collins told CNBC's Squawk Box.

"Wouldn't it be good if they'd actually open up their lab books and let us know what they were actually doing there and find out more about those cases of

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U.S. intelligence reports first reported by the Wall Street Journal indicated that in November 2019, three workers at the Wuhan Institute of Virology fell ill with symptoms similar to those seen in Covid-19 infections, a report that China said was "completely untrue."

About three months ago, President Joe Biden [initiated an investigation](#) of his own and gave his intelligence community 90 days to further the investigation the virus' origins and report the findings. The deadline is Tuesday.

"It will be an interesting week because tomorrow is the day of the 90-day deadline that President Biden set for the intelligence community to do all their poking around that they could to see if they could come up with anymore insight as to how this virus got started in China," Collins said.

Most of the information gathered will likely remain classified, but some information from the report will be released, according to Collins.

"We don't know what they're going to come up with either, but we're intensely interested," Collins said.

Collins also weighed in on the debate over whether or not the U.S. funded so-called gain-of-function research at the Wuhan lab, a debate that Republican Sen. Rand Paul of Kentucky and medical advisor to the president, Dr. Anthony Fauci, [have engaged in](#) time and time again. Gain-of-function research is when scientists take a pathogen and make it more contagious, deadly or both to study how to combat it.

"The kind of gain-of-function research that's under very careful scrutiny is when you take a pathogen for humans, and you do something with it that would enhance its virulence or its transmissibility," Collins said. "They were not studying a pathogen that was a pathogen for humans, these are bat viruses."

Some of the research at the Wuhan Institute of Virology that was funded, in part, by the NIH through a grant to non-profit EcoHealth Alliance studied how bat viruses could infect humans.

"So by the strict definition, and this was look at exquisitely carefully by all the reviewers of that research in anticipation that this might come up, was that this did not meet the official description of what's called gain-of-function research

that requires oversight,” Collins said. “I know this has gotten lots of attention, but I think it’s way out of place.”

Cheers,

Peter

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

From: Morens, David (NIH/NIAID) [E] (b)(6)
Sent: Monday, August 23, 2021 5:33 PM
To: Peter Daszak ((b)(6)); (b)(6); Keusch, Jerry ((b)(6)); (b)(6); Kessler, Robert ((b)(6)); (b)(6)
Subject: FW: Vice: Why China Is Struggling to Make the Lab Leak Theory Go Away




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

Sent: Sunday, August 22, 2021 12:29 AM

Subject: Vice: Why China Is Struggling to Make the Lab Leak Theory Go Away

Why China Is Struggling to Make the Lab Leak Theory Go Away

U.S. spy agencies are about to report on COVID-19's origins, but don't hold your breath.

by [Alan Wong](#)

by [Viola Zhou](#)

August 20, 2021, 9:38am

Robert Redfield has a lot of questions. The virologist and former director of the U.S. Centers for Disease Control and Prevention wants to know what happened at the Wuhan Institute of Virology, especially in the months before the emergence of COVID-19 in the same city. But China's answers didn't satisfy him. "On Sept. 12, 2019, coronavirus bat sequences were deleted from the institute's database. Why? It changed the security protocols for the lab. Why? It put out requests for more than \$600 million for a new ventilation system. What prompted this new need?"

Redfield, who [believes](#) that the coronavirus escaped from the lab in Wuhan, asked those questions in the *Wall Street Journal* on Sunday, alluding to the possibility that something bad happened at the facility as early as September that year and caused a pandemic that has killed more than 4 million people worldwide. To bolster this view, he said a Harvard study of satellite images revealed a shutdown of traffic around the Wuhan lab around that time and that hospital parking lots in the city were filling up—signs, perhaps, of a lab accident and a subsequent surge in sick people.

But almost all of those insinuations are disputed, inaccurate, or just plain wrong.

The opinion article offers a stark illustration of the limits of circumstantial evidence as the search for the origins of COVID-19 enters a contentious new phase.

U.S. spy agencies are preparing to release a report on their findings on whether the pandemic started from human contact with an infected animal or a laboratory accident in China. The report is expected no later than next week, after President Joe Biden in May gave the U.S. intelligence community a 90-day deadline to further collect and analyze information that could “bring us closer to a definitive conclusion” on the origins of COVID-19.

But China is not keen to cooperate. Further muddling the search is Beijing’s renewed push of an unsubstantiated, alternative theory that the virus could have originated in a U.S. army lab at Fort Detrick, Maryland. The move has only fueled suspicions that the Chinese government is hiding something.

Unless U.S. spies uncovered substantial evidence—such as proof that the Wuhan lab possessed the virus that caused COVID-19 or evidence that it created the virus—the [debate on the pathogen’s origins](#) is likely to persist.

Redfield co-authored the *Journal* article with Marc Siegel, a physician and *Fox News* contributor who last March said the coronavirus was [no worse than the flu](#). It was riddled with mistakes.

For example, the planned ventilation system upgrade at the Wuhan Institute of Virology cost about \$600,000, not \$600 million as the authors stated. The figure was [corrected](#) on Friday, a day after VICE World News emailed questions to the *Journal*’s opinion desk. That number came from a report by Republicans that [exaggerated the amounts of several other projects by orders of magnitude](#) and has been cited in several other [prominent news outlets](#).

The Trump-appointed former director of the CDC apparently also misattributed the findings of a military contractor’s report to Harvard. The [Harvard study](#) he links to analyzed satellite images of hospital parking lots in Wuhan, but it did not once mention the Wuhan Institute of Virology. It was also criticized for its [poor dataset, abuse of statistical methods, and mistranslation](#).

The analysis of traffic outside the Wuhan institute used commercial satellite imagery and phone location data to conclude that traffic was unusually thin around the Wuhan institute and was the result of containment efforts following a hazardous event. But the report’s key assertions were [found to be false](#) as early as June last year.

These are just a few examples, from one article, showing the challenges of investigating the origins of the coronavirus without being in China and without the country’s full cooperation.

The closest thing to a field study the world has seen was the World Health Organization (WHO) trip to China early this year, but the global health body has complained about not being able to access the complete raw data from the early COVID-19 patients that could give researchers insights into how the virus emerged.

Last month, the WHO chief urged Beijing to share the data, but Chinese officials said the information could not be disclosed due to patients’ privacy. Some scientists are not convinced by the argument, citing the possibility of disclosing the data while keeping the patients’ anonymous.

Beijing’s obsession with a theory that the coronavirus could have been brought into China through frozen food imports has also raised doubts. Officials have kept calling for more research into such

potential [cold-chain transmission](#), although few scientists abroad have found it credible enough to justify further investigation.

“In my opinion, it’s even less likely than lab origin,” Angela Rasmussen, a virologist at the University of Saskatchewan in Canada, told VICE World News. Rasmussen, who has argued in favor of a natural origin of the coronavirus, said the Chinese government might be trying to distract people from the [wildlife trade](#) that could have led to a virus zoonotic spillover.

Scientists say only greater transparency will help Chinese authorities fend off all these suspicions. “We are being asked to take their words for it, without seeing any data,” said Alina Chan, a biologist at the Broad Institute in Cambridge, Massachusetts, who has promoted the lab leak hypothesis. Chan told VICE World News she would like to see all of the sequences of the pathogens that were processed at the Wuhan lab. If the data could not be made public, she said, they should at least be reviewed by an international team of scientists.

“This situation is setting precedents for how future outbreaks are tracked,” she said. “If every single country does this, and refuses to let international investigators check where the virus came from, we would just be facing a future where viruses are just exploding everywhere, and we are just getting a new pandemic every five or ten years.”

Some other scientists still maintain that the lab leak theory is unlikely, in contrast with what they have called a “substantial body of scientific evidence” supporting a natural origin for the coronavirus, according to a [peer-reviewed paper](#) published in *Cell* this week.

Still, with few new data points to inform the origins probe, scientists on both sides of the debate have called for greater transparency.

WHO Director-General Tedros Adhanom Ghebreyesus in July said the lack of raw data on the early days of the outbreak was hampering the investigations into the origin of the virus and urged China to be more transparent. Tedros suggested further studies into Chinese laboratories in the next phase of studies.

But the Chinese government would not feel comfortable with this degree of transparency. The Communist Party leadership is used to conducting investigations and making decisions behind closed doors, and sees the call for openness as a political threat.

“That is not atypical in China’s crisis management,” Yanzhong Huang, a senior fellow for global health at the Council on Foreign Relations, told VICE World News. “The U.S. could push for more transparency, but they fail to recognize that the lack of transparency itself is part of the authoritarian governance in the country.”

This mindset could hurt China’s reputation—the pandemic is not a small crisis but one that has upended almost everyone’s life. “Even if the virus is caused by a natural spillover event,” Huang said, “when you don’t show transparency, when you are perceived as unwilling to share the data, people naturally will think you have something to hide.”

The Chinese government has remained intransigent to the mounting calls for more transparency. At the press conference last month, Chinese officials said they were “shocked” to hear about WHO’s proposal for fresh audits into Chinese labs, adding the suggestion indicated “disrespect for common sense and an arrogant attitude toward science.”

The same month, state media quoted a Facebook post by a self-claimed Swiss biologist named Wilson Edwards as saying that researchers faced intimidation from the U.S. for supporting the WHO-China origin-tracing study. The Swiss embassy said [no such person exists](#).

It’s unclear whether the U.S. intelligence probe, which was condemned by Chinese state media as a “political witch-hunt,” would yield anything more than circumstantial evidence.

By the time a preliminary report was drafted, the intelligence community was still divided over the lab leak theory and the natural origin one, CNN reported this month. The outlet cited a source as saying that the draft contained “[nothing too earth shattering](#).”

In September 2019, the Wuhan Institute of Virology shut off public access to its database, which holds thousands of genetic sequences of bat coronaviruses it studied.

Shi Zhengli, director of the Center for Emerging Infectious Diseases at the institute, said the online database was shut down after cyberattacks—believe it or not, that’s the answer to ex-CDC director Robert Redfield’s first question. But almost two years later, the database remains offline. It’s no wonder that people are asking questions.

Follow [Alan Wong](#) and [Viola Zhou](#) on Twitter.

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From: Peter Daszak
Sent: Mon, 23 Aug 2021 23:51:46 -0400
To: Roberts, Rich; Morens, David (NIH/NIAID) [E]; Keusch, Jerry; Robert Kessler
Subject: RE: Francis Collins on CNBC today

Yes, you're right – he didn't throw us under the bus completely to be fair...

Cheers,

Peter

Peter Daszak
President

EcoHealth Alliance
520 Eighth Avenue, Suite 1200
New York, NY 10018-6507
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Tel.: (b)(6)
Website: www.ecohealthalliance.org
Twitter: [@PeterDaszak](https://twitter.com/PeterDaszak)

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

From: Roberts, Rich (b)(6)
Sent: Monday, August 23, 2021 9:06 PM
To: Peter Daszak (b)(6); Morens, David (NIH/NIAID) [E]
(b)(6); Keusch, Jerry (b)(6); Robert Kessler
(b)(6)
Subject: RE: Francis Collins on CNBC today

Peter:

It could have been much worse.

Rich

Richard J. Roberts
New England Biolabs
240 County Road
Ipswich, MA 01938-2723
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Tel: (b)(6)
Fax: (978) 412 9910
email: (b)(6)

From: Peter Daszak (b)(6)
Sent: Monday, August 23, 2021 8:35 PM
To: Morens, David (NIH/NIAID) [E] (b)(6); Keusch, Jerry (b)(6); Robert Kessler (b)(6); Roberts, Rich (b)(6)
Subject: Francis Collins on CNBC today

EXTERNAL SENDER

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NIH director says Covid likely came from nature, but doesn’t rule out it

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PUBLISHED MON, AUG 23 2021 12:53 PM EDT UPDATED MON, AUG 23 2021 11:08 PM EDT
[Rich Mendez@RICHMENDEZCNBC](mailto:Rich.Mendez@RICHMENDEZCNBC)

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Some of the research at the Wuhan Institute of Virology that was funded, in part, by the NIH through a grant to non-profit EcoHealth Alliance studied how bat viruses could infect humans.

"So by the strict definition, and this was look at exquisitely carefully by all the reviewers of that research in anticipation that this might come up, was that this did not meet the official description of what's called gain-of-function research

that requires oversight,” Collins said. “I know this has gotten lots of attention, but I think it’s way out of place.”

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](https://twitter.com/PeterDaszak)

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


From: Morens, David (NIH/NIAID) [E] (b)(6)
Sent: Monday, August 23, 2021 5:33 PM
To: Peter Daszak ((b)(6)); (b)(6); Keusch, Jerry
((b)(6)); (b)(6); Kessler, Robert ((b)(6))
(b)(6)
Subject: FW: Vice: Why China Is Struggling to Make the Lab Leak Theory Go Away




David M. Morens, M.D.

CAPT, United States Public Health Service
Senior Advisor to the Director
Office of the Director
National Institute of Allergy and Infectious Diseases
National Institutes of Health

Building 31, Room 7A-03
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Bethesda, MD 20892-2520

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

 301 496 4409

 (b)(6)

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

Sent: Sunday, August 22, 2021 12:29 AM

Subject: Vice: Why China Is Struggling to Make the Lab Leak Theory Go Away

Why China Is Struggling to Make the Lab Leak Theory Go Away

U.S. spy agencies are about to report on COVID-19's origins, but don't hold your breath.

by [Alan Wong](#)

by [Viola Zhou](#)

August 20, 2021, 9:38am

Robert Redfield has a lot of questions. The virologist and former director of the U.S. Centers for Disease Control and Prevention wants to know what happened at the Wuhan Institute of Virology, especially in the months before the emergence of COVID-19 in the same city. But China's answers didn't satisfy him. "On Sept. 12, 2019, coronavirus bat sequences were deleted from the institute's database. Why? It changed the security protocols for the lab. Why? It put out requests for more than \$600 million for a new ventilation system. What prompted this new need?"

Redfield, who [believes](#) that the coronavirus escaped from the lab in Wuhan, asked those questions in the *Wall Street Journal* on Sunday, alluding to the possibility that something bad happened at the facility

as early as September that year and caused a pandemic that has killed more than 4 million people worldwide. To bolster this view, he said a Harvard study of satellite images revealed a shutdown of traffic around the Wuhan lab around that time and that hospital parking lots in the city were filling up—signs, perhaps, of a lab accident and a subsequent surge in sick people.

But almost all of those insinuations are disputed, inaccurate, or just plain wrong.

The opinion article offers a stark illustration of the limits of circumstantial evidence as the search for the origins of COVID-19 enters a contentious new phase.

U.S. spy agencies are preparing to release a report on their findings on whether the pandemic started from human contact with an infected animal or a laboratory accident in China. The report is expected no later than next week, after President Joe Biden in May gave the U.S. intelligence community a 90-day deadline to further collect and analyze information that could “bring us closer to a definitive conclusion” on the origins of COVID-19.

But China is not keen to cooperate. Further muddling the search is Beijing’s renewed push of an unsubstantiated, alternative theory that the virus could have originated in a U.S. army lab at Fort Detrick, Maryland. The move has only fueled suspicions that the Chinese government is hiding something.

Unless U.S. spies uncovered substantial evidence—such as proof that the Wuhan lab possessed the virus that caused COVID-19 or evidence that it created the virus—the [debate on the pathogen’s origins](#) is likely to persist.

Redfield co-authored the *Journal* article with Marc Siegel, a physician and *Fox News* contributor who last March said the coronavirus was [no worse than the flu](#). It was riddled with mistakes.

For example, the planned ventilation system upgrade at the Wuhan Institute of Virology cost about \$600,000, not \$600 million as the authors stated. The figure was [corrected](#) on Friday, a day after VICE World News emailed questions to the *Journal*’s opinion desk. That number came from a report by Republicans that [exaggerated the amounts of several other projects by orders of magnitude](#) and has been cited in several other [prominent news outlets](#).

The Trump-appointed former director of the CDC apparently also misattributed the findings of a military contractor’s report to Harvard. The [Harvard study](#) he links to analyzed satellite images of hospital parking lots in Wuhan, but it did not once mention the Wuhan Institute of Virology. It was also criticized for its [poor dataset, abuse of statistical methods, and mistranslation](#).

The analysis of traffic outside the Wuhan institute used commercial satellite imagery and phone location data to conclude that traffic was unusually thin around the Wuhan institute and was the result of containment efforts following a hazardous event. But the report’s key assertions were [found to be false](#) as early as June last year.

These are just a few examples, from one article, showing the challenges of investigating the origins of the coronavirus without being in China and without the country’s full cooperation.

The closest thing to a field study the world has seen was the World Health Organization (WHO) trip to China early this year, but the global health body has complained about not being able to access the complete raw data from the early COVID-19 patients that could give researchers insights into how the virus emerged.

Last month, the WHO chief urged Beijing to share the data, but Chinese officials said the information could not be disclosed due to patients’ privacy. Some scientists are not convinced by the argument, citing the possibility of disclosing the data while keeping the patients’ anonymous.

Beijing’s obsession with a theory that the coronavirus could have been brought into China through frozen food imports has also raised doubts. Officials have kept calling for more research into such potential [cold-chain transmission](#), although few scientists abroad have found it credible enough to justify further investigation.

“In my opinion, it’s even less likely than lab origin,” Angela Rasmussen, a virologist at the University of Saskatchewan in Canada, told VICE World News. Rasmussen, who has argued in favor of a natural origin of the coronavirus, said the Chinese government might be trying to distract people from the [wildlife trade](#) that could have led to a virus zoonotic spillover.

Scientists say only greater transparency will help Chinese authorities fend off all these suspicions. “We are being asked to take their words for it, without seeing any data,” said Alina Chan, a biologist at the Broad Institute in Cambridge, Massachusetts, who has promoted the lab leak hypothesis. Chan told VICE World News she would like to see all of the sequences of the pathogens that were processed at the Wuhan lab. If the data could not be made public, she said, they should at least be reviewed by an international team of scientists.

“This situation is setting precedents for how future outbreaks are tracked,” she said. “If every single country does this, and refuses to let international investigators check where the virus came from, we would just be facing a future where viruses are just exploding everywhere, and we are just getting a new pandemic every five or ten years.”

Some other scientists still maintain that the lab leak theory is unlikely, in contrast with what they have called a “substantial body of scientific evidence” supporting a natural origin for the coronavirus, according to a [peer-reviewed paper](#) published in *Cell* this week.

Still, with few new data points to inform the origins probe, scientists on both sides of the debate have called for greater transparency.

WHO Director-General Tedros Adhanom Ghebreyesus in July said the lack of raw data on the early days of the outbreak was hampering the investigations into the origin of the virus and urged China to be more transparent. Tedros suggested further studies into Chinese laboratories in the next phase of studies.

But the Chinese government would not feel comfortable with this degree of transparency. The Communist Party leadership is used to conducting investigations and making decisions behind closed doors, and sees the call for openness as a political threat.

“That is not atypical in China’s crisis management,” Yanzhong Huang, a senior fellow for global health at the Council on Foreign Relations, told VICE World News. “The U.S. could push for more transparency, but they fail to recognize that the lack of transparency itself is part of the authoritarian governance in the country.”

This mindset could hurt China’s reputation—the pandemic is not a small crisis but one that has upended almost everyone’s life. “Even if the virus is caused by a natural spillover event,” Huang said, “when you don’t show transparency, when you are perceived as unwilling to share the data, people naturally will think you have something to hide.”

The Chinese government has remained intransigent to the mounting calls for more transparency. At the press conference last month, Chinese officials said they were “shocked” to hear about WHO’s proposal for fresh audits into Chinese labs, adding the suggestion indicated “disrespect for common sense and an arrogant attitude toward science.”

The same month, state media quoted a Facebook post by a self-claimed Swiss biologist named Wilson Edwards as saying that researchers faced intimidation from the U.S. for supporting the WHO-China origin-tracing study. The Swiss embassy said [no such person exists](#).

It’s unclear whether the U.S. intelligence probe, which was condemned by Chinese state media as a “political witch-hunt,” would yield anything more than circumstantial evidence.

By the time a preliminary report was drafted, the intelligence community was still divided over the lab leak theory and the natural origin one, CNN reported this month. The outlet cited a source as saying that the draft contained “[nothing too earth shattering](#).”

In September 2019, the Wuhan Institute of Virology shut off public access to its database, which holds thousands of genetic sequences of bat coronaviruses it studied.

Shi Zhengli, director of the Center for Emerging Infectious Diseases at the institute, said the online database was shut down after cyberattacks—believe it or not, that’s the answer to ex-CDC director Robert Redfield’s first question. But almost two years later, the database remains offline. It’s no wonder that people are asking questions.

Follow [Alan Wong](#) and [Viola Zhou](#) on Twitter.

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From: (b)(6)
Sent: Sun, 25 Jul 2021 19:32:18 -0400
To: Peter Daszak
Cc: Gerald Keusch
Bcc: Morens, David (NIH/NIAID) [E]
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 (b)(6) 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

(b)(6)

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,

(b)(6)

(b)(6)

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

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

From: Morens, David (NIH/NIAID) [E] (b)(6)
Sent: Friday, July 23, 2021 8:07 AM
To: Peter Daszak (b)(6); Gerald Keusch
(b)(6)
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

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From: Morens, David (NIH/NIAID) [E]
Sent: Wed, 23 Jun 2021 14:37:10 +0000
To: Peter Daszak; Keusch, Jerry; Rich Roberts
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.

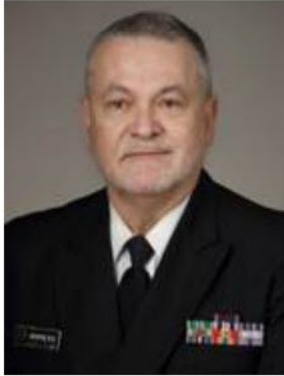
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Office of the Director
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From: Peter Daszak (b)(6)
Sent: Wednesday, June 23, 2021 10:11 AM
To: Morens, David (NIH/NIAID) [E] (b)(6); Keusch, Jerry (b)(6); Rich Roberts (b)(6)
Subject: RE: Hi David

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

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520 Eighth Avenue, Suite 1200
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Tel.: (b)(6)

Website: www.ecohealthalliance.org

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

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

Sent: Wednesday, June 23, 2021 9:16 AM

To: Peter Daszak (b)(6); Keusch, Jerry (b)(6); Rich Roberts (b)(6)

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 appear 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 symptoms 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 sequences 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 know much about the origin isn't that surprising to me. Nature does its business away from our gaze....


David

David M. Morens, M.D.

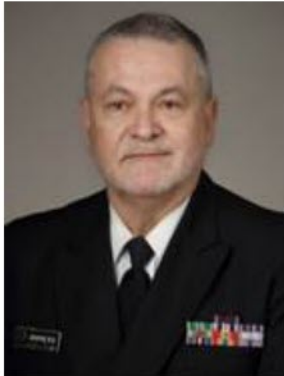
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From: Peter Daszak (b)(6)
Sent: Wednesday, June 23, 2021 8:48 AM
To: Morens, David (NIH/NIAID) [E] (b)(6); Keusch, Jerry (b)(6); Rich Roberts (b)(6); Taubenberger, Jeffery (NIH/NIAID) [E] (b)(6)
Subject: RE: Hi David

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
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Website: www.ecohealthalliance.org
Twitter: [@PeterDaszak](https://twitter.com/PeterDaszak)

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From: Morens, David (NIH/NIAID) [E] (b)(6)
Sent: Wednesday, June 23, 2021 7:22 AM
To: Peter Daszak ((b)(6)); (b)(6); Keusch, Jerry ((b)(6)); (b)(6); Rich Roberts ((b)(6)); (b)(6); Taubenberger, Jeffery (NIH/NIAID) [E] (b)(6)
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 (b)(6) and (b)(6) (b)(6), and he has already contacted (b)(6) while I contacted (b)(6) myself. They are both horrified, to use (b)(6) 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. (b)(6) 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. (b)(6) is apparently upset, and Jason also contacted (b)(6), who I don't know personally, and he had some really choice words to unload....


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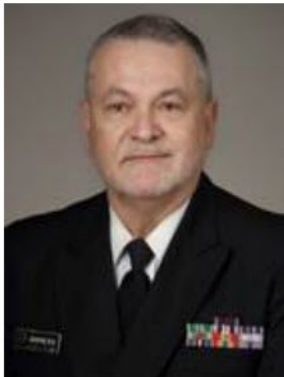
 (b)(6) (assistant: Whitney Robinson)

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From: Jason Gale (BLOOMBERG/ NEWSROOM:) <j.gale@bloomberg.net>
Sent: Tuesday, June 22, 2021 6:28 PM
To: Morens, David (NIH/NIAID) [E] (b)(6)
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 (b)(6)
@jwgale | LinkedIn: <http://www.linkedin.com/pub/jason-gale/6/249/a56>

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From: Peter Daszak
Sent: Wed, 23 Jun 2021 11:51:14 -0400
To: Morens, David (NIH/NIAID) [E]; Keusch, Jerry; Rich Roberts
Subject: Bizarre witness list! RE: House Select Subcommittee Republicans Announce Expert Witness Forum on COVID-19 Origins

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

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

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

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

Cheers,

Peter

Peter Daszak
President

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Tel.: (b)(6)
Website: www.ecohealthalliance.org
Twitter: [@PeterDaszak](https://twitter.com/PeterDaszak)


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

From: Morens, David (NIH/NIAID) [E] (b)(6)
Sent: Wednesday, June 23, 2021 10:46 AM
To: Peter Daszak ((b)(6)) ((b)(6)); Keusch, Jerry
((b)(6)) ((b)(6)); Rich Roberts ((b)(6)) ((b)(6))
Subject: FW: House Select Subcommittee Republicans Announce Expert Witness Forum on COVID-19
Origins


David

David M. Morens, M.D.

CAPT, United States Public Health Service
Senior Advisor to the Director
Office of the Director
National Institute of Allergy and Infectious Diseases
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Building 31, Room 7A-03
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 (b)(6) (assistant: Whitney Robinson)

 301 496 4409

 (b)(6)

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

Sent: Wednesday, June 23, 2021 10:07 AM

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

Press Release Published: Jun 23, 2021

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

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

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

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

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

It was recently **reported** that three researchers from the Wuhan lab became ill with symptoms consistent with COVID-19 and sought hospital care in November 2019. Additionally, Dr. Fauci’s

recently released emails from February 2020 reveal that scientists raised the possibility of a lab leak and also expressed concern the virus appeared to be engineered.

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

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

WHERE: HVC-215, Capitol Visitors Center

WHO:

Witness Panel I

- **The Honorable Brett P. Giroir, former Assistant Secretary for Health, U.S. Department of Health and Human Services:** Admiral Giroir brings firsthand knowledge about the public health response to the COVID-19 pandemic. As COVID-19 testing czar, he oversaw creating a nationwide testing apparatus from scratch which was made particularly difficult by China’s lack of transparency. Admiral Giroir will also discuss the investigatory failures of the World Health Organization and why a U.S.-led origins investigation is vital.
- **Dr. David Asher, Senior Fellow, Hudson Institute:** Dr. Asher has decades of national security experience and most recently led the U.S. Department of State’s COVID-19 origins investigation. His testimony will provide inside information into the origins investigation and the role of the Chinese government’s efforts to block a thorough and impartial investigation.
- **Dr. Richard Muller, Emeritus Professor of Physics, University of California Berkeley:** Dr. Muller is an acclaimed scientist that used his own research to study available data in attempting to determine the origins of COVID-19. He recently penned an op-ed in the [*Wall Street Journal*](#) pointing out there is strong evidence COVID-19 was developed in a laboratory using gain-of-function acceleration.
- **Dr. Steven Quay, Founder, Atossa Therapeutics:** Dr. Quay is one of a growing number of scientists dedicated to finding the origins of COVID-19. He has conducted his own research using the publicly available viral data and reached conclusions apart from outside influence. He brings significant scientific expertise to this endeavor including over 87 patents and hundreds of published scientific articles.

Member Panel

- **The Honorable Cathy McMorris Rodgers, Member of Congress**
- **The Honorable Michael McCaul, Member of Congress**

- **The Honorable Devin Nunes, Member of Congress**
- **The Honorable Mike Gallagher, Member of Congress**

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

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

WATCH: A livestream will be available [HERE](#).

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From: Morens, David (NIH/NIAID) [E]
Sent: Tue, 5 Oct 2021 14:04:44 +0000
To: Peter Daszak; Roberts, Rich; Taubenberger, Jeffery (NIH/NIAID) [E]; Gerald Keusch
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.

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From: Peter Daszak (b)(6)
Sent: Tuesday, October 5, 2021 9:18 AM
To: Roberts, Rich (b)(6); Morens, David (NIH/NIAID) [E] (b)(6);
Taubenberger, Jeffery (NIH/NIAID) [E] (b)(6); Gerald Keusch
(b)(6)
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

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

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

From: Roberts, Rich (b)(6)
Sent: Tuesday, October 5, 2021 9:04 AM
To: Morens, David (NIH/NIAID) [E] (b)(6); Taubenberger, Jeffery (NIH/NIAID) [E]
(b)(6); Peter Daszak (b)(6); Gerald Keusch
Subject: RE: Stepping Down as NIH Director

Best news I’ve heard in a long time.

Rich

Richard J. Roberts
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240 County Road
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Tel: (b)(6)
Fax: (978) 412 9910
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From: Morens, David (NIH/NIAID) [E] (b)(6)
Sent: Tuesday, October 5, 2021 7:45 AM
To: Taubenberger, Jeffery (NIH/NIAID) [E] (b)(6) Peter Daszak
(b)(6); Gerald Keusch (b)(6); Roberts, Rich (b)(6)
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 unflinching 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

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From: Morens, David (NIH/NIAID) [E] [b6]
Sent: 6/5/2016 10:24:21 PM
To: 'Kevin Olival, PhD' [b6]
CC: [b6]
Subject: RE: Viruses | Free Full-Text | Filoviruses in Bats: Current Knowledge and Future Directions | HTML
Attachments: Singh Ruzek VHF Book ch7.pdf

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

David

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

From: Kevin Olival, PhD [mailto:[b6]]
Sent: Friday, June 03, 2016 6:39 PM
To: Morens, David (NIH/NIAID) [E] [b6]
Subject: Viruses | Free Full-Text | Filoviruses in Bats: Current Knowledge and Future Directions | HTML

Cheers,
Kevin

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

7 Role of Rodents and Bats in Human Viral Hemorrhagic Fevers

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

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7.1 RODENTS

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

7.1.1 ARENAVIRUSES

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

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

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

7.1.1.1 Lassa Virus

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

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

7.1.1.2 Machupo Virus

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

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

7.1.1.3 Junín Virus

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

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

7.1.1.4 Guanarito Virus

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

7.1.1.5 Conclusion

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

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

7.1.2 HANTAVIRUSES

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

TABLE 7.1
Hantaviruses Causing HFRS

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

7.1.2.1 Brief History of Hemorrhagic Fever with Renal Syndrome

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

7.1.2.2 Epidemiology

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

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

7.1.2.3 China, Korea, and Far Eastern Russia

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

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

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

7.1.2.4 Western Russia and Eastern Europe

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

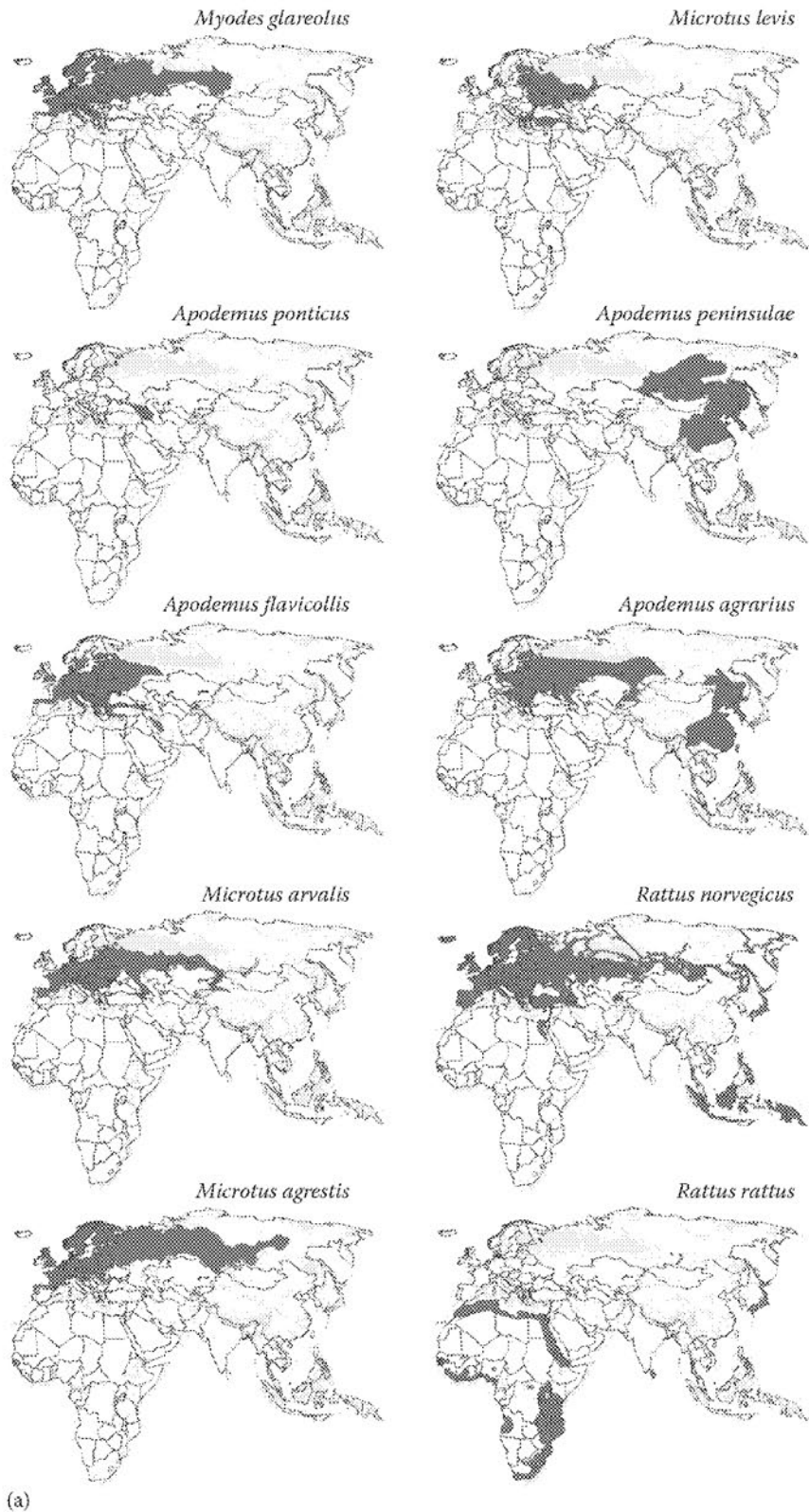


FIGURE 7.1 Distribution of rodents that are associated with HFRS is shown in individual (a) as well as a single composite map (b). All data used to generate maps were obtained from IUCN 2012. (From IUCN, The IUCN red list of threatened species, version 2012.1, 2012, <http://www.iucnredlist.org>.)

(continued)

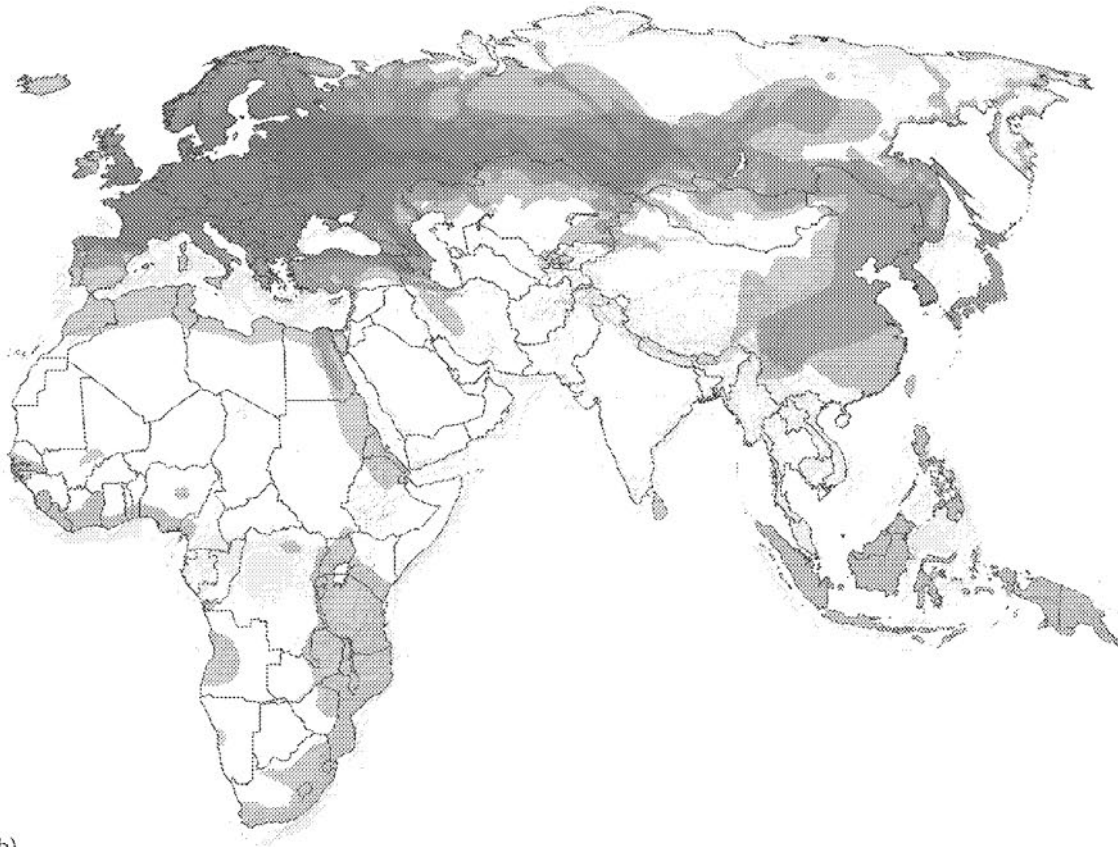


FIGURE 7.1 (continued) Distribution of rodents that are associated with HFRS is shown in individual (a) as well as a single composite map (b). All data used to generate maps were obtained from IUCN 2012. (From IUCN, The IUCN red list of threatened species, version 2012.1, 2012, <http://www.iucnredlist.org>.)

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

7.1.2.5 Northern and Central Europe/Scandinavia

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

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

7.1.2.6 Southern Europe/Balkans

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

7.1.2.7 Prospects for the Future

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

7.2 BATS

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

7.2.1 FILOVIRUSES

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

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

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

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

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

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

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

TABLE 7.2
Bats Screened for Filoviruses with Negative Results

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

(continued)

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

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

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

(continued)

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

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

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

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

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

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

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

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

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

TABLE 7.3
Evidence for an Association of Filoviruses with Bats

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

(continued)

TABLE 7.3 (continued)

Evidence for an Association of Filoviruses with Bats

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

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

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

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

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

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

DISCLAIMER

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REFERENCES

- Abu Sin, M., Stark, K., van Treeck, U., Dieckmann, H., Uphoff, H., Hautmann, W., Bornhofen, B., Jensen, E., Pfaff, G., Koch, J., 2007. Risk factors for hantavirus infection in Germany, 2005. *Emerg Infect Dis* **13**, 1364–1366.
- Adams, M.J., Carstens, E.B., 2012. Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2012). *Arch Virol* **157**, 1411–1422.
- Adjemian, J., Farnon, E.C., Tschioke, F., Wamala, J.F., Byaruhanga, E., Bwire, G.S., Kansime, E. et al., 2011. Outbreak of Marburg hemorrhagic fever among miners in Kamwenge and Ibanda districts, Uganda, 2007. *J Infect Dis* **204**(suppl. 3), S796–S799.
- Agnarsson, I., Zambrana-Torrel, C.M., Flores-Saldana, N.P., May-Collado, L.J., 2011. A time-calibrated species-level phylogeny of bats (Chiroptera, Mammalia). *PLoS Curr* **3**, RRN1212.
- Avsic-Zupanc, 1998. Hantaviruses and hemorrhagic fever with renal syndrome in the Balkans, in: J.F. Saluzzo, B.D. (Ed.), *Emergence and Control of Rodent-borne Viral Diseases (Hantaviral and Arenal Diseases)*. Elsevier, Veyrier-du-lac, Annecy, France, pp. 93–98.
- Avsic-Zupanc, T., Xiao, S.Y., Stojanovic, R., Gligic, A., van der Groen, G., LeDuc, J.W., 1992. Characterization of Dobrava virus: A Hantavirus from Slovenia, Yugoslavia. *J Med Virol* **38**, 132–137.
- Bausch, D.G., Nichol, S.T., Muyembe-Tamfum, J.J., Borchert, M., Rollin, P.E., Sleurs, H., Campbell, P. et al., for the International Scientific and Technical Committee for Marburg Hemorrhagic Fever Control in the Democratic Republic of the Congo, 2006. Marburg hemorrhagic fever associated with multiple genetic lineages of virus. *New Engl J Med* **355**, 909–919.
- Benda, P., Aulagnier, S., Hutson, A.M., Amr, Z.S., Kock, D., Sharifi, M., Karatas, A., Mickleburgh, S., Bergmans, W., Howell, K., 2008. *Rousettus aegyptiacus*, IUCN 2012. IUCN Red List of Threatened Species. Version 2012.1. www.iucnredlist.org. Downloaded on July 16, 2012.

- Biek, R., Walsh, P.D., Leroy, E.M., Real, L.A., 2006. Recent common ancestry of Ebola Zaire virus found in a bat reservoir. *PLoS Pathog* **2**, e90.
- Bowen, M.D., Peters, C.J., Nichol, S.T., 1996. The phylogeny of New World (Tacaribe complex) arenaviruses. *Virology* **219**, 285–290.
- Breman, J.G., Johnson, K.M., van der Groen, G., Robbins, C.B., Szczeniowski, M.V., Ruti, K., Webb, P.A. et al., 1999. A search for Ebola virus in animals in the democratic Republic of the Congo and Cameroon: Ecologic, Virologic, and Serologic Surveys, 1979–1980. *J Infect Dis* **179**(suppl. 1), S139–S147.
- Briese, T., Paweska, J.T., McMullan, L.K., Hutchison, S.K., Street, C., Palacios, G., Khristova, M.L. et al., 2009. Genetic detection and characterization of Lujo virus, a new hemorrhagic fever-associated arenavirus from southern Africa. *PLoS Pathog* **5**, e1000455.
- Brummer-Korvenkontio, M., Henttonen, H., Vaheri, A., 1982. Hemorrhagic fever with renal syndrome in Finland: Ecology and virology of nephropathia epidemica. *Scand J Infect Dis Suppl* **36**, 88–91.
- Brummer-Korvenkontio, M., Vaheri, A., Hovi, T., von Bonsdorff, C.H., Vuorimies, J., Manni, T., Penttinen, K., Oker-Blom, N., Lahdevirta, J., 1980. Nephropathia epidemica: Detection of antigen in bank voles and serologic diagnosis of human infection. *J Infect Dis* **141**, 131–134.
- Buchmeier, M.J., de La Torre, J.C., Peters, C.J., 2006. Arenaviridae: The viruses and their replication. In: Knipe, D.M., Howley, P.M. (Eds.). *Fields Virology*, 5th edn. Lippincott Williams & Wilkins, Philadelphia, PA, pp. 1791–1827.
- van Cakenberghe, V., de Vree, F., Leirs, H., 1999. On a collection of bats (Chiroptera) from Kikwit, Democratic Republic of the Congo. With French abstract. *Mammalia* **63**, 291–322.
- Calisher, C.H., Childs, J.E., Field, H.E., Holmes, K.V., Schountz, T., 2006. Bats: Important reservoir hosts of emerging viruses. *Clin Microbiol Rev* **19**, 531–545.
- Calisher, C.H., Holmes, K.V., Dominguez, S.R., Schountz, T., Cryan, P., 2008. Bats prove to be rich reservoirs for emerging viruses. *Microbe* (Washington, DC) **3**, 521–528.
- Carballal, G., Videla, C.M., Merani, M.S., 1988. Epidemiology of Argentine hemorrhagic fever. *Eur J Epidemiol* **4**, 259–274.
- Centers for Disease Control and Prevention, 2009. Imported case of Marburg hemorrhagic fever—Colorado, 2008. *MMWR Morb Mortal Wkly Rep* **58**, 1377–1381.
- Charrel, R.N., de Lamballerie, X., 2003. Arenaviruses other than Lassa virus. *Antiviral Res* **57**, 89–100.
- Charrel, R.N., Lemasson, J.J., Garbutt, M., Khelifa, R., De Micco, P., Feldmann, H., de Lamballerie, X., 2003. New insights into the evolutionary relationships between arenaviruses provided by comparative analysis of small and large segment sequences. *Virology* **317**, 191–196.
- Clegg, J.C., 2002. Molecular phylogeny of the arenaviruses. *Curr Top Microbiol Immunol* **262**, 1–24.
- Coetsee, C.G., 1975. The biology, behaviour, and ecology of *Mastomys natalensis* in southern Africa. *Bull WHO* **52**, 637–644.
- Csorba, G., Rosell-Ambal, G., Ingle, N., 2008. *Rousettus amplexicaudatus*, IUCN 2012. IUCN Red List of Threatened Species. Version 2012.1. www.iucnredlist.org. Downloaded on July 16, 2012.
- Delgado, S., Erickson, B.R., Agudo, R., Blair, P.J., Vallejo, E., Albarino, C.G., Vargas, J. et al., 2008. Chapare virus, a newly discovered arenavirus isolated from a fatal hemorrhagic fever case in Bolivia. *PLoS Pathog* **4**, e1000047.
- Demby, A.H., Inapogui, A., Kargbo, K., Koninga, J., Kourouma, K., Kanu, J., Coulibaly, M. et al., 2001. Lassa fever in Guinea: II. Distribution and prevalence of Lassa virus infection in small mammals. *Vector Borne Zoonotic Dis* **1**, 283–297.
- DisWeb, C.D.I.S., 2003. Communicable diseases statistics. Major statistics, reported cases by year National Institutes of Health.
- Downs, W.G., Anderson, C.R., Spence, L., Aitken, T.H., Greenhall, A.H., 1963. Tacaribe virus, a new agent isolated from Artibeus bats and mosquitoes in Trinidad, West Indies. *Am J Trop Med Hyg* **12**, 640–646.
- Dybas, C.L., 2007. Russia Sees III Effects of ‘General Winter’s’ Retreat, Washington Post.
- Enria, D.A., Briggiler, A.M., Sanchez, Z., 2008. Treatment of Argentine hemorrhagic fever. *Antiviral Res* **78**, 132–139.
- Erickson, B.R., Delgado, S., Aguda, R., Vallejo, E., Vargas, J., Blair, P.J., Albarino, C. et al., 2006. A newly discovered arenavirus associated with a fatal hemorrhagic fever case in Bolivia, Abstracts of the *XIIIth International Conference on Negative Strand Viruses*, Salamanca, Spain, p. 165.
- Fang, L., Yan, L., Liang, S., de Vlas, S.J., Feng, D., Han, X., Zhao, W. et al., 2006. Spatial analysis of hemorrhagic fever with renal syndrome in China. *BMC Infect Dis* **6**, 77.
- Fichet-Calvet, E., Lecompte, E., Koivogui, L., Daffis, S., Ter Meulen, J., 2008. Reproductive characteristics of *Mastomys natalensis* and Lassa virus prevalence in Guinea, West Africa. *Vector Borne Zoonotic Dis* **8**, 41–48.

- Fichet-Calvet, E., Lecompte, E., Koivogui, L., Soropogui, B., Dore, A., Kourouma, F., Sylla, O., Daffis, S., Koulemou, K., Ter Meulen, J., 2007. Fluctuation of abundance and Lassa virus prevalence in *Mastomys natalensis* in Guinea, West Africa. *Vector Borne Zoonotic Dis* **7**, 119–128.
- Fichet-Calvet, E., Rogers, D.J., 2009. Risk maps of Lassa fever in west Africa. *PLoS Negl Trop Dis* **3**, e388.
- Fulhorst, C.E., Bowen, M.D., Salas, R.A., de Manzione, N.M., Duno, G., Utrera, A., Ksiazek, T.G. et al., 1997. Isolation and characterization of pirital virus, a newly discovered South American arenavirus. *Am J Trop Med Hyg* **56**, 548–553.
- Fulhorst, C.F., Cajimat, M.N.B., Milazzo, M.L., Paredes, H., de Manzione, N.M.C., Salas, R.A., Rollin, P.E., Ksiazek, T.G., 2008. Genetic diversity between and within the arenavirus species indigenous to western Venezuela. *Virology* **378**, 205–213.
- Fulhorst, C.F., Ksiazek, T.G., Peters, C.J., Tesh, R.B., 1999. Experimental infection of the cane mouse *Zygodontomys brevicauda* (family Muridae) with Guanarito virus (*Arenaviridae*), the etiologic agent of Venezuelan hemorrhagic fever. *J Infect Dis* **180**, 966–969.
- García, J., Calderon, G., Sabattini, M., Enria, D., 1996. Infección por virus Junin (JV) de *Calomys musculinus* (Cm) en áreas con diferente situación epidemiológica para la Fiebre Hemorrágica Argentina (FHA). *Medicina (B Aires)* **56**, 624.
- Germain, M., 1978. Collection of mammals and arthropods during the epidemic of haemorrhagic fever in Zaire. In: Pattyn, S.R. (Ed.), *Ebola Virus Haemorrhagic Fever—Proceedings of an International Colloquium on Ebola Virus Infection and Other Haemorrhagic Fevers held in Antwerp, Belgium, December 6–8, 1977*. Elsevier, Amsterdam, the Netherlands, pp. 185–189.
- Grard, G., Biek, R., Muyembe Tamfum, J.J., Fair, J., Wolfe, N., Formenty, P., Paweska, J., Leroy, E., 2011. Emergence of divergent Zaire Ebola virus strains in Democratic Republic of the Congo in 2007 and 2008. *J Infect Dis* **204**(suppl. 3), S776–S784.
- Gresikova, M., Rajcani, J., Sekeyova, M., Brummer-Korvenkontio, M., Kozuch, O., Labuda, M., Turek, R., Weismann, P., Nosek, J., Lysy, J., 1984. Haemorrhagic fever virus with renal syndrome in small rodents in Czechoslovakia. *Acta Virol* **28**, 416–421.
- van der Groen, G., Piot, P., Desmyter, J., Colaert, J., Muylle, L., Tkachenko, E.A., Ivanov, A.P., Verhagen, R., van Ypersele de Strihou, C., 1983. Seroepidemiology of Hantaan-related virus infections in Belgian populations. *Lancet* **2**, 1493–1494.
- Hayman, D.T., Emmerich, P., Yu, M., Wang, L.F., Suu-Ire, R., Fooks, A.R., Cunningham, A.A., Wood, J.L., 2010. Long-term survival of an urban fruit bat seropositive for Ebola and Lagos bat viruses. *PLoS One* **5**, e11978.
- Hayman, D.T., Yu, M., Cramer, G., Wang, L.F., Suu-Ire, R., Wood, J.L., Cunningham, A.A., 2012. Ebola virus antibodies in fruit bats, Ghana, West Africa. *Emerg Infect Dis* **18**, 1207–1209.
- Henderson, W.W., Monroe, M.C., St Jeor, S.C., Thayer, W.P., Rowe, J.E., Peters, C.J., Nichol, S.T., 1995. Naturally occurring Sin Nombre virus genetic reassortants. *Virology* **214**, 602–610.
- Heyman, P., Ceianu, C.S., Christova, I., Tordo, N., Beersma, M., Joao Alves, M., Lundkvist, A. et al., 2011. A five-year perspective on the situation of haemorrhagic fever with renal syndrome and status of the hantavirus reservoirs in Europe, 2005–2010. *Euro Surveill* **16**(36).
- Heyman, P., Cochez, C., Ducoffre, G., Mailles, A., Zeller, H., Abu Sin, M., Koch, J. et al., 2007. Haemorrhagic Fever with Renal Syndrome: An analysis of the outbreaks in Belgium, France, Germany, the Netherlands and Luxembourg in 2005. *Euro surveillance: Bulletin europeen sur les maladies transmissibles = Eur. Commun. Dis. Bull.* **12**, E15–E16.
- Hooper, J.W., Ferro, A.M., Wahl-Jensen, V., 2008. Immune serum produced by DNA vaccination protects hamsters against lethal respiratory challenge with Andes virus. *J Virol* **82**, 1332–1338.
- Hugot, J.P., Gonzalez, J.P., Denys, C., 2001. Evolution of the Old World Arenaviridae and their rodent hosts: Generalized host-transfer or association by descent? *Infect Genet Evol* **1**, 13–20.
- Isaacson, M., 1975. The ecology of *Praomys (Mastomys) natalensis* in southern Africa. *Bull World Health Organ* **52**, 629–636.
- Jay, M.T., Glaser, C., Fulhorst, C.F., 2005. The arenaviruses. *J Am Vet Med Assoc* **227**, 904–915.
- Johnson, K.M., 2001. Hantaviruses: History and overview. *Curr Top Microbiol Immunol* **256**, 1–14.
- Johnson, E.D., Johnson, B.K., Silverstein, D., Tukei, P., Geisbert, T.W., Sanchez, A., Jahrling, P.B., 1996. Characterization of a new Marburg virus isolate from a 1987 fatal case in Kenya. In: Schwarz, T.F., Siegl, G. (Eds.), *Imported Virus Infections*. Springer-Verlag, Vienna, Austria, pp. 101–114.
- Johnson, K.M., Kuns, M.L., Mackenzie, R.B., Webb, P.A., Yunker, C.E., 1966. Isolation of Machupo virus from wild rodent *Calomys callosus*. *Am J Trop Med Hyg* **15**, 103–106.
- Johnson, K.M., Mackenzie, R.B., Webb, P.A., Kuns, M.L., 1965. Chronic infection of rodents by Machupo virus. *Science (New York)* **150**, 1618–1619.

- Jordan, I., Horn, D., Oehmke, S., Leendertz, F.H., Sandig, V., 2009. Cell lines from the Egyptian fruit bat are permissive for modified vaccinia Ankara. *Virus Res* **145**, 54–62.
- Jordan, I., Munster, V.J., Sandig, V., 2012. Authentication of the R06E fruit bat cell line. *Viruses* **4**, 889–900.
- Jung, Y.T., Kim, G.R., 1995. Genomic characterization of M and S RNA segments of hantaviruses isolated from bats. *Acta Virol* **39**, 231–233.
- Justines, G., Johnson, K.M., 1969. Immune tolerance in *Calomys callosus* infected with Machupo virus. *Nature* **222**, 1090–1091.
- Kallio, E.R., Voutilainen, L., Vapalahti, O., Vaheri, A., Henttonen, H., Koskela, E., Mappes, T., 2007. Endemic hantavirus infection impairs the winter survival of its rodent host. *Ecology* **88**, 1911–1916.
- Kariwa, H., Yoshimatsu, K., Arikawa, J., 2007. Hantavirus infection in East Asia. *Comp Immunol Microbiol Infect Dis* **30**, 341–356.
- Keenlyside, R.A., McCormick, J.B., Webb, P.A., Smith, E., Elliott, L., Johnson, K.M., 1983. Case-control study of *Mastomys natalensis* and humans in Lassa virus-infected households in Sierra Leone. *Am J Trop Med Hyg* **32**, 829–837.
- Klempa, B., Meisel, H., Rath, S., Bartel, J., Ulrich, R., Kruger, D.H., 2003. Occurrence of renal and pulmonary syndrome in a region of northeast Germany where Tula hantavirus circulates. *J Clin Microbiol* **41**, 4894–4897.
- Krähling, V., Dolnik, O., Kolesnikova, L., Schmidt-Chanasit, J., Jordan, I., Sandig, V., Gunther, S., Becker, S., 2010. Establishment of fruit bat cells (*Rousettus aegyptiacus*) as a model system for the investigation of filoviral infection. *PLoS Negl Trop Dis* **4**, e802.
- Kuhl, A., Hoffmann, M., Muller, M.A., Munster, V.J., Gnirss, K., Kiene, M., Tsegaye, T.S. et al., 2011. Comparative analysis of Ebola virus glycoprotein interactions with human and bat cells. *J Infect Dis* **204**(suppl. 3), S840–S849.
- Kuhn, J.H., 2008. Filoviruses. A compendium of 40 years of epidemiological, clinical, and laboratory studies. *Arch Virol Suppl* **20**. Springer Wien New York, Vienna, Austria.
- Kuhn, J.H., Becker, S., Ebihara, H., Geisbert, T.W., Jahrling, P.B., Kawaoka, Y., Netesov, S.V. et al., 2011. Family *Filoviridae*. In: King, A.M.Q., Adams, M.J., Carstens, E.B., Lefkowitz, E.J. (Eds.), *Virus Taxonomy—Ninth Report of the International Committee on Taxonomy of Viruses*. Elsevier/Academic Press, London, U.K., pp. 665–671.
- Kuhn, J.H., Becker, S., Ebihara, H., Geisbert, T.W., Johnson, K.M., Kawaoka, Y., Lipkin, W.I. et al., 2010. Proposal for a revised taxonomy of the family *Filoviridae*: Classification, names of taxa and viruses, and virus abbreviations. *Arch Virol* **155**, 2083–2103.
- Kuns, M.L., 1965. Epidemiology of Machupo virus infection. II. Ecological and control studies of hemorrhagic fever. *Am J Trop Med Hyg* **14**, 813–816.
- Kuzmin, I.V., Bozick, B., Guagliardo, S.A., Kunkel, R., Shak, J.R., Tong, S., Rupprecht, C.E., 2011. Bats, emerging infectious diseases, and the rabies paradigm revisited. *Emerg Health Threats J* **4**, 7159.
- Lalis, A., Leblois, R., Lecompte, E., Denys, C., Ter Meulen, J., Wirth, T., 2012. The impact of human conflict on the genetics of *Mastomys natalensis* and Lassa virus in West Africa. *PLoS One* **7**, e37068.
- Laming, F., Prinz, A., 2010. Bats and other reservoir hosts of *Filoviridae*. Danger of epidemic on the African continent? A deductive literature analysis. *Wien Klin Wochenschr* **122**(suppl. 3), 19–30.
- Lecompte, E., Fichet-Calvet, E., Daffis, S., Koulemou, K., Sylla, O., Kourouma, F., Dore, A. et al., 2006. *Mastomys natalensis* and Lassa fever, West Africa. *Emerg Infect Dis* **12**, 1971–1974.
- Lecompte, E., Ter Meulen, J., Emonet, S., Daffis, S., Charrel, R.N., 2007. Genetic identification of Kodoko virus, a novel arenavirus of the African pigmy mouse (*Mus Nannomys minutoides*) in West Africa. *Virology* **364**, 178–183.
- Lee, H.W., 1996. Hantaviruses: An emerging disease. *Phil J Microbiol Infect Dis* **25**, S19–S24.
- Lee, H.W., Lee, P.W., Johnson, K.M., 1978. Isolation of the etiologic agent of Korean hemorrhagic fever. *J Infect Dis* **137**, 298–308.
- Lee, J.S., Lahdevirta, J., Koster, F., Levy, H., 1999. Clinical manifestations and treatment of HFRS and HPS. In: Lee, H.W., Calisher, C., Schmaljohn, C. (Eds.), *Manual of Hemorrhagic Fever with Renal Syndrome and Hantavirus Pulmonary Syndrome*. ASAN Institute for Life Sciences, Seoul, South Korea, pp. 17–38.
- Leirs, H., Mills, J.N., Krebs, J.W., Childs, J.E., Akaibe, D., Woollen, N., Ludwig, G. et al., 1999. Search for the Ebola virus reservoir in Kikwit, democratic Republic of the Congo: Reflections on a vertebrate collection. *J Infect Dis* **179**(suppl. 1), S155–S163.
- Leroy, E.M., Epelboin, A., Mondonge, V., Pourrut, X., Gonzalez, J.P., Muyembe-Tamfum, J.J., Formenty, P., 2009. Human Ebola outbreak resulting from direct exposure to fruit bats in Luebo, Democratic Republic of Congo, 2007. *Vector Borne Zoonotic Dis* **9**, 723–728.

- Leroy, E.M., Kumulungui, B., Pourrut, X., Rouquet, P., Hassanin, A., Yaba, P., Délicat, A., Paweska, J.T., Gonzalez, J.-P., Swanepoel, R., 2005. Fruit bats as reservoirs of Ebola virus. *Nature* **438**, 575–576.
- Li, D., Schmaljohn, A.L., Anderson, K., Schmaljohn, C.S., 1995. Complete nucleotide sequences of the M and S segments of two hantavirus isolates from California: Evidence for reassortment in nature among viruses related to hantavirus pulmonary syndrome. *Virology* **206**, 973–983.
- Lundkvist, A., Hukic, M., Horling, J., Gilljam, M., Nichol, S., Niklasson, B., 1997. Puumala and Dobrava viruses cause hemorrhagic fever with renal syndrome in Bosnia-Herzegovina: Evidence of highly cross-neutralizing antibody responses in early patient sera. *J Med Virol* **53**, 51–59.
- Lyubsky, S., Gavrilovskaya, I., Luft, B., Mackow, E., 1996. Histopathology of *Peromyscus leucopus* naturally infected with pathogenic NY-1 hantaviruses: Pathologic markers of HPS viral infection in mice. *Lab Invest J Tech Methods Pathol* **74**, 627–633.
- Maganga, G.D., Bourgarel, M., Ebang Ella, G., Drexler, J.F., Gonzalez, J.P., Drosten, C., Leroy, E.M., 2011. Is Marburg virus enzootic in Gabon? *J Infect Dis* **204**(suppl. 3), S800–S803.
- Maiztegui, J.I., 1975. Clinical and epidemiological patterns of Argentine haemorrhagic fever. *Bull World Health Organ* **52**, 567–575.
- de Manzione, N., Salas, R.A., Paredes, H., Godoy, O., Rojas, L., Araoz, F., Fulhorst, C.F. et al., 1998. Venezuelan hemorrhagic fever: Clinical and epidemiological studies of 165 cases. *Clin Infect Dis* **26**, 308–313.
- McCormick, J.B., Fisher-Hoch, S.P., 2002. Lassa fever. *Curr Top Microbiol Immunol* **262**, 75–109.
- McCormick, J.B., Webb, P.A., Krebs, J.W., Johnson, K.M., Smith, E.S., 1987. A prospective study of the epidemiology and ecology of Lassa fever. *J Infect Dis* **155**, 437–444.
- Mercado, R., 1975. Rodent control programmes in areas affected by Bolivian haemorrhagic fever. *Bull World Health Organ* **52**, 691–696.
- Messenger, S.L., Rupprecht, C.E., Smith, J.S., 2003. Bats, emerging virus infections, and the rabies paradigm. In: Kunz, T.H., Fenton, M.B. (Eds.), *Bat Ecology*. The University of Chicago Press, Chicago, IL, pp. 622–679.
- Milazzo, M.L., Cajimat, M.N.B., Duno, G., Duno, F., Utrera, A., Fulhorst, C.F., 2011. Transmission of Guanarito and Pirital viruses among wild rodents, Venezuela. *Emerg Infect Dis* **17**, 2209–2215.
- Mills, J.N., Ellis, B.A., Childs, J.E., McKee, K.T., Jr., Maiztegui, J.I., Peters, C.J., Ksiazek, T.G., Jahrling, P.B., 1994. Prevalence of infection with Junin virus in rodent populations in the epidemic area of Argentine hemorrhagic fever. *Am J Trop Med Hyg* **51**, 554–562.
- Mills, J.N., Ellis, B.A., McKee, K.T., Jr., Calderon, G.E., Maiztegui, J.I., Nelson, G.O., Ksiazek, T.G., Peters, C.J., Childs, J.E., 1992. A longitudinal study of Junin virus activity in the rodent reservoir of Argentine hemorrhagic fever. *Am J Trop Med Hyg* **47**, 749–763.
- Mills, J.N., Ellis, B.A., McKee, K.T., Jr., Ksiazek, T.G., Oro, J.G., Maiztegui, J.I., Calderon, G.E., Peters, C.J., Childs, J.E., 1991. Junin virus activity in rodents from endemic and nonendemic loci in central Argentina. *Am J Trop Med Hyg* **44**, 589–597.
- Monath, T.P., 1999. Ecology of Marburg and Ebola Viruses: Speculations and Directions for Future Research. *J Infect Dis* **179**(suppl. 1), S127–S138.
- Monath, T.P., Newhouse, V.F., Kemp, G.E., Setzer, H.W., Cacciapuoti, A., 1974. Lassa virus isolation from *Mastomys natalensis* rodents during an epidemic in Sierra Leone. *Science* (Washington, DC) **185**, 263–265. PMID: 4833828.
- Mulic, R., Ropac, D., 2002. Epidemiologic characteristics and military implications of hemorrhagic fever with renal syndrome in Croatia. *Croat Med J* **43**, 581–586.
- Negredo, A., Palacios, G., Vazquez-Moron, S., Gonzalez, F., Dopazo, H., Molero, F., Juste, J. et al., 2011. Discovery of an ebolavirus-like filovirus in Europe. *PLoS Pathog* **7**, e1002304.
- Netski, D., Thran, B.H., St Jeor, S.C., 1999. Sin Nombre virus pathogenesis in *Peromyscus maniculatus*. *J Virol* **73**, 585–591.
- Niklasson, B., Hornfeldt, B., Mullaart, M., Settergren, B., Tkachenko, E., Myasnikov Yu. A., Ryltceva, E.V., Leschinskaya, E., Malkin, A., Dzagurova, T., 1993. An epidemiologic study of hemorrhagic fever with renal syndrome in Bashkortostan (Russia) and Sweden. *Am J Trop Med Hyg* **48**, 670–675.
- Nowak, R.M., Walker, E.P., 1994. *Walker's Bats of the World*. Johns Hopkins University Press, Baltimore, MD.
- Okumura, M., Yoshimatsu, K., Kumperasart, S., Nakamura, I., Ogino, M., Taruishi, M., Sungdee, A. et al., 2007. Development of serological assays for Thottapalayam virus, an insectivore-borne Hantavirus. *Clin Vaccine Immunol* **14**, 173–181.
- Olds, N., 1988. A revision of the genus *Calomys* (Rodentia: Muridae). PhD dissertation. University of New York, New York.
- Oldstone, M.B., 2002. Arenaviruses. I. The epidemiology molecular and cell biology of arenaviruses. Introduction. *Curr Top Microbiol Immunol* **262**, V–XII.

- Omatsu, T., Watanabe, S., Akashi, H., Yoshikawa, Y., 2007. Biological characters of bats in relation to natural reservoir of emerging viruses. *Comp Immunol Microbiol Infect Dis* **30**, 357–374.
- Pensiero, M.N., Sharefkin, J.B., Dieffenbach, C.W., Hay, J., 1992. Hantaan virus infection of human endothelial cells. *J Virol* **66**, 5929–5936.
- Peralta, L.A., Laguens, R.P., Cossio, P.M., Sabattini, M.S., Maiztegui, J.I., Arana, R.M., 1979. Presence of viral particles in the salivary gland of *Calomys musculinus* infected with Junin virus by a natural route. *Intervirology* **11**, 111–116.
- Peterson, A.T., Bauer, J.T., Mills, J.N., 2004. Ecologic and geographic distribution of Filovirus disease. *Emerg Infect Dis* **10**, 40–47.
- Peterson, A.T., Ryan Lash, R., Carroll, D.S., Johnson, K.M., 2006. Geographical potential for outbreaks of Marburg hemorrhagic fever. *Am J Trop Med Hyg* **75**, 9–15.
- Pettersson L., K.J., Hardestam J, Lundkvist Å, Ahlm C, Evander M., 2008. Hantavirus RNA in saliva from patients with hemorrhagic fever with renal syndrome. *Emerg Infect Dis* **14**(3), 406–411.
- Pourrut, X., Delicat, A., Rollin, P.E., Ksiazek, T.G., Gonzalez, J.P., Leroy, E.M., 2007. Spatial and temporal patterns of Zaire ebolavirus antibody prevalence in the possible reservoir bat species. *J Infect Dis* **196**(suppl. 2), S176–S183.
- Pourrut, X., Leroy, E., Gonzalez, J.P., 2006. Ebola: From bats to Gorillas. *Gorilla J* **19**.
- Pourrut, X., Souris, M., Towner, J.S., Rollin, P.E., Nichol, S.T., Gonzalez, J.P., Leroy, E., 2009. Large serological survey showing cocirculation of Ebola and Marburg viruses in Gabonese bat populations, and a high seroprevalence of both viruses in *Rousettus aegyptiacus*. *BMC Infect Dis* **9**, 159.
- Rowe, W.P., Pugh, W.E., Webb, P.A., Peters, C.J., 1970. Serological relationship of the Tacaribe complex of viruses to lymphocytic choriomeningitis virus. *J Virol* **5**, 289–292.
- Sabattini, M.S., Gonzalez, L.E., 1967. Direct identification of Junin's virus in infected wild rodents in nature. *Rev Soc Argent Biol* **43**, 252–260.
- Sabattini, M.S., Gonzales del Rio, L., Diaz, G., Vega, V.R., 1977. Infeccion natural y experimental de roedores con virus Junin. *Medicina (B Aires)* **37** (suppl. 3), 149–161.
- Salazar-Bravo, J., Dragoo, J.W., Bowen, M.D., Peters, C.J., Ksiazek, T.G., Yates, T.L., 2002a. Natural nidality in Bolivian hemorrhagic fever and the systematics of the reservoir species. *Infect Genet Evol* **1**, 191–199.
- Salazar-Bravo, J., Ruedas, L.A., Yates, T.L., 2002b. Mammalian reservoirs of arenaviruses. *Curr Top Microbiol Immunol* **262**, 25–63.
- Salvato, M.S., Clegg, J.C.S., Buchmeier, M.J., Charrel, R.N., Gonzalez, J.P., Lukashevich, I.S., Peters, C.J., Romanowski, V., 2011. Family *Arenaviridae*. In: King, A.M.Q., Adams, M.J., Carstens, E.B., Lefkowitz, E.J. (Eds.), *Virus Taxonomy—Ninth Report of the International Committee on Taxonomy of Viruses*. Elsevier, London, U.K., pp. 715–723.
- Settergren, B., Juto, P., Wadell, G., Trollfors, B., Norrby, S.R., 1988. Incidence and geographic distribution of serologically verified cases of nephropathia epidemica in Sweden. *Am J Epidemiol* **127**, 801–807.
- Simmons, N.B., 2005. Order Chiroptera. In: Wilson, D.E., Reeder, D.M. (Eds.), *Mammal Species of the World: A Taxonomic and Geographic Reference*, 3rd edn. Johns Hopkins University Press, Baltimore, MD.
- Sinclair, J.R., Carroll, D.S., Montgomery, J.M., Pavlin, B., McCombs, K., Mills, J.N., Comer, J.A. et al., 2007. Two cases of hantavirus pulmonary syndrome in Randolph County, West Virginia: A coincidence of time and place? *Am J Trop Med Hyg* **76**, 438–442.
- Sluydts, V., Crespin, L., Davis, S., Lima, M., Leirs, H., 2007. Survival and maturation rates of the African rodent, *Mustomys natalensis*: Density-dependence and rainfall. *Integr Zool* **2**, 220–232.
- Smith, D.H., Johnson, B.K., Isaacson, M., Swanepoel, R., Johnson, K.M., Killey, M., Bagshawe, A., Siongok, T., Koinange Keruga, W., 1982. Marburg-virus disease in Kenya. *Lancet* **319**, 816–820.
- Strong, J.E., Wong, G., Jones, S.E., Grolla, A., Theriault, S., Kobinger, G.P., Feldmann, H., 2008. Stimulation of Ebola virus production from persistent infection through activation of the Ras/MAPK pathway. *Proc Natl Acad Sci U S A* **105**, 17982–17987.
- Sumibcay, L., Kadjo, B., Gu, S.H., Kang, H.J., Lim, B.K., Cook, J.A., Song, J.W., Yanagihara, R., 2012. Divergent lineage of a novel hantavirus in the banana pipistrelle (*Neoromicia nanus*) in Cote d'Ivoire. *Virol J* **9**, 34.
- Swanepoel, R., Leman, P.A., Burt, F.J., Zachariades, N.A., Braack, L.E.O., Ksiazek, T.G., Rollin, P.E., Zaki, S.R., Peters, C.J., 1996. Experimental inoculation of plants and animals with Ebola virus. *Emerg Infect Dis* **2**, 321–325.
- Taniguchi, S., Watanabe, S., Masangkay, J.S., Omatsu, T., Ikegami, T., Alviola, P., Ueda, N. et al., 2011. Reston ebolavirus antibodies in bats, the Philippines. *Emerg Infect Dis* **17**, 1559–1560.
- Teeling, E.C., Springer, M.S., Madsen, O., Bates, P., O'Brien S, J., Murphy, W.J., 2005. A molecular phylogeny for bats illuminates biogeography and the fossil record. *Science (New York)* **307**, 580–584.

- Ter Meulen, J., Lukashevich, I., Sidibe, K., Inapogui, A., Marx, M., Dorlemann, A., Yansane, M.L., Koulemou, K., Chang-Claude, J., Schmitz, H., 1996. Hunting of peridomestic rodents and consumption of their meat as possible risk factors for rodent-to-human transmission of Lassa virus in the Republic of Guinea. *Am J Trop Med Hyg* **55**, 661–666.
- Tesh, R.B., Wilson, M.L., Salas, R., De Manzione, N.M., Tovar, D., Ksiazek, T.G., Peters, C.J., 1993. Field studies on the epidemiology of Venezuelan hemorrhagic fever: Implication of the cotton rat *Sigmodon alstoni* as the probable rodent reservoir. *Am J Trop Med Hyg* **49**, 227–235.
- Timen, A., Koopmans, M.P.G., Vossen, A.C.T.M., van Doornum, G.J.J., Gunther, S., van den Berkmortel, F., Verduin, K.M. et al., 2009. Response to imported case of Marburg hemorrhagic fever, the Netherlands. *Emerg Infect Dis* **15**, 1171–1175.
- Tkachenko, E., Dekonenko, A., Ivanov, A., Dzagouva, T., Ivanov, L., Slonova, R., Nurgaleeva, R., Stepanenko, A., Ivanidze, E., Zagidullin, I., 1998. Hemorrhagic fever with renal syndrome and hantaviruses in Russia. In: J.F. Saluzzo, B.D. (Ed.), *Emergence and Control of Rodent-Borne Viral Diseases (Hantaviral and Arenal Diseases)*. Elsevier, Veyrier-du-lac, Annecy, France, pp. 63–72.
- Tkachenko, E., Ivanidze, E., Zagidullin, I., Dekonenko, A., 1999. HFRS in Eurasia: Russia and the Republics of the former USSR. In: H. W. Lee, C.C., C. Schmaljohn (Ed.), *Manual of Hemorrhagic Fever with Renal Syndrome and Hantavirus Pulmonary Syndrome*. WHO Collaborating Center for Virus Reference and Research (Hantaviruses), Asian Institute for Life Sciences, Seoul, pp. 49–57.
- Towner, J.S., Amman, B.R., Sealy, T.K., Carroll, S.A., Comer, J.A., Kemp, A., Swanepoel, R. et al., 2009. Isolation of genetically diverse Marburg viruses from Egyptian fruit bats. *PLoS Pathog* **5**, e1000536.
- Towner, J.S., Pourrut, X., Albariño, C.G., Nkogue, C.N., Bird, B.H., Grard, G., Ksiazek, T.G., Gonzalez, J.-P., Nichol, S.T., Leroy, E.M., 2007. Marburg virus infection detected in a common African bat. *PLoS One* **2**, e764.
- Vapalahti, O., Lundkvist, A., Kukkonen, S.K., Cheng, Y., Gilljam, M., Kanerva, M., Manni, T. et al., 1996. Isolation and characterization of Tula virus, a distinct serotype in the genus Hantavirus, family *Bunyaviridae*. *J Gen Virol* **77** (Pt 12), 3063–3067.
- Vapalahti, O., Mustonen, J., Lundkvist, A., Henttonen, H., Plyusnin, A., Vaheri, A., 2003. Hantavirus infections in Europe. *Lancet Infect Dis* **3**, 653–661.
- Vapalahti, K., Paunio, M., Brummer-Korvenkontio, M., Vaheri, A., Vapalahti, O., 1999. Puumala virus infections in Finland: Increased occupational risk for farmers. *Am J Epidemiol* **149**, 1142–1151.
- de Villafañe, G., Kravetz, F.O., Donadio, O., Persich, R., Knecher, L., Torrs, M.P., Fernandez, N., 1977. Dinámica de las comunidades de roedores en agroecosistemas pampásicos. *Medicina (B Aires)* **37**, 128–140.
- Vitullo, A.D., Hodara, V.L., Merani, M.S., 1987. Effect of persistent infection with Junin virus on growth and reproduction of its natural reservoir, *Calomys musculinus*. *Am J Trop Med Hyg* **37**, 663–669.
- Vitullo, A.D., Marani, M.S., 1987. Mecanismos de transmisión del virus Junín en su resrvorio natural, *Calomys musculinus*. *Medicina (B Aires)* **47**, 440.
- Vitullo, A.D., Merani, M.S., 1988. Is vertical transmission sufficient to maintain Junin virus in nature? *J Gen Virol* **69**, 1437–1440.
- Vitullo, A.D., Merani, M.S., 1990. Vertical transmission of Junin virus in experimentally infected adult *Calomys musculinus*. *Intervirology* **31**, 339–344.
- Walker, D.H., Wulff, H., Lange, J.V., Murphy, F.A., 1975. Comparative pathology of Lassa virus infection in monkeys, guinea-pigs, and *Mastomys natalensis*. *Bull World Health Organ* **52**, 523–534.
- Wang, L.F., Walker, P.J., Poon, L.L., 2011. Mass extinctions, biodiversity and mitochondrial function: Are bats 'special' as reservoirs for emerging viruses? *Curr Opin Virol* **1**, 649–657.
- Weaver, S.C., Salas, R.A., de Manzione, N., Fulhorst, C.F., Duno, G., Utrera, A., Mills, J.N., Ksiazek, T.G., Tovar, D., Tesh, R.B., 2000. Guanarito virus (*Arenaviridae*) isolates from endemic and outlying localities in Venezuela: Sequence comparisons among and within strains isolated from Venezuelan hemorrhagic fever patients and rodents. *Virology* **266**, 189–195.
- Webb, P.A., Justines, G., Johnson, K.M., 1975. Infection of wild and laboratory animals with Machupo and Latino viruses. *Bull World Health Organ* **52**, 493–499.
- Weiss, S., Witkowski, P.T., Auste, B., Nowak, K., Weber, N., Fahr, J., Mombouli, J.V. et al., 2012. Hantavirus in bat, Sierra Leone. *Emerg Infect Dis* **18**, 159–161.
- Wilson, D.E., Reeder, D.M., 2005. *Mammal Species of the World: A Taxonomic and Geographic Reference*. Johns Hopkins University Press, Baltimore, MD.
- Wong, S., Lau, S., Woo, P., Yuen, K.-Y., 2007. Bats as a continuing source of emerging infections in humans. *Rev Med Virol* **17**, 67–91.

- Yan, L., Fang, L.Q., Huang, H.G., Zhang, L.Q., Feng, D., Zhao, W.J., Zhang, W.Y., Li, X.W., Cao, W.C., 2007. Landscape elements and Hantaan virus-related hemorrhagic fever with renal syndrome, People's Republic of China. *Emerg Infect Dis* **13**, 1301–1306.
- Zaki, S.R., Nolte, K.B., 1999. Pathology, Immunohistochemistry and in situ hybridization. In: Lee, H.W., Calisher, C.E., Schmaljohn, C. (Eds.), *Manual of Hemorrhagic Fever with Renal Syndrome and Hantavirus Pulmonary Syndrome*. ASAN Institute for Life Sciences, Seoul, South Korea, pp. 143–154.
- Zhang, Y.Z., Zou, Y., Fu, Z.F., Plyusnin, A., 2010. Hantavirus infections in humans and animals, China. *Emerg Infect Dis* **16**, 1195–1203.

From: Kevin Olival, PhD [b6]
Sent: 6/6/2016 1:49:19 PM
To: Morens, David (NIH/NIAID) [E] [b6]
CC: Jon Epstein [b6]
Subject: Re: Viruses | Free Full-Text | Filoviruses in Bats: Current Knowledge and Future Directions | HTML

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

Kevin J. Olival, PhD
Associate Vice President for Research

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

[b6] (direct)
[b6] (mobile)
1.212.380.4465 (fax)
@nycbat (twitter)
www.ecohealthalliance.org

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

On Jun 5, 2016, at 6:51 PM, Morens, David (NIH/NIAID) [E] [b6]
wrote:

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

Thasnks,

david

David M. Morens, M.D.
CAPT, United States Public Health Service
Senior Advisor to the Director
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 [b6] (assistants: Kelley, Meaghan)
(301 496 4409)

3 [b6]

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

From: Kevin Olival, PhD [mailto:[b6]]
Sent: Sunday, June 05, 2016 6:50 PM
To: Morens, David (NIH/NIAID) [E] [b6]
Cc: Jon Epstein [b6]
Subject: Re: Viruses | Free Full-Text | Filoviruses in Bats: Current Knowledge and Future Directions | HTML

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

Best,
Kevin

On Jun 5, 2016, at 6:24 PM, Morens, David (NIH/NIAID) [E] [b6] wrote:

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

David

David M. Morens, M.D.
CAPT, United States Public Health Service Senior Advisor to the
Director Office of the Director National Institute of Allergy and
Infectious Diseases National Institutes of Health Building 31, Room
7A-03
31 Center Drive, MSC 2520
Bethesda, MD 20892-2520
B [b6] (assistants: Kelley, Meaghan) (301 496 4409
3 [b6]

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the intended recipient, any dissemination, distribution, or copying is strictly prohibited. If you have received this communication in error, please erase all copies of the message and its attachments and notify us immediately.

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

From: Kevin Olival, PhD [mailto:b6]

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

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

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

Cheers,
Kevin

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

From: Morens, David (NIH/NIAID) [E] [b6]
Sent: 6/5/2016 10:15:42 PM
To: 'Kevin Olival, PhD' [b6]
Subject: RE: Viruses | Free Full-Text | Filoviruses in Bats: Current Knowledge and Future Directions | HTML

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

David M. Morens, M.D.
CAPT, United States Public Health Service
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 [b6] (assistants: Kelley, Meaghan)
(301 496 4409
3 [b6]

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

From: Kevin Olival, PhD [mailto:[b6]]
Sent: Friday, June 03, 2016 6:39 PM
To: Morens, David (NIH/NIAID) [E] [b6]
Subject: Viruses | Free Full-Text | Filoviruses in Bats: Current Knowledge and Future Directions | HTML

Cheers,
Kevin

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

From: Jon Epstein [b6]
Sent: 1/17/2021 7:15:19 PM
To: Morens, David (NIH/NIAID) [E] [b6]
[b6]
Subject: Re: Request for support [b6] letter

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

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

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](https://twitter.com/epsteinjon)

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

--

Jonathan H. Epstein DVM, MPH, PhD

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From: Morens, David (NIH/NIAID) [E] [b6]
([b6])
Sent: 1/18/2021 9:50:06 PM
To: Jon Epstein [b6]
BCC: Morens, David (NIH/NIAID) [E] [b6]
([b6])
Subject: Re: Request for support [b6] letter
Attachments: Jonathan H Epstein full CV 2021.pdf

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

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

On Jan 18, 2021, at 16:41, Jon Epstein [b6] wrote:

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]

b6

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

b6

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,

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Thanks, in advance, for considering.

Cheers,
Jon

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From: Morens, David (NIH/NIAID) [E] [b6]
([b6])
Sent: 1/18/2021 10:21:27 PM
To: Jon Epstein [b6]
BCC: Morens, David (NIH/NIAID) [E] [b6]
([b6])
Subject: Re: Request for support [b6] letter
Attachments: Epstein NIH BioSketch R24 2021.pdf

TY. I will be on it tomorrow. Today am [b6] D

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

On Jan 18, 2021, at 17:15, Jon Epstein [b6] wrote:

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

On Mon, Jan 18, 2021 at 5:04 PM Jon Epstein [b6] wrote:
Same here - [b6]
[b6]

Stay safe :)

On Mon, Jan 18, 2021 at 5:00 PM Morens, David (NIH/NIAID) [E] [b6] wrote:
That should be all i need, if not i will get back to you. It is due by Wednesday night

[b6] No one i know at nih
has been vaccinated, only the ill patients, plus the folks taking care of covid patients plus the
nih police and fire fighters

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

On Jan 18, 2021, at 16:54, Jon Epstein [b6] wrote:

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

Jon

p.S. [b6]

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

[b6] wrote:

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

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

On Jan 18, 2021, at 16:41, Jon Epstein

[b6] wrote:

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]

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

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

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From: Jon Epstein [b6]
Sent: 2/1/2021 2:11:03 PM
To: Morens, David (NIH/NIAID) [E] [b6]
[b6]
CC: Taubenberger, Jeffery (NIH/NIAID) [E] [b6]
[b6]
Subject: Re: bioRxiv: A novel SARS-CoV-2 related coronavirus in bats from Cambodia

Hi David,

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

Cheers,
Jon

Jonathan Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
New York

(e) [b6]
(o)
(m)
[b6]

On Tue, Jan 26, 2021, 7:20 PM Morens, David (NIH/NIAID) [E] [b6] wrote:
Jon, are you aware of our niaid field group in Cambodia? The site has Rhinophilus bats and humans with sarbecovirus antibodies. They have been doing dengue work but have recently started doing a few coronavirus studies

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

Begin forwarded message:

From: "Morens, David (NIH/NIAID) [E]" [b6]
Date: January 26, 2021 at 19:15:29 EST
To: "Manning, Jessica (NIH/NIAID) [E]" [b6], "Taubenberger, Jeffery (NIH/NIAID) [E]" [b6]
Subject: Fwd: bioRxiv: A novel SARS-CoV-2 related coronavirus in bats from Cambodia

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

Begin forwarded message:

From: "Folkers, Greg (NIH/NIAID) [E]" b6
Date: January 26, 2021 at 18:59:37 EST
Subject: bioRxiv: A novel SARS-CoV-2 related coronavirus in bats from Cambodia

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

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

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

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Abstract

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

Competing Interest Statement

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

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

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

From: Jon Epstein [b6]
Sent: 1/18/2021 10:14:03 PM
To: Morens, David (NIH/NIAID) [E] [b6]
[b6]
Subject: Re: Request for support [b6] letter
Attachments: Epstein NIH BioSketch R24 2021.pdf

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

On Mon, Jan 18, 2021 at 5:04 PM Jon Epstein [b6] wrote:
[b6] have been able to get vaccinated.

[b6]

Stay safe :)

On Mon, Jan 18, 2021 at 5:00 PM Morens, David (NIH/NIAID) [E] [b6] wrote:
That should be all i need, if not i will get back to you. It is due by Wednesday night

(b) (6) [b6] No one i know at nih has been vaccinated, only the ill patients, plus the folks taking care of covid patients plus the nih police and fire fighters

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

On Jan 18, 2021, at 16:54, Jon Epstein [b6] wrote:

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

p.S. [b6]

On Mon, Jan 18, 2021 at 4:50 PM Morens, David (NIH/NIAID) [E] [b6] wrote:

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b6

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Cheers,
Jon

Describe

b6

b6

250 words

b6

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

b6

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

Thanks, in advance, for considering.

Cheers,
Jon

--

Jonathan H. Epstein DVM, MPH, PhD

Vice President for Science and Outreach

EcoHealth Alliance
520 Eighth Avenue, Ste. 1200

New York, NY 10018

b6

(direct)

(mobile)

web: ecohealthalliance.org

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

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

--

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b6

b6

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b6

b6

From: Morens, David (NIH/NIAID) [E] [b6]
([b6])
Sent: 1/20/2021 9:36:17 PM
To: Jon Epstein [b6]
BCC: Morens, David (NIH/NIAID) [E] [b6]
([b6])
Subject: Re: Request for support [b6] letter

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

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

On Jan 20, 2021, at 16:33, Jon Epstein [b6] wrote:

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

It would be good to get that grant decision reversed.

On Wed, Jan 20, 2021 at 3:32 PM Morens, David (NIH/NIAID) [E] [b6] wrote:

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

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

On Jan 20, 2021, at 15:29, Jon Epstein [b6] wrote:

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

See you soon.
-Jon

On Wed, Jan 20, 2021 at 3:24 PM Morens, David (NIH/NIAID) [E] [b6] wrote:

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

David

David M. Morens, M.D.

CAPT, United States Public Health Service

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

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From: Morens, David (NIH/NIAID) [E]
Sent: Wednesday, January 20, 2021 3:23 PM
To: Jon Epstein [b6]
Subject: RE: Request for support [b6] letter

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

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


David

David M. Morens, M.D.

CAPT, United States Public Health Service

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

 [b6] (assistant: Whitney Robinson)

 301 496 4409

 [b6]

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From: Jon Epstein [b6]
Sent: Wednesday, January 20, 2021 2:53 PM
To: Morens, David (NIH/NIAID) [E] [b6]
Subject: Re: Request for support [b6] letter

haha - I'll send 'em your way if they don't!

Anyway, that's really kind of you to say, and I'm sincerely grateful for your support, and friendship.

Cheers,

Jon

On Wed, Jan 20, 2021 at 2:48 PM Morens, David (NIH/NIAID) [E]
[b6] wrote:


Jon, will do. I just finished it but need to proof read and go over it one more time. Writing this thing reminded me all over again what a great and promising scientist you are. If the [b6] don't take you, it will be a travesty.


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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 **b6** (assistant: Whitney Robinson)

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From: Jon Epstein **b6**

Sent: Wednesday, January 20, 2021 2:45 PM

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

Subject: Re: Request for support **b6** letter

Hi David

I hope that you were able to enjoy today's events.

Would you mind ping me when you submit the **b6** letter of reference? The system won't let me submit the application until your letter is received.

Thanks,

Jon

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

b6 wrote:

TY. I will be on it tomorrow. Today am

b6 D

b6

Sent from my iPhone

David M Morens

OD, NIAID, NIH

On Jan 18, 2021, at 17:15, Jon Epstein

b6 wrote:

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

-Jon

On Mon, Jan 18, 2021 at 5:04 PM Jon Epstein

b6 wrote:

b6

b6 have been able to get vaccinated.

b6

Stay safe :)

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p.S. [b6]

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Describe

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250 words

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*EcoHealth
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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,

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From: Morens, David (NIH/NIAID) [E] [b6]
[b6]
Sent: 1/18/2021 10:12:04 PM
To: Jon Epstein [b6]
BCC: Morens, David (NIH/NIAID) [E] [b6]
[b6]
Subject: Re: Request for support [b6] letter

U2! All we have to do is [b6] and then get thru a few more months of shit, and life as we knew it will start to return. Not soon enough for me... d

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

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[b6]

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From: Jon Epstein [b6]
Sent: 9/22/2021 5:39:40 PM
To: Morens, David (NIH/NIAID) [E] [b6]
([b6])
Subject: Re: Request for support [b6] etter

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

I'm certainly as focused as ever on the work. And there's plenty to do. [b6] and please pass on my gratitude to Tony, as well.

Talk soon,
Jon

On Wed, Sep 22, 2021 at 1:16 PM Morens, David (NIH/NIAID) [E] [b6] wrote:

Jon, [b6]
[b6]

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

Slowly, an important area of science is catching up to you. [b6]


[b6]

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
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Building 31, Room 7A-03
31 Center Drive, MSC 2520
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 **b6** (assistant: Whitney Robinson)

 301 496 4409

 **b6**

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From: Jon Epstein **b6**

Sent: Wednesday, September 22, 2021 12:48 PM

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

Subject: Re: Request for support **b6** letter

Hey David,

I hope you're doing well. I wanted to get back to you to let you know that

b6

b6

b6

I wanted to sincerely thank you for writing a letter of support.

b6

b6

It would be nice to engage with the

b6

a bit more in the upcoming years.

Looking forward to the next opportunity to get together.

Cheers,

Jon

On Wed, Jan 20, 2021 at 3:23 PM Morens, David (NIH/NIAID) [E] b6 wrote:

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

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



David 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**

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From: Jon Epstein **b6**

Sent: Wednesday, January 20, 2021 2:53 PM

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

Subject: Re: Request for support **b6** letter

haha - I'll send 'em your way if they don't!

Anyway, that's really kind of you to say, and I'm sincerely grateful for your support, and friendship.

Cheers,

Jon

On Wed, Jan 20, 2021 at 2:48 PM Morens, David (NIH/NIAID) [E] b6 wrote:

Jon, will do. I just finished it but need to proof read and go over it one more time. Writing this thing reminded me all over again what a great and promising scientist you are. If the b6 don't take you, it will be a travesty.



David M. Morens, M.D.

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 b6

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From: Jon Epstein [b6]
Sent: Wednesday, January 20, 2021 2:45 PM
To: Morens, David (NIH/NIAID) [E] [b6]
Subject: Re: Request for support [b6] letter

Hi David

I hope that you were able to enjoy today's events.

Would you mind ping me when you submit the [b6] letter of reference? The system won't let me submit the application until your letter is received.

Thanks,

Jon

On Mon, Jan 18, 2021 at 5:21 PM Morens, David (NIH/NIAID) [E] [b6] wrote:

TY. I will be on it tomorrow. Today am [b6] D

Sent from my iPhone

David M Morens

OD, NIAID, NIH

On Jan 18, 2021, at 17:15, Jon Epstein [b6] wrote:

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

-Jon

On Mon, Jan 18, 2021 at 5:04 PM Jon Epstein [b6] wrote:

[b6] have been able to get vaccinated.

b6

Stay safe :)

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

b6

wrote:

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

b6

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

D

Sent from my iPhone

David M Morens

OD, NIAID, NIH

On Jan 18, 2021, at 16:54, Jon Epstein
wrote:

b6

perfect - and sincerely appreciated.

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

Cheers,

Jon

p.S.

b6

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

b6

wrote:

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

Sent from my iPhone

David M Morens

OD, NIAID, NIH

On Jan 18, 2021, at 16:41, Jon Epstein

b6

wrote:

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

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

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](https://twitter.com/epsteinjon)

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

--

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From: Morens, David (NIH/NIAID) [E] [b6]
[b6]
Sent: 2/1/2021 11:25:20 PM
To: Aguilar, Patricia V. [b6]
CC: [b6]
BCC: Morens, David (NIH/NIAID) [E] [b6]
[b6]
Subject: Re: ACAV webinar on COVID-19 variants

Peter, i meant to email earlier about this and the other matter we discussed. On the latter, i spoke with Tony and he would like for you to brief him on your return from Wuhan, when convenient for yiu

Hope all is well. Don't drink the Mao Tai!!!!!!!

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

On Feb 1, 2021, at 17:51, Aguilar, Patricia V. [b6] wrote:

Dear Dr. Daszak:

On behalf of The American Committee on Arthropod-borne and zoonotic viruses (ACAV), we are honored to invite you to speak at the webinar on COVID-19 variants. The event will be scheduled for late February or early March.

We believe your voice would be a critical addition to our panel of renowned speakers. Please let me know whether or not you would be interested in participating as part of our panel. Thank you in advance for your consideration; we very much look forward to hearing from you.

Best Regards,

Patricia Aguilar, PhD
ACAV Chair 2021
Associate Professor, Department of Pathology
Associate Director, Center for Tropical Diseases
University of Texas Medical Branch
301 University Blvd
Galveston, Texas 77550

[b6]
Ph: [b6]

From: Morens, David (NIH/NIAID) [E] [b6]
[b6]
Sent: 6/19/2020 12:36:40 PM
To: Ellen Carlin [b6]
CC: Sarah Babcock [b6]
Subject: Re: I've arrived!

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

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

> On Jun 19, 2020, at 08:22, Ellen Carlin [b6] wrote:
>
> I'm in a video piece with Dr. Fauci! https://www.washingtonpost.com/video/health/worried-about-a-second-wave-of-coronavirus-were-still-in-the-first/2020/06/18/35d25e0d-863f-4735-9915-a88773bfd06f_video.html
>
> I need to remember to look at the pinpoint camera on the top of my computer when doing interviews. It's so awkward.
>
> Hope you guys are well.
>
> Ellen
>

From: Morens, David (NIH/NIAID) [E] [redacted] b6
[redacted] b6
Sent: 7/1/2020 1:19:55 AM
To: Bloom, Marshall (NIH/NIAID) [E] [redacted] b6
[redacted] b6
BCC: Taubenberger, Jeffery (NIH/NIAID) [E] [redacted] b6
[redacted] b6]; Peter Daszak
Subject: Re: great article [redacted] b6

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

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

On Jun 30, 2020, at 20:51, Bloom, Marshall (NIH/NIAID) [E] [redacted] b6 wrote:

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

Marshall E.Bloom, M.D.
RML Associate Director for Scientific Management
Division of Intramural Research
Chief, Biology of Vector-borne Viruses Section
Laboratory of Virology
Rocky Mountain Laboratories
National Institute of Allergy and Infectious Diseases
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From: Morens, David (NIH/NIAID) [E] [b6]
[b6]
Sent: 3/4/2020 7:58:49 PM
To: Robert Kessler [b6]
CC: Peter Daszak [b6]; Tara Hoda [b6]; Aleksei Chmura [b6]; Alison Andre [b6]
Subject: RE: Cosmos Club EcoHealth Alliance Event

Thanks!

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
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[b6] (assistants: Kimberly Barasch; Whitney Robinson)

301 496 4409

[b6]

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From: Robert Kessler [b6]
Sent: Wednesday, March 4, 2020 2:35 PM
To: Morens, David (NIH/NIAID) [E] [b6]
Cc: Peter Daszak [b6]; Tara Hoda [b6]; Aleksei Chmura

b6

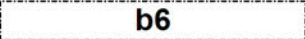
Alison Andre

b6

Subject: Re: Cosmos Club EcoHealth Alliance Event

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

Thanks,
Robert

On Wed, Mar 4, 2020 at 2:22 PM Morens, David (NIH/NIAID) [E]  wrote:

Hi Peter, I'd love to do that but as things stand now, I am scheduled to be at UCLA from 5/27-5/29 giving a keynote lecture and then various stuff with faculty and students over the next couple days. Everything is of course up in the air with this coronavirus, but I am on the hook for that 3 day event. Always love to get together with you guys, so yes, you can count on me in the future



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  (assistants: Kimberly Barasch; Whitney Robinson)

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From: Peter Daszak [redacted] **b6**
Sent: Monday, March 2, 2020 4:57 PM
To: Morens, David (NIH/NIAID) [E] [redacted] **b6**
Cc: Robert Kessler [redacted] **b6**; Tara Hoda [redacted] **b6**; Aleksei Chmura [redacted] **b6**; Alison Andre [redacted] **b6**
Subject: Cosmos Club EcoHealth Alliance Event

Hi, David,

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

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

Cheers,

Peter

Peter Daszak

President

EcoHealth Alliance

460 West 34th Street – 17th Floor

New York, NY 10001

Tel. b6

Website: www.ecohealthalliance.org

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

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--

Robert Kessler

Communications Manager

he/him

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

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

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

From: Peter Daszak [REDACTED] b6
Sent: 8/15/2021 5:48:49 PM
To: Morens, David (NIH/NIAID) [E] [REDACTED] b6
([REDACTED] b6); Robert Kessler
[REDACTED] b6 Keusch, Gerald T [REDACTED] b6
Subject: RE: Sunday Wash Post editorial

He's claiming he said nothing new, but it's now being used by the press – see article below from the UK Times today.

I wouldn't mind if they just stuck to slagging off the DG, WHO, Peter Ben Embarek etc., but of course they do a hit-job on me as well. It's just disgusting. I can't get through a week without more of this garbage, despite zero communication with the press.

China, the WHO and the power grab that fuelled a pandemic

In early 2020, the world missed its chance to stop Covid-19. Insight exposes how Beijing's ten-year takeover of the global health watchdog sowed the seeds of disaster

Play Video

Jonathan Calvert

and

George Arbuthnott

| Insight

Saturday August 14 2021, 6.00pm BST, The Sunday Times

Share

After being heavily criticised by the World Health Organisation for its response to Sars in

2003, China decided it would not accept such public humiliation again. What followed was a concerted campaign over many years to seize power within the organisation.

A Sunday Times investigation raises serious concerns that the independence and leadership of the WHO were severely compromised by the time the first cases of a mysterious new coronavirus appeared in Wuhan in 2019 — with profound consequences for the course of the Covid-19 pandemic and the world.

Our investigation reveals:

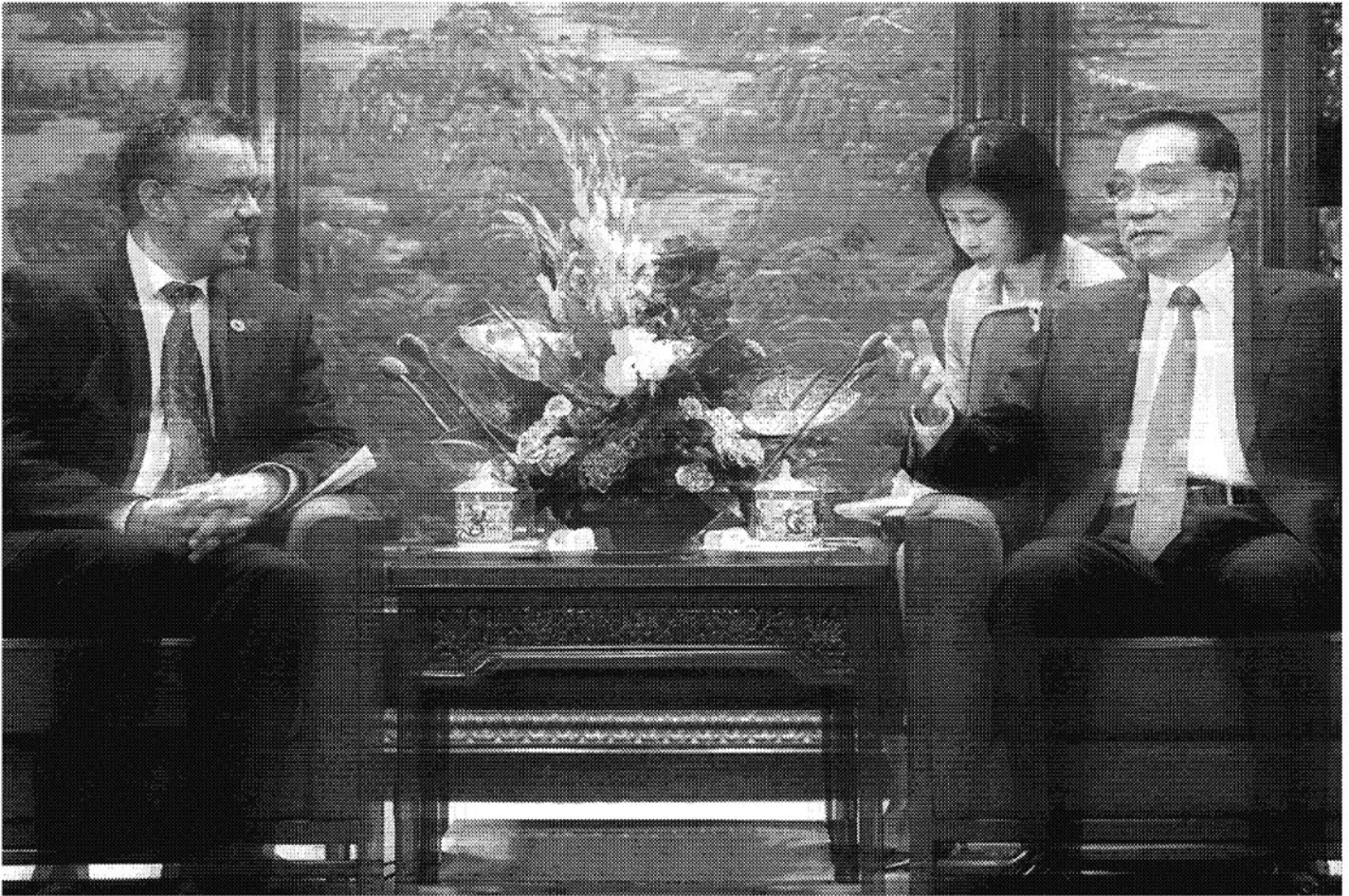
- China secured WHO votes to install its chosen candidates as director-general.
- The WHO leadership prioritised China's economic interests over halting the spread of the virus when Covid-19 first emerged.
- China exerted ultimate control over the WHO investigation into the origins of Covid-19, appointing its chosen experts and negotiating a backroom deal to water down the mandate.

A catastrophe in the making

Barely eight months after taking charge, the director-general of the WHO gave a speech that would prove extraordinarily prophetic. Tedros Adhanom Ghebreyesus warned that all nations were facing the ever-present threat that a new respiratory illness, such as the Spanish flu, might emerge and spread across the globe in weeks or months, killing millions.

It was why, the Ethiopian told the audience at his keynote speech in Dubai in February 2018, he had made it his daily priority since becoming the WHO's chief to make sure he was up to date on the thousands of reports the health body received every month that might flag up signs of an outbreak.

The WHO, a Geneva-based United Nations agency with a £5 billion budget from 194 member states, was on a war footing. Tedros said it would act fast and decisively, because ignoring the signs of an outbreak could "be the difference between global spread of a deadly disease and rapid interruption of transmission". So far this "new tighter focus" was working, he added.



Tedros Adhanom Ghebreyesus with Chinese premier Li Keqiang in 2017

GETTY IMAGES

So when the first alert of a mysterious respiratory illness in China, exactly as Tedros had described, was reported by health monitors in Taiwan at the end of December 2019, the health agency should have been prepared and ready for action.

In fact the WHO would receive considerable criticism for failing to help stop the spread of the Sars-CoV-2 virus in the opening weeks of the Covid-19 pandemic. Not only did the organisation fail to act but it also promulgated misinformation about the virus originating from China and even discouraged other nations from taking steps that might have contained the spread. For all his foresight, Tedros would be accused of being ineffective when the big test came.

The world paid a heavy price for the WHO's inaction. As Tedros predicted, the virus has killed more than four million people, and there will be many more. The body that is charged with looking after the world's health seriously malfunctioned in those opening weeks, when humanity most needed it to come to the rescue. Why?

Our investigation reveals today how a concerted campaign over many years by Beijing to grab power inside the WHO appears to have fatally compromised its ability to respond to the crisis. It raises serious concerns about the extent of Beijing's influence over the WHO and its director-general, and how this undermined the organisation's capacity — and willingness — to take the steps necessary to avert a global pandemic. Its leadership put China's economic interests before public health concerns. The results have been nothing short of catastrophic.



Disinfection in a Chinese village in January 2020, when hospitals were being overwhelmed with Covid patients

CNSPHOTO/REUTERS

Beijing's man

It is a story that stretches back many years before the Covid-19 crisis. After being strongly criticised by the health agency for attempting to cover up the 2003 Sars crisis, China set out to increase its influence over the WHO. By applying financial and diplomatic leverage over some of the world's poorest nations, Beijing won a global power struggle to get its favoured candidates installed at the very top of the organisation.

As a result, years later, a body that was set up with the lofty goal of “attainment by all peoples of the highest possible level of health” has been co-opted into aiding the Chinese state’s campaign for global economic dominance. Its leadership began to speak differently, espousing statements and pursuing policies that were markedly convenient to China — even praising Beijing’s questionable allies such as North Korea, despite its appalling health and human rights record.

Beijing had been instrumental in installing Tedros as the £170,000-a-year head of the agency by pulling strings and calling in favours during the 2017 election for the job.

Tedros himself caused outrage by bestowing the role of WHO goodwill ambassador on Robert Mugabe, the notorious former Zimbabwean dictator, an appointment said to have had strong backing by the Chinese government, a long-standing close ally of the despot.

As hospitals became flooded with patients in Wuhan in January 2020, the health agency repeatedly relayed to the world the Chinese government’s false claims that there was no evidence the virus could pass between humans. It made a specific point of cautioning countries not to impose bans on travel to and from the virus hotspots — which meant many weeks were lost before countries independently decided to seal their borders. The WHO’s approach ensured that China’s short-term economic prospects were protected. Meanwhile, the virus was allowed to spread round the globe like wildfire.

More recently, we can reveal, a backroom deal negotiated between the WHO and China has seriously damaged the chances of the world getting to the bottom of one of the most important questions facing mankind today: the origin of the Covid-19 pandemic.

When the world’s nations gave Tedros the job of discovering how the virus first came to infect humans, his team struck an agreement in secret with China that emasculated the inquiry. It meant that the WHO’s “independent” mission — its fact-finding team travelled to Wuhan early this year to carry out an investigation — was, in the words of one expert, little more than a “shameful charade”. There may well be no second chance.

Legacy of Sars

The health agency's reaction to Sars, the first pandemic crisis of the 21st century, had been very different. In many ways that lay at the root of the later difficulties that would come to a head with China.

The Sars outbreak started in November 2002, when a number of people in Guangdong province, southern China, began to fall ill with flu-like respiratory symptoms; by January 2003 infected patients were streaming into the region's hospitals.

The Chinese government had immediately enforced its strict laws, which classified all new infectious diseases as a state secret before they were officially announced by the ministry of health. As a result, the WHO was kept largely in the dark about the outbreak until the son of one of its former employees emailed the agency in February 2003 with some alarming news. The message described a mysterious virus in Guangdong that had already killed 100 people but claimed the authorities were insisting "it was not allowed to be made known to the public".

The cat was out of the bag, and after stern questions from the health agency China did share some limited information about the new virus the following day. However, government officials in Guangzhou, the city at the centre of the outbreak, were still maintaining that the illness was under control. This was untrue. Sars had already spread to other parts of China.

The Chinese were still anxious to play down the extent of the outbreak. At one stage 30 patients with the virus were said to have been driven round Beijing in ambulances, and 40 others were moved out of a hospital into a hotel to hide their existence from a visiting team of WHO scientists.



Tough on China: former WHO director-general Gro Harlem Brundtland

PAUL HILTON/EPA/REX/SHUTTERSTOCK

China's reluctance to disclose the duration, scale and evolution of the disease led Gro Harlem Brundtland, then the WHO director-general, to get tough. She was a former prime minister of Norway and not scared of ruffling feathers. "Brundtland was a very brave politician with a lot of legitimacy," recalls Gian Luca Burci, a legal adviser to the WHO at the time. "She didn't shy away from criticising China and basically saying, 'We don't believe you. You should come clean.'"

Brundtland put pressure on China and took the brave decision to issue strong advice against travelling to the affected areas, which included Hong Kong and Toronto as the virus spread.

"The WHO really stepped into a vacuum, and it really exerted its authority as an emergency manager," Burci said. "I would say the unanimous perception is that the WHO played a central role and essential role in allowing Sars to be controlled in a matter of months."

Brundtland publicly criticised China's cover-up and said the outbreak might have been contained if the WHO had been alerted earlier. "Next time something strange and new comes anywhere in the world, let us come in as quickly as possible," she urged.

The virus was brought under control in the early summer with only 8,000 cases and just under 800 deaths. The public ticking-off had been humiliating for Beijing. There was also an economic price for China: the health agency's travel advice had contributed to an estimated \$6 billion loss to the country's GDP.

China began taking a keen interest in the WHO after the bruising it received over Sars. A senior source now working at the health agency has described how in 2005 Beijing was behind a group of countries that attempted to "limit" the authority of its director-general.

Their efforts led to new regulations for the WHO's governance, which compel the director-general to consult an emergency committee — made up of international experts and often including a China representative — before he or she calls an international public health emergency or recommends travel restrictions.

A further opportunity for China to extend its influence within the agency presented itself a year later when Brundtland's recently appointed successor as director-general, the Korean doctor Lee Jong-wook, suddenly died after undergoing brain surgery.

One of the leading candidates was Dr Margaret Chan, a Chinese national. She was a former Hong Kong health director who had been criticised during the Sars crisis for her supine attitude to mainland China. The Hong Kong legislative council found she had been too slow to respond to the Sars outbreak and too unquestioning of the misleading information from Beijing. Hong Kong suffered a higher Sars death rate than anywhere else in the world.

Chan had, nonetheless, moved to a new job with the WHO in Geneva, and when Jong-wook died, the Beijing government rallied behind her candidacy, ordering its embassies to lobby international friends to get behind her in the November 2006 election to choose a replacement.



Margaret Chan drew criticism as Hong Kong's health chief for believing China's claims about the 2002-04 Sars outbreak

FABRICE COFFRINI/AFP/GETTY IMAGES

Just five days before the vote, a summit was held in Beijing for leaders of the African nations. China pledged to cancel large amounts of their debts and double aid donations to the continent in a move that was openly acknowledged by state-backed analysts in the country as designed to secure backing for Chan.

It was an “extraordinarily aggressive campaign”, according to Professor Lawrence Gostin, the director of the WHO’s Collaborating Centre on Public Health Law and Human Rights. “[China] got burnt really badly during Sars,” he said, adding: “It wanted someone much more friendly and gentle if an outbreak came again.”

Chan won with two thirds of the votes in the final ballot. China had succeeded in getting its candidate to the top “precisely to avoid another humiliation”, according to a source working at the WHO at the time.

The African link

During her 10-year reign in the agency's top job, Chan certainly gave the appearance that she was very grateful to China for propelling her into the role. In April 2010 she made a trip to North Korea, one of China's neighbours and allies, and made the extraordinary claim the country's health system was the "envy" of most developing nations.

A few months later a report by the human rights group Amnesty International described the shambolic state of North Korea's "crumbling" health system. Hospitals at times lacked heat, power and medicines, the report said, and amputations were sometimes performed in candlelight without anaesthesia by doctors who were living on the poverty line because their wages were not paid.

Chan made a number of key appointments that appeared carefully calculated to please the Chinese government. In 2011 she made the Chinese soprano Peng Liyuan a WHO goodwill ambassador, praising the singer's "world-famous voice" and "compassionate heart". The other reason Chan might have selected Peng was not mentioned.

Peng is married to Xi Jinping, China's president. She holds the rank of major-general in the People's Liberation Army and wore her uniform to sing for the troops after they quashed the pro-democracy protests in Tiananmen Square. Chinese state censors have since attempted to erase these pictures from the internet.

Chan also chose to appoint China Central Television's James Chau a goodwill ambassador. Later, during the 2020 pandemic, more than 100 UN-affiliated associations would write to the WHO calling for him to be removed from the role because he was a well-known propagandist for the Chinese government.

The biggest test for Chan was also the moment she drew the most criticism — and there was a Beijing link to this too. She took two months to declare an international emergency over the 2014 ebola outbreak despite repeated warnings from her own experts.

Leaked emails obtained by the Associated Press revealed that the delay was caused by WHO officials who did not want to upset the African countries hit by the outbreak and damage their economies. More than 1,000 people died during the delay.

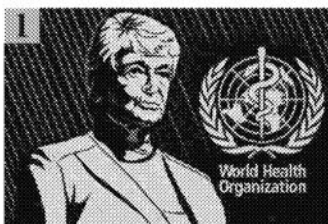
One of the countries affected, Guinea, had struck a big mining rights deal that allowed a state-backed Chinese firm to excavate one of the world's biggest untapped iron ore reserves. Fearing that the foreign investors might be scared away, Alpha Condé, then the country's president, claimed that ebola was under control in Guinea in a speech at the WHO's Geneva headquarters.

His lie went unchallenged. "Margaret Chan's WHO was accused of being too close to Alpha Condé," the senior source from the WHO said. In the end the UN took the highly unusual step of appointing David Nabarro, a British doctor, to co-ordinate the international effort on ebola because it was so concerned about the WHO's failure to get to grips with the outbreak.

In 2017 Chan crowned her final year in office by welcoming Xi to Geneva. While he was there, she signed an agreement that committed the WHO to working alongside China on health as part of the country's Belt and Road initiative. It was the first time any UN agency had signed up to the initiative, which seeks to extend Chinese influence and trade in more than 70 developing countries by financing infrastructure projects.

The initiative is highly controversial because its critics argue that China uses it to shackle countries, particularly in Africa, to "unsustainable debt" as a way of gaining access to the continent's raw materials and buying political favours.

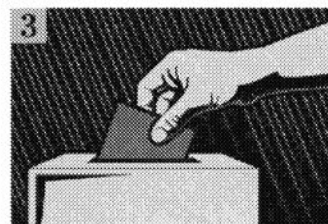
"I think health is too special to get into the really seedy politics that Belt and Road is part of, and I wouldn't want the WHO to be associated with it," Gostin argues. "The cost in terms of human rights and debt, and other adverse events for Africa, was a bridge too far."



2003
The World Health Organisation's director-general, Gro Harlem Brundtland, takes strong and decisive action during the Sars crisis, exposing China's cover-up of the outbreak and recommending restrictions on travel to virus hotspots. Fearless leadership by Brundtland, a former Norwegian prime minister, helps to bring a swift end to the pandemic, which causes 800 deaths



2006
As Brundtland's five-year term as head of the WHO comes to an end, China is alleged to have used its financial and diplomatic muscle, including by doubling aid commitments to Africa, to ensure that its candidate, Margaret Chan, will be elected the agency's new director-general. She has previously been censured for failing to question Beijing's misleading claims about the Sars crisis



2007-2017
During her two terms in the top job, Chan supports China's allies and agenda. She describes North Korea's health system as the "envy" of the world and appoints the Chinese president's wife a WHO goodwill ambassador. A new, secretive, FIFA-style voting procedure — giving small, easily swayed nations as much say as any other country — is introduced to determine her successor



2017
The former Ethiopian foreign minister Tedros Adhanom Ghebreyesus, a good friend of China, is Beijing's chosen candidate to succeed Chan. On the eve of the leadership election China announces a big boost in funding to poorer countries taking part in the vote, just as it did before Chan's victory. Tedros wins by 133 votes to 50 against Britain's David Nabarro

Graphic: The Times and The Sunday Times

Turning on the money taps

Under bright skies in the rolling parkland on the banks of Lake Geneva a large group of protesters with placards gathered outside the Palace of Nations for the 70th meeting of the World Health Assembly (WHA), the body with representatives from all UN member states that controls the WHO.

The protest that day — May 22, 2017 — was against Tedros standing to replace Chan, who had served her final term. The demonstrators were highlighting human rights abuses by the Ethiopian regime, which was reported to have tortured dissidents, displaced villages and ordered police massacres of protesters. Until the previous year Tedros had been a minister in that Ethiopian government.

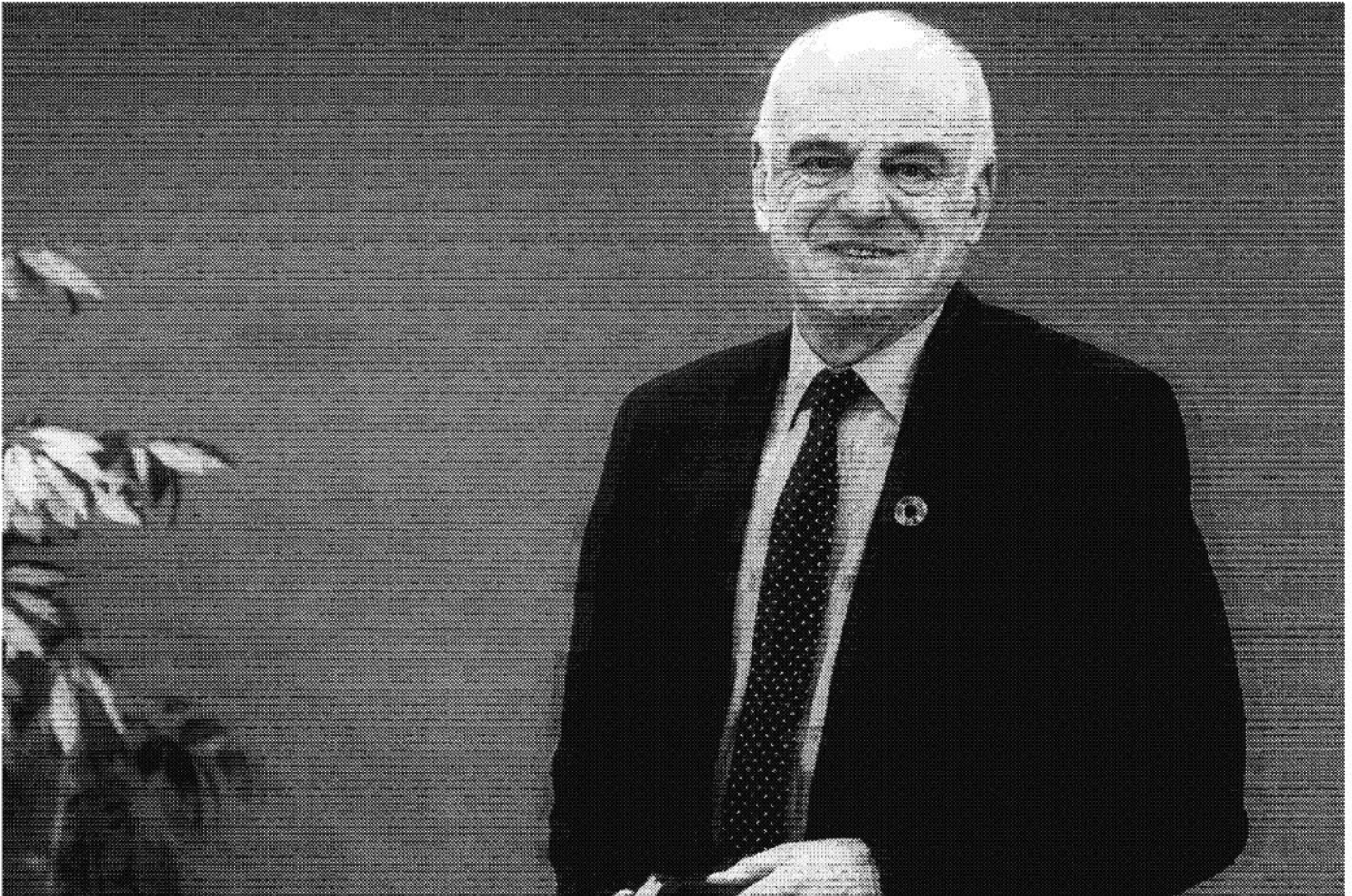
Tedros, a former epidemiologist then aged 52, had been the health and then foreign minister after joining the government in 2005. Last year David Steinman, a US economist nominated for the Nobel peace prize, called for Tedros to be personally prosecuted for genocide over his alleged involvement directing Ethiopia's security forces. He denies any involvement in human rights abuses despite his lengthy period in government.

As foreign minister Tedros had formed a close relationship with China. He would often praise the Chinese leadership, which invested more money in Ethiopia than any other country did. In 2014 he wrote a joint article with the Chinese foreign minister in the state-controlled China Daily newspaper that waxed lyrical about the bond between the countries. "We are sincere friends, reliable partners and good brothers who share both happiness and adversity, each rejoicing in the successes the other has achieved," they wrote.

The African Union countries had wanted their candidate to replace Chan as director-general. They had previously helped Chan get elected, and it was now their turn. As an African with close links to China, Tedros was the perfect candidate.

As the election approached, China had again turned on the money taps. A month before the vote, a multinational ministerial conference was held in Pretoria ostensibly with the aim of stepping up China-Africa co-operation in health. During the conference China agreed to offer a cataract surgery programme for free to the African countries.

Then, nine days before polling, Xi hosted an event in Beijing at which he pledged more than \$100 billion in extra funding for its Belt and Road initiative — a large portion of which would be channelled into investment in developing countries. This included new investment in Kenya, Indonesia and Hungary.



David Nabarro witnessed at first hand the WHO leadership's incompetence during the Ebola crisis

FABRICE COFFRINI/AFP/GETTY IMAGES

Tedros's main opponent was Nabarro, whose first-hand experience of the WHO leadership's incompetence during the ebola crisis had convinced him of the need for reform. Nabarro was not alone in his concerns about the WHO, and he reportedly received support from the US, the UK and Canada. This appears to have been the first time the West had woken up to China's creeping influence over the health agency.

The contest between the two men for the WHO director-generalship took place under new rules that had been introduced by Chan. Previously, the director-general had been chosen by the 34 members of the WHA executive board, but the new rules gave an equal vote to all the assembly's 194 member states.

Critics of the rule change, such as J Michael Cole of the Canadian think tank the Macdonald-Laurier Institute, have pointed out that the WHO was essentially copying the electoral system that propped up the famously corrupt regime of the former Fifa president Sepp Blatter.

As with football's governing body, tiny countries that might be susceptible to financial aid were given an equal vote to countries many times their size. Cole said tiny island countries such as those in the Pacific were "easy targets" for Chinese influence.

During the campaign Gostin, who was supporting Nabarro, accused Tedros of covering up three cholera outbreaks during his time as Ethiopia's health minister. Tedros again strongly denied the allegations. Certainly the mud did not stick. With China's help he won by 133 votes to Nabarro's 50.

'Model' China

Within a month of taking over in July 2017, Tedros was on his way to China to emphasise the health agency's continued commitment to the partnership under the Belt and Road initiative.

"China's long experience and expertise in health systems and policies will be invaluable to achieving the WHO's global priorities, especially in health crisis management," he wrote in the China Daily. "China can share its lessons learnt and best practices with other countries, offering them models of success."

Months later Tedros made an extraordinary announcement, seemingly without consulting colleagues. He had appointed Mugabe, the tyrannical Zimbabwean president, as a goodwill ambassador for the WHO. Diplomatic sources affiliated to the health agency have told us that the honouring of Mugabe was made at the behest of Beijing as a political payoff for the dictator's years as a staunch ally of the Chinese government.

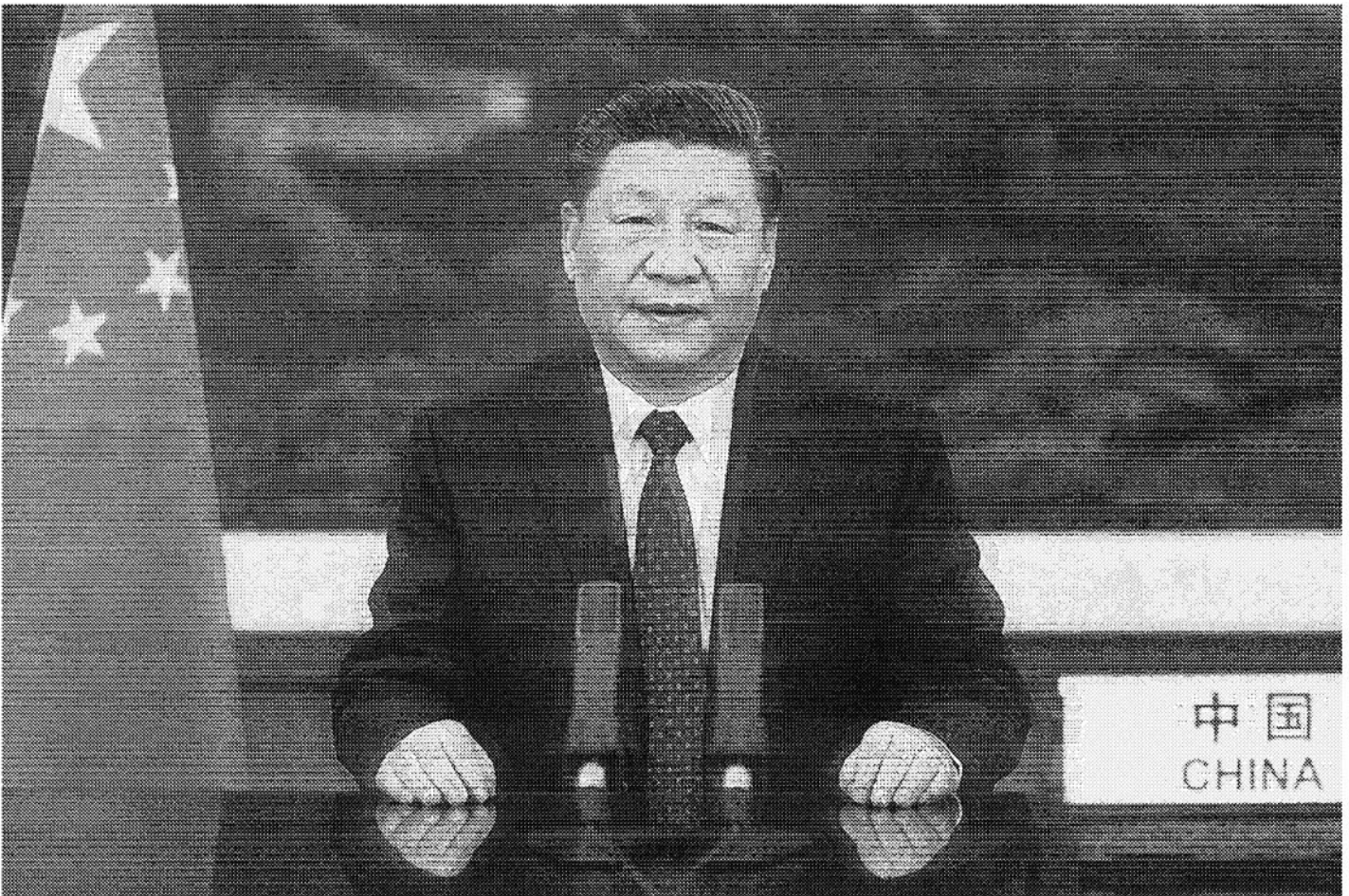
Xi has described Zimbabwe as China's "all-weather friend". In turn Mugabe called Xi "a God-sent person". The Chinese government's connection to Mugabe stretches back to the 1970s, when it helped fund his guerrilla war in Zimbabwe before he took power. More recently it ploughed cash into his regime when it was struggling under western sanctions.

It was an ill-judged move by Tedros. The Canadian prime minister, Justin Trudeau, described the announcement as a “bad April Fool’s joke”, Ireland’s health minister said it was “offensive and bizarre” and the UK prime minister’s office said it was “surprising and disappointing, particularly in light of the current US and EU sanctions against [Mugabe]”.

There was particular bemusement because Zimbabwe’s healthcare system had deteriorated so badly under Mugabe’s rule that he himself had sought treatment at a luxurious private hospital in Singapore rather than trust his own country’s doctors. A report by the group Physicians for Human Rights in 2009 gave examples of how Mugabe had damaged his own health system in his efforts to cling on to power.

The appointment was withdrawn just four days after Tedros announced it. But it did not stop him continuing to lavish praise on China’s leaders. Nine months later, on another trip to Beijing in July 2018, he described China’s health reforms as “a model for universal health coverage” and “a bulwark against health emergencies”. In other words, they would help to prevent a future pandemic.

One of the oddities of China’s influence within the WHO was that it managed to achieve it while paying little money towards the running of the organisation. In 2018-19 China gave the health agency \$89 million, whereas the UK contributed \$464 million and the US \$853 million.



Tedros praised President Xi's 'rare leadership' as Covid spread across the world in January 2020

LI XUEREN/XINHUA/AP

Gostin described the vast shortfall as “galling”. He is critical of the way China instead uses its money to pay for health projects in deals it negotiates directly with individual countries. This gives Beijing more diplomatic and economic leverage with the countries themselves. “China’s foreign policy is extraordinarily mercantile and self-interested,” he said. “It’s all done on bilateral country negotiations, where [China] has got a ton of leverage.”

China has used this approach to take over other parts of the UN system. In June 2019 a Chinese candidate was elected head of the Food and Agricultural Organisation, after reports that Beijing had cancelled \$78 million of Cameroon’s debt in exchange for the withdrawal from the race of a candidate from the country. It meant that, of the UN’s 15 specialised agencies, four were headed by Chinese nationals.

The cover-up begins

The main “bulwark” at the beginning of the Covid-19 pandemic was a wall of secrecy in China. On December 30, 2019, Dr Li Wenliang, an ophthalmologist at Wuhan Central Hospital, sent a message to medical colleagues in an online chat forum suggesting they wear protective clothing because he had seen several cases of a virus that appeared to be transmitted between humans like Sars.

Li was summoned for an inquisition by the authorities, with seven of his friends. They were investigated for “spreading rumours” and warned against “publishing fictitious discourse”. Li would later die from Covid-19.

The following day — the last of the year — the Wuhan Municipal Health Commission publicly admitted for the first time that a number of people had been struck down with a similar illness in a bland public announcement reporting 27 cases of pneumonia-like infection.

What the statement did not say was that the illness had already been identified by the Chinese authorities as a new coronavirus — not unlike Sars — that appeared to be passing between humans. This crucial information — as well as any indication of the alarm already secretly felt by scientific and health officials in China — was withheld from the world.

However, earlier that day Taiwan had been closely monitoring reports in the Chinese media that might indicate a new medical phenomenon and it noted that an internal hospital alert had been reported in an obscure business publication. The Taiwanese authorities sent the WHO an email raising concerns about a number of “atypical pneumonia cases” in Wuhan that had been “isolated for treatment”. The only reason patients would need to be isolated was that Chinese hospitals feared the virus could pass between humans.

The health agency did not heed the Taiwanese warning. The island’s relations with the WHO were strained because of China’s claims of sovereignty over its territory.

In the months before the pandemic Beijing had used its influence to block the island from attending meetings of the WHA for a third year in a row. The UK and the US were among a number of nations that wanted Taiwan to be given access and had warned Tedros that the country’s absence “created serious gaps in the global health security system”.

Taiwan's vice-president, Chen Chien-jen, an epidemiologist by training, would later accuse the WHO of brushing aside this early evidence it had provided on suspected human-to-human transmission and of failing to pass the early warning on to the world. In the weeks that followed, the island's relationship with the WHO deteriorated further when Tedros wrongly claimed in public that it was behind a series of racist online attacks against him.

In the first two weeks of January desperate scenes were unfolding at Wuhan hospitals as patients with flu-like symptoms began to flood in. The mayhem and death were described by Dr Peng Zhiyong, the director of the intensive care unit in Wuhan University's Zhongnan Hospital, several weeks later in an interview he gave to the Chinese media outlet Caixin Global.

Within four days of the arrival of the first patient, Peng said, all 16 intensive care beds were full and the situation was "dire". More than 40 members of his team then contracted the disease from patients. Things were even worse at another hospital in the city, where two thirds of intensive care staff had reportedly been infected.

The doctors fought the epidemic in gruelling conditions. Some wore nappies inside their protective suits to avoid taking breaks. Peng said many patients were turned away because the hospitals could not cope. "Some patients even knelt down to beg me to accept [them]. But there was nothing I could do since all the beds were occupied," he said. "I shed tears while I turned them down. I have run out of tears now."

The doctors were in no doubt the virus was passing rapidly between humans. Few of Peng's colleagues went home after their shifts, for fear they would infect their families.

Yet the Chinese authorities systematically tried to cover up the human spread by issuing diktats, suppressing whistleblowers and scrubbing social media. On January 3 a confidential notice was issued forbidding labs to publish details of the virus without authorisation. On January 6 the hashtag #WuhanSARS appeared online, but posts on Twitter were swiftly censored.

The authorities also withheld work that had been done to sequence the coronavirus's genome, which had been completed by January 3 — a decision that delayed international scientists from developing tests for the virus.

It was the beginning of exactly the type of crisis that Tedros had warned of in his 2018 Dubai speech. He had been clear at the time that ignoring the signs of an outbreak could be the difference between containing a deadly disease and allowing it to spread.

But, at the beginning of the biggest pandemic for more than a hundred years, the health agency simply took the Chinese explanations about the outbreak at face value. On January 10 the WHO issued a statement saying: “From the currently available information, preliminary investigation suggests that there is no significant human-to-human transmission, and no infections among healthcare workers have occurred.”

Both statements were untrue, and the agency did not even attempt to couch its language in a way that would have made clear that these were merely claims made by China. Instead it was mindful of the need to avoid taking measures that might damage the Chinese economy. “WHO advises against the application of any travel or trade restrictions on China,” its statement went on.

However, staff at the Shanghai Public Health Clinical Centre laboratory were growing increasingly anxious about the need to develop tests for the virus in the hope they might be available before millions of people crisscrossed the country for the lunar new year celebrations later that month. So they took matters into their own hands and shared the genetic code they had sequenced on a US computer database called GenBank, which is available to scientists around the world. It was published on January 11. When the Chinese authorities learnt of the leak, the Shanghai lab was instantly closed for “rectification”. But China’s secret was out and the Wuhan Institute of Virology was forced to share its information on the coronavirus with the health agency.

By now some officials inside the WHO were becoming frustrated that their repeated requests for data from China were being rebuffed. Leaked recordings of one of the health agency’s meetings in the second week of January show that Dr Michael Ryan, the WHO’s Irish chief of emergencies, wanted to apply more pressure on China as he could see that the crisis was becoming a repeat of the 2003 Sars disaster.



Chinese authorities desperately tried to cover up the spread of the coronavirus

NOEL CELIS/AFP/GETTY IMAGES

“This is exactly the same scenario — endlessly trying to get updates from China about what was going on,” he said in the recording obtained by the AP news agency. “The WHO barely got out of that one with its neck intact, given the issues that arose around transparency in southern China.”

Ryan appears to have been keen to raise the lack of co-operation by China in public, pointing out that the health agency had criticised Tanzania a few months earlier for withholding details of an ebola outbreak. “We have to be consistent,” Ryan said. “The danger now is that despite our good intent ... especially if something does happen, there will be a lot of finger-pointing at the WHO.”

But such behind-the-scenes concerns did not alter the WHO’s public messaging. “WHO is reassured of the quality of the ongoing investigations and the response measures implemented in Wuhan, and the commitment to share information regularly,” it said in a statement on January 12. “At this stage there is no infection among healthcare workers, and no clear evidence of human-to-human transmission,” it added calmly.

Deadly delay

On the morning of January 13 the first case of an infection outside China was found in Thailand. That day Tedros announced that he was giving thought to whether he should call a meeting of the WHO emergency committee, which consists of about 20 international experts, including one from China.

The emergency body plays a key role in deciding whether the director-general should declare an infectious outbreak as a public health emergency of international concern (PHEIC). Meetings are held in confidence because PHEIC declarations can damage business, travel and tourism in an affected country, according to a source on the committee.

The growing outbreak in China could have been declared an emergency under the health agency's criterion, which requires a crisis to be "an extraordinary event" that might cause "a public health risk to other states through the international spread of disease".

But Tedros decided to wait, and nine more days passed before he even gathered the committee members for their advice. During this period he was talking directly on the phone about the outbreak to Ma Xiaowei, the Chinese minister of health, whom he had described warmly as his "brother" in a tweet on January 11.

According to the health agency's official timeline of events, it first warned that the virus might be transmitted between people on January 14. It is certainly true that Maria Van Kerkhove, the American acting head of emerging diseases, acknowledged in a briefing that there might be some evidence of "limited human-to-human transmission, potentially among families". But she was corrected by the WHO official Twitter account a few hours later: "Investigations conducted by the Chinese authorities have found no clear evidence of human-to-human transmission of the novel #coronavirus." A further five days would go by in which the WHO issued another denial about hospital staff in Wuhan contracting the virus.

Finally on January 19 the health agency's regional office in the western Pacific announced clearly that the virus could pass between humans, albeit with the qualification that the transmission was "limited".

By now the emergency situation in Wuhan was so desperate that the Chinese authorities were preparing to build the 1,000-bed Huoshenshan Hospital in just 10 days. The virus had spread to Beijing, and it was no longer credible to pretend it could not pass between humans.

Therefore, on January 20 — three weeks after Taiwan’s warning — China’s health ministry admitted that it did have evidence that medical staff had been infected. It meant the health agency could no longer delay. Tedros summoned a meeting of the emergency committee, which deliberated on January 22 and 23.

The number of known cases jumped from 314 to 581 during those two days and the virus had spread to 24 regions of China, killing 18 people. The true figures will have been many times greater because of underreporting by China. And the virus had now escaped the country’s borders: ten cases had been identified in four other countries.

For reasons that are unclear because of the secrecy of its meetings, the members of the emergency committee were split on what action to take after an update on the crisis was provided by the Chinese representative. The advice they gave Tedros was equivocal, and he decided to avoid taking the diplomatically fraught decision of imposing an international public health emergency on China.

In a press briefing on January 23 he reasoned that there was “an emergency in China ... but it has not yet become a global health emergency”, adding that he wished to thank the country’s government for its “co-operation and transparency”.

The protection of Beijing’s interests continued the following day when the health agency issued a statement reiterating that countries should not impose travel restrictions on China, even though the situation in Wuhan had become so dire that the city had imposed a full lockdown, then unprecedented in modern times. Yet the inaction by the health body sent a clear signal to the world that this new coronavirus might not be as serious as was feared.

The calm ripples of this cool approach were felt in Britain a day later. Matt Hancock, the health minister, chaired the first meeting of the Cobra national security committee, which spent an hour discussing the virus before concluding that the risk to the UK public was “low”. Hancock had first been alerted to the unusual pneumonia-like cases on January 3 but the government had done little in

the meantime to prepare for the potential arrival of the virus. Downing Street would later defend Boris Johnson's decision to skip the Cobra meeting — the first of five the prime minister missed — by pointing out that the WHO had not considered the crisis sufficiently serious to declare a global emergency.

By Tuesday January 28 four weeks had passed since Taiwan raised the initial alarm and there was still no evidence of the fast and decisive action that Tedros had said was necessary to combat an outbreak in his Dubai speech. That day he met Xi, the Chinese president, in Beijing and emerged from the encounter full of praise for his hosts.

He said Xi had shown “rare leadership” and deserved “gratitude and respect” for acting to contain the outbreak at the epicentre. These “extraordinary steps” had prevented further spread of the virus, and this was why, he said, there were only “a few cases of human-to-human transmission outside China, which we are monitoring very closely”.

Tedros even claimed that China was “completely committed to transparency”, pointing out that it had shared the genomic sequence of the virus “immediately” — when in fact the lab that leaked the sequence had been punished by the country's authorities for defying the censors.

If the words of Tedros's speech suggested he and China had everything under control, nothing could have been further from the truth. The virus was spreading fast across the globe.

By this point a crucial four weeks had been lost because China had covered up the highly infectious nature of Sars-CoV-2 while the WHO had repeated its claims unquestioningly. The health agency had failed in its single most important job — to swiftly sound the alarm.

Professor Richard Ebright, of Rutgers University's Waksman Institute of Microbiology in New Jersey, a fellow of the Infectious Disease Society of America, believes China's influence over the WHO played “a decisive role” in the agency's failure to act decisively at the start of the pandemic.

“Not only did it have a role; it has had a decisive role,” he said. “It was the only motivation. There was no scientific or medical or policy justification for the stance that the WHO took in January and February 2020. That was entirely premised on maintaining satisfactory ties to the Chinese government. So at every step of the way, the WHO promoted the position that was sought by the

Chinese government ... the WHO actively resisted and obstructed efforts by other nations to implement effective border controls that could have limited the spread or even contained the spread of the outbreak.”

He added: “It is impossible for me to believe that the officials in Geneva, who were making those statements, believed those statements accorded with the facts that were available to them at the time the statements were made.

“It’s hard not to see that the direct origin of that is the support of the Chinese government for Tedros’s election as director-general ... This was a remarkably high return on [China’s] investment with the relatively small sums that were invested in supporting his election. It paid off on a grand scale for the Chinese government.”

David Fidler, a former WHO legal adviser, is scathing about Tedros’s “obsequious” praise for Xi and suspects that “the WHO knew China was not being transparent, particularly about information related to human-to-human transmission”. He added: “The praise that he heaped on China gave them no incentive to change their behaviour.”

Tedros finally declared an international public health emergency on January 30. By then the virus had been detected in 18 countries and was almost certainly lurking undetected in many others.

The WHO’s failure to act had blown the world’s only chance to contain the pandemic at source, Ebright believes. “Ironically, China’s success in curbing the spread and containing the spread by implementing appropriate border controls ... tells us that, had this been done globally, in January, this outbreak could have been potentially contained,” he said.

“We can see what happened when Taiwan, cut off from WHA guidance and shunned by the WHO, made its own decisions and was largely Covid-free for 2020 and even through 2021. Had other nations implemented tight border restrictions by the middle of January, the situation would have been very different.”

A year later a report by an independent panel set up at the request of the WHA was critical of the delay in calling the emergency. The panel, led by the former New Zealand prime minister Helen

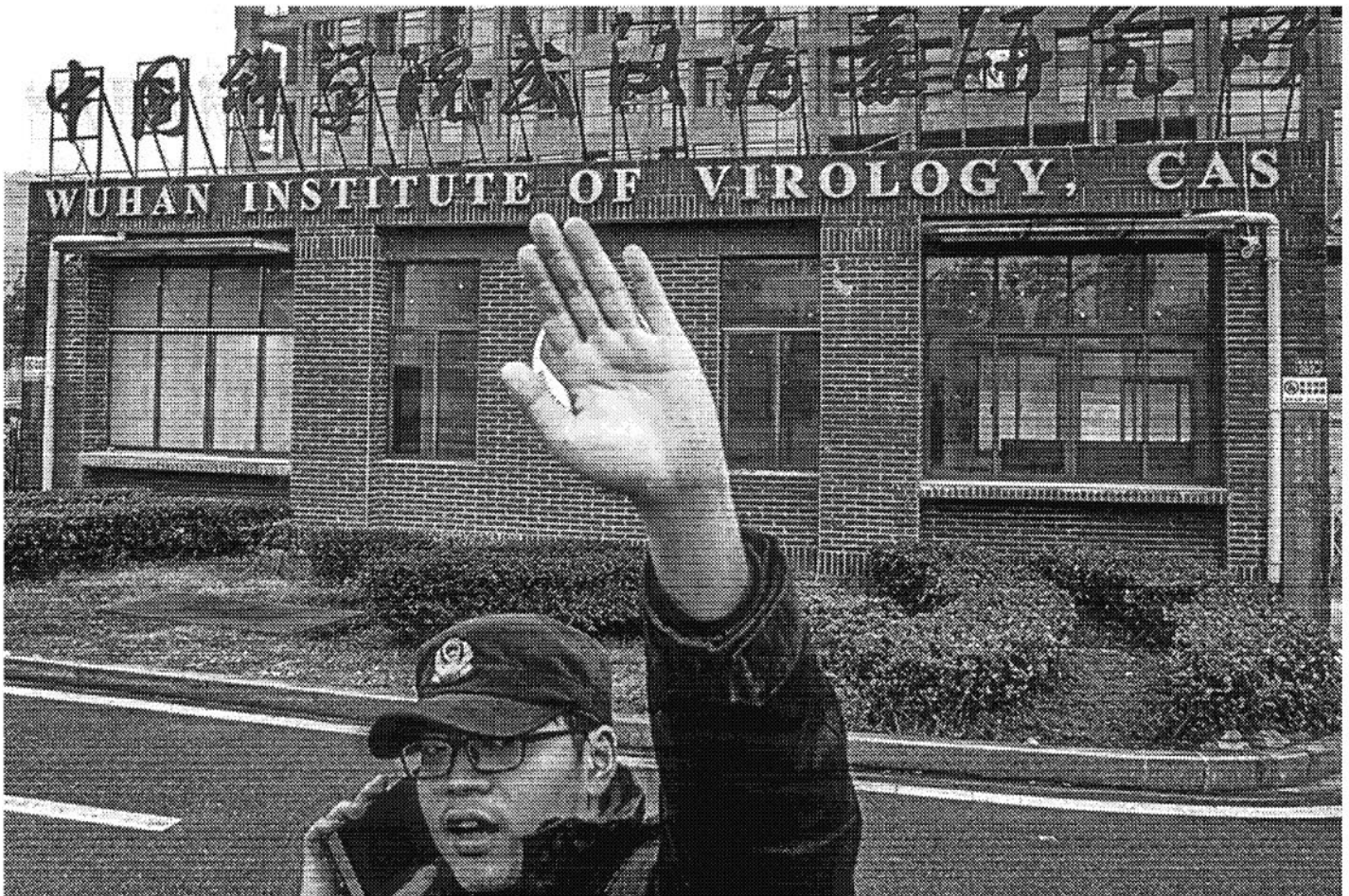
Clark, said the health agency should have assumed human-to-human transmission and issued warnings as a precaution, given what was known about respiratory infections.

Even after the global emergency was declared, the travel advice remained the same. At a meeting of the WHO executive board in Geneva on February 3, Tedros claimed the spread of the virus outside China was “minimal and slow” and there was no need to introduce measures that “unnecessarily interfere with international travel and trade”.

This prompted an outburst from the appreciative Chinese delegate to the board. Li Song, an ambassador to the UN, leapt to his feet and denounced countries that were blocking the entry of travellers from Hubei, the province of which Wuhan is the capital. “All these measures are seriously against recommendation by the WHO,” he fumed.

In fact, while the health agency did later give advice that travellers should be screened to detect flu symptoms at airports, it never did explicitly support any restrictions on travel to and from China. By the end of March 2020 many countries across the world had ignored the health agency’s advice and instituted some form of travel ban.

Gostin believes China’s cover-up in January was “the singular important event in the course of the pandemic” because it blew the world’s “only shot” of containing the crisis at source.



The Wuhan institute was meant to develop vaccines in advance of outbreaks

ROMAN PILIPEY/EPA

A flawed investigation

If the cordial relationship between Tedros and China had survived the opening months of the pandemic, the strength of their friendship would be tested once again in the early summer of 2020. It was over the very important, yet highly sensitive, issue of how and where the virus originated. The Sars outbreak in 2003 is thought to have originated in bats in Yunnan province, southwest China, and to have been introduced into markets in the surrounding area through an intermediary host animal. Sars-CoV-2 is believed to have had similar beginnings because of its resemblance to other bat coronaviruses.

However, the caves in Yunnan province are more than a thousand miles from Wuhan, and no bats containing such viruses have ever been found near that city. If an intermediate animal, or indeed a human, had been infected by a bat in Yunnan, how could this very infectious virus be carried on such a long journey to Wuhan without causing a single noticeable outbreak along the way?

The Chinese had tested thousands of animals in Wuhan and the surrounding areas, but not one had come up positive for the virus. Chinese scientists had also rejected the suggestion that the virus entered through the Huanan seafood market in the city, which was connected to some of the cases in December 2019.

Extensive sample-testing at the market failed to show a link between any of the animals there and the virus. It was also clear that many of the early human cases had no link to the market, and the conclusion was that the market was a crowded environment in which the virus had spread, rather than the point of introduction into Wuhan.

But there was an elephant in the room. Coronaviruses found in the Yunnan bat caves, including the world's closest known match to Sars-CoV-2, were being kept at the Wuhan Institute of Virology at the time of the outbreak. To many it seemed a remarkable coincidence that, of all the 600 cities in China, the virus began in Wuhan, the home of an institute that houses the world's largest collection of coronaviruses from wild bats and has a team of scientists who often travel to those same Yunnan caves.

The scientists had been seeking out coronavirus-infected bats and then transporting the viruses back to the laboratory in Wuhan. There they carried out highly controversial "gain of function" experiments to make the viruses more infectious to humans. The work was designed to help develop vaccines to pre-empt a potential coronavirus outbreak, but many scientists had warned that one safety lapse could itself cause a deadly pandemic.

Only a tiny handful of labs in the world carried out such high-risk experiments, and in 2018 inspectors sent by the US embassy in Beijing to the Wuhan institute had flagged serious safety concerns there. A US diplomatic cable leaked to The Washington Post stated: "During interactions with scientists at the WIV laboratory, they noted the new lab has a serious shortage of appropriately trained technicians and investigators needed to safely operate this high-containment laboratory."

There were therefore questions about whether the pandemic had been caused by a leak from the Wuhan institute or one of its researchers who had been infected in the bat caves and then accidentally carried the virus back to the city. It was certainly not inconceivable: the Sars virus had

leaked from the National Institute of Virology lab in Beijing in 2004. Nine people were infected by the outbreak and one died.

There were serious concerns about what the Wuhan institute had been doing with the world's closest known match to the Covid-19 virus, which was the strongest lead in the hunt for the pandemic's origin. It had been found eight years ago by Wuhan scientists in an abandoned mine, where it had been linked to deaths caused by a coronavirus-type respiratory illness. But the significance of the deaths had been kept secret by the Chinese authorities until a Sunday Times investigation uncovered them in the summer of last year. The lab has refused to answer questions on whether it was experimenting on the virus in the run-up to the pandemic.

Indeed China had been reluctant to address many questions about the pandemic's origins since January 2020, other than to issue blanket denials. It did not want the ignominy of being found culpable for the world's worst pandemic for a century.

The subject had become politically charged. Donald Trump, then the US president, had weighed in and alleged China might be culpable. Right-wingers in America were calling for multibillion-dollar reparations from China if it was proved to have caused the pandemic.

So a demand for an investigation of the origins of the virus by the Australian prime minister, Scott Morrison, on April 22 was not welcomed in Beijing. Morrison called for the WHO to appoint independent investigators, akin to weapons inspectors, and urged the international community to back a plan to track down the virus's origins in China. In the weeks that followed, China imposed trade sanctions on Australia's beef and barley.

Morrison had started a hare running. It was important to find the origin of the virus but there was much resistance by China, leading to some tough negotiating behind the scenes at the WHA. Many countries wanted an investigation to start immediately, but Chinese diplomats managed to fight that off. In the end it was the EU countries that brokered a compromise. "There were negotiations over every word," said a source in the WHO.

On May 19 the assembly agreed on a form of words for the inquiry. The resolution required the director-general of the WHO to work closely with member states to "identify the zoonotic source of

the virus and the route of introduction to the human population”. There was no mention of the word “investigation” or the timescale.



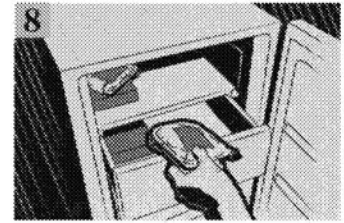
2017
 Tedros causes outrage by appointing Robert Mugabe, the tyrannical Zimbabwean president, a WHO goodwill ambassador. Sources say the appointment was encouraged by China, which was a close ally of Mugabe, having helped to fund his guerrilla war in Zimbabwe before he took power and ploughed cash into his sanctions-hit regime. After an outcry, the appointment is rescinded



January 2020
 China tries to cover up the Covid-19 outbreak by menacing whistleblowers, scrubbing social media and withholding evidence. The WHO amplifies China's denials of clear evidence the virus is passing between humans and explicitly advises against travel restrictions on virus hotspots, which would slow the virus's spread but harm China's economy



January 2020
 Tedros travels to Beijing to meet Xi Jinping. He gushes that the Chinese president has shown "rare leadership" and deserves "gratitude and respect". Tedros claims China is "completely committed to transparency" and shared the genomic sequence of the virus immediately. In fact, the lab that leaked the sequence was punished by the country's authorities for defying the censors



May-August 2020
 Tedros is instructed by the World Health Assembly to launch an inquiry into how the Covid-19 virus first infected humans. But the WHO strikes a backroom deal with Chinese authorities over the terms of reference, excluding the laboratory leak theory from the remit. China's preferred theory that the virus arrived in Wuhan on frozen food from abroad is examined, despite the lack of evidence

Graphic: The Times and The Sunday Times

There are those such as Jamie Metzl, a former member of the Clinton administration and an adviser to the WHO, who believe Tedros’s hands were tied from the beginning by the resolution. He says it had strong backing from China because it authorised “a Chinese-controlled joint study into a single-origin hypothesis, namely, that of zoonosis in the wild, and that is what I call the original sin, because there was a broad public perception that there was a WHO-led investigation, and there was no investigation that was ever authorised”.

However, the wording did not say this specifically, and it was left to Tedros and his team to draw up the terms of the inquiry with the Chinese authorities between May and July, which they did without seeking the opinions of the member states. The two sides took the decision to jointly interpret the loose wording — referring to “scientific and collaborative field missions” — as a mandate for a “study” rather than a proper independent investigation.

“It was never an investigation. Investigations are something different,” said the WHO source with knowledge of the negotiations. “With a study it’s not that you go and look for some wrongdoing ... You’re not looking backwards trying really to do a forensic audit of things and say, ‘Give me everything; show me everything.’ It doesn’t work like that.”

In July, Peter Ben Embarek, a WHO expert on infections that jump from animals to people, spent three weeks in China with a colleague horse-trading over the terms of reference of the “study”. Two weeks were spent in quarantine in a gloomy hotel on the outskirts of Beijing, and their

requests to interview Chinese researchers on Zoom were largely rebuffed. “It was a real struggle to get this going while they were on the ground and really depressing,” said the WHO source.

WHO insiders say Beijing held the trump card in the negotiations as it could always simply refuse to allow any of the scientific team to enter the country. That is why Tedros was averse to criticising the country’s leadership publicly, the insiders claim in his defence.

Behind closed doors the health agency ruled out any work on a matter that might make Beijing jumpy: the question of a possible laboratory leak. The study would concentrate on the zoonotic source of the virus, which the WHO argued was its narrow remit from the original WHA resolution.

But the resolution was clearly wider than the health agency’s interpretation. Even a virus that had leaked from the lab would have had a zoonotic origin before, for example, it was taken back to Wuhan by researchers. The crucial point was the second part of the resolution, which clearly states that the director-general was charged with finding out how such an animal virus would be then transmitted to humans.

The terms of reference were finalised between the WHO and China on August 2 last year. Yet, according to the US government, they were not shared with the other countries until the beginning of November.

That was when Garrett Grigsby, the US representative on the WHO executive board, immediately raised objections that the terms were “not negotiated in a transparent way with all WHO member states” and appeared to be “inconsistent” with the mandate. The complaints were ignored.

When asked why other nations had not been consulted about the terms, a WHO spokesman said: “In general, terms of reference for in-country scientific studies are not discussed by member states.”

By then the team of scientists had already been selected for the study. The health agency had deliberately chosen zoonotic experts rather than scientists who might be qualified to examine laboratory leaks. The team consisted of 34 scientists, and the agreement reached with Beijing was

that it would include 17 members from China, who would mostly be employed by the Chinese state.

The team turned out to contain a majority of Chinese nationals because the health agency chose Li Jian — one of its technical officers, who is from China — among its 17. Gostin says allowing so many Chinese scientists to be part of the WHO team “undermined the credibility and objectivity” of the inquiry.

Furthermore, China was given a veto over the choice of the non-Chinese experts. When the US put forward three scientists, including a laboratory expert, they were all rejected by the WHO without even a phone call. The only US representative chosen by the WHO was Peter Daszak, a New Yorker originally from Dukinfield, near Manchester.

Daszak was a controversial choice. He had been working with the Wuhan Institute of Virology on hunting down coronaviruses for more than 15 years and he headed the EcoHealth Alliance charity, which had redirected large grants from the US government to the Wuhan lab to fund some of its controversial coronavirus work.

The institute’s lead virologist, Shi Zhengli — nicknamed “Bat Woman” — described Daszak as her “collaborator” in an email to this newspaper that summer. However, the health agency regarded this conflict of interest as an irrelevance because it had already ruled out the possibility that the team would follow any lines of inquiry into the Wuhan institute.

A capable communicator, Daszak had already been vocal with his view that the virus first infected humans directly from an animal — possibly in one of China’s cramped live markets. He had even secretly orchestrated a statement rejecting the “conspiracy” theory that the virus did not have a natural origin, which was signed by 27 scientists and published by the medical journal *The Lancet* in February 2020. When his role in organising the letter was revealed this year, Daszak stepped down from a UN-backed *Lancet* commission that was separately looking into the origins of the virus, and the medical periodical retrospectively published a detailed disclosure document on his work in China.



Peter Daszak had been hunting viruses with the Wuhan Institute of Virology for 15 years

ALY SONG/REUTERS

The stakes were high for Daszak when the WHO chose him for the joint mission in late summer 2020. If it was concluded that the virus passed naturally from animals to humans, it would vindicate much of his life's work. However, all that work would be seriously undermined if the pandemic had begun at the laboratory he was so closely associated with.

Metzl, who has been campaigning for a proper investigation of the origins of the virus, believes Daszak's selection was "simply outrageous". He said: "So his entire career is ... in large part based on his collaboration with the Wuhan Institute of Virology. So he's the last person who should be on a committee that is examining the possibility of whether experiments that his organisation may have supported played a role in sparking this global pandemic."

Ebright added: "Shameful terms of reference were negotiated between WHO and China. Terms of reference that in essence ended up being the Chinese position without any change. Again it is hard not to see this as a repayment, or as a return on investment on the support the Chinese government provided for [Tedros's] election."

The centrepiece of the first phase of the WHO study was the long-awaited field trip to Wuhan, which finally began on January 14. It had been delayed by the Chinese government for reasons that were opaque: a year had passed since the original outbreak by the time the international scientists were allowed to set foot in the city where the first known Covid-19 cases were recorded.

According to the American magazine *Vanity Fair*, it was in the weeks before the trip that the US State Department had acquired its explosive — and hotly disputed — intelligence that three researchers from the Wuhan institute had fallen ill.

The researchers were alleged to be connected to the laboratory’s “gain of function” experiments on coronaviruses and appeared to have been taken to hospital with Covid-19-type pneumonia symptoms in November 2019. The timing of the cases is significant: this is exactly the time the outbreak is believed to have started and, if the intelligence is true, it would be a smoking gun in favour of the laboratory theory.

It is not clear when this information was conveyed to the WHO, but Tedros surprisingly decided to move the goalposts at about that time. According to WHO sources close to him, he agreed with China that the international team would now be allowed to briefly visit the Wuhan institute — while fully aware that the scientists that had been chosen were not qualified to assess the potential of a laboratory leak.

The Chinese had not acceded to every request by the health agency. They refused entry to a WHO communications officer who would have acted as spokesperson for the joint mission. The result was that the team’s most media-savvy communicator, Daszak, became the default spokesman for the group.

While the joint mission was in quarantine in a Wuhan hotel on January 15 this year, the US government publicly released its information about the researchers’ illnesses and raised concerns about the experiments that had been carried out at the laboratory on the closest known match to the Covid-19 virus. The US further claimed that the Wuhan institute had been engaged in secret projects with China’s military, including laboratory animal experiments, since 2017.

“For more than a year, the Chinese Communist Party has systematically prevented a transparent and thorough investigation of the Covid-19 pandemic’s origin, choosing instead to devote enormous resources to deceit and disinformation,” said the statement by the US State Department. “Nearly two million people have died. Their families deserve to know the truth.”

Joe Biden was due to be inaugurated as president in five days, and there was no sign that he would deviate from this hard line. It raised the stakes for the WHO team even higher.

Playing politics

As it was, the team’s visit to the Wuhan Institute of Virology lasted only a few hours. It was a smoggy day, and Daszak was filming the press pack outside the institute for his regular Twitter update. He would later claim that the joint mission had asked “tough” questions of the director and senior staff. “And the answers we got were consistent with everything that’s been put out there,” he said.

What actually happened was that the scientists asked a string of questions and appeared to take the answers from senior figures from the Wuhan institute at face value without seeking evidential proof.

Professor Thea Fischer, a Danish virologist who was part of the team, has described how she felt impolite asking direct questions. In an interview for a virology podcast she said the team concluded that it was not obvious that anything untoward had been “going on” but admitted: “This was based on questioning and not us coming with swabs or testing, or serology follow-up, or looking into lab logs, because it was not a lab audit.”

Before the trip there had been widespread disquiet in scientific circles about why the institute had, on September 12, 2019, taken offline a database that itemised its collection of 22,000 virus samples and sequences. The institute claimed it had taken the database down because it had feared hacking attacks, but it was a notable coincidence that it happened just before the pandemic is thought to have started.

Yet the joint mission team did not even demand access to the database. Daszak later explained that he had told the team there was no need to request the information as his charity had done a lot of work with the institute. “We do basically know what’s in those databases,” he said. They appear to have accepted his word and moved on.

Even WHO sources acknowledge that the lab visit was cursory. “They walk through the door, they talk to people and they walk out,” the source said. “I think they were there for about two hours. And it was better than nothing, but it was close to nothing.”

The team toured hospitals, a communicable disease centre, a propaganda museum and the empty Wuhan seafood market. When it finished in early February this year, it decided to conduct a straw poll of all the international and Chinese members on the relative likelihood of four theories on how the virus originated.

On the ground the Chinese were 17-strong as originally intended but the team were down to 14 as three of their experts were having to keep in contact remotely from outside China.

The ranking of possible theories took place in a Wuhan conference centre on February 8, with the two sets of scientists sitting in rows of chairs facing each other. They were given five options to categorise each theory, in a sliding scale from “very likely” to “likely”, “possible”, “unlikely” and “extremely unlikely”.



WHO investigators at the Huanan seafood market in January this year

GETTY IMAGES

It is not known how many people favoured each theory, but the results were announced at a press conference in Wuhan on February 9. The favoured theory, which was backed as “likely” to “very likely”, was that the virus spread from a bat into another host animal, possibly through intensive farming, and was then passed on to humans.

In a sense this was a leap of faith, as the joint mission had found no evidence of such an intermediary animal or any clues as to how it might have travelled the huge distance to Wuhan. It was just that the scientists believed that this was the way these outbreaks had happened in the past. But then laboratory leaks had happened too.

The decision was perhaps unsurprising, given this was a team that had been specifically picked to concentrate solely on the natural animal causes of the pandemic. In addition, the joint mission’s Chinese contingent were under pressure from their government to dismiss any suggestion of culpability.

Therefore the joint mission found the idea that a virus could have leaked from an institution in Wuhan “extremely unlikely” and unworthy of further investigation. Even the theory that the virus might have entered China on frozen food was ranked higher and classed as “possible”. The Chinese scientists had been pushing this theory and claimed to have evidence of a small number of cases in which the virus had been reintroduced to China on frozen food packaging.

The implausibility of the theory was later highlighted when the team’s more detailed report was released. But the joint mission’s “possible” verdict had given the theory a semblance of credibility, which was welcomed in Beijing because it suggested the virus might have originated outside its borders.

Sources close to Tedros say he was taken by surprise when Embarek, the mission’s joint leader, dismissed the lab leak theory at the press conference. “That was the first time when we realised back in Geneva that there was an agreement among the totality of terminology that did not feel grounded in science, specifically this relative weighting of hypotheses,” said the source.

The WHO insiders admit that the team was not even qualified to make that judgment. They point out that the health agency has a specialist “lab audit team”, which, for example, regularly checks Russian and American smallpox labs. “And that group had not fed into the choice of the team,” the source said. “Nor had any of those people gone [to Wuhan], because we weren’t able to negotiate something like that in the terms of reference.”

A second WHO source was even more damning. “These guys should have not gone into the labs at all. They had not been given proper access to these labs. They didn’t have expertise. They didn’t have a mandate,” they said. “And then they came out with this ‘extremely unlikely’ thing. We were all surprised. I was listening and I had no idea why they would say that. I think it was a little bit naive, honestly.”

Last week, Emabarek gave an extraordinary interview for a Danish television documentary in which he disclosed that the joint mission had been forced to rule out a lab leak because of pressure from Beijing. He said the final report had been vetted by the Chinese government employees and

the team were only allowed to mention the theory if they agreed that they would not pursue it further.

Embarek said it was possible that a laboratory employee may have been infected while collecting samples from bats in the wild. “We consider that hypothesis a likely one,” he added. This was not what the team had told the world.

It is still not clear why Tedros organised for the team to visit the laboratory in his last-minute negotiations. But the director-general was under pressure after the joint mission’s press conference in February. He was only too aware the new US president held more sway among America’s international allies than Trump. While Biden had reversed his predecessor’s decision to stop funding the health agency, he was not backing down on the confrontation with China over the origin investigation.

With the WHO’s credibility on the line, Tedros decided to take a diplomatic approach to the joint mission’s findings. He called a press conference to praise the team for its work while making clear that “all hypotheses remain open and require further analysis and studies”.

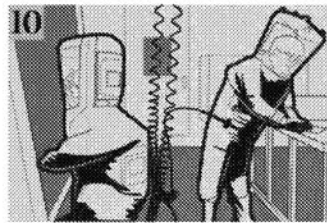
When the joint mission produced its report in March, it was clear that there had been a lack of rigour in the team’s reasoning for ruling out the Wuhan laboratory as a possible source.

It made two main arguments. The first was that there “was no record of viruses closely related to Sars-CoV-2 in any laboratory before December 2019”. Yet it had not been given access to the Wuhan institute’s virus database. Second, it observed that staff at the institute had claimed nobody at the lab had been ill with respiratory symptoms. But the WHO joint mission had not been given access to research staff or their personnel records.

The report prompted a further joint statement by the US and 13 allies, including Britain, Australia and Japan, which expressed concerns about its findings and alleged the scientists’ work had been hampered by significant delays and “lacked access to complete, original data and samples”.



9
August-November 2020
 China is given a veto over the make-up of the inquiry team, which ends up with more Chinese than non-Chinese scientists and is made up of experts qualified to examine the animal-to-human transmission and frozen meat theories rather than those trained to do lab audits. The zoologist Peter Daszak, who has a close relationship with the Wuhan Institute of Virology, is one of them



10
January 2021
 As the WHO team arrives in Wuhan, the US discloses that three researchers at the institute had fallen ill with Covid-19-style symptoms in autumn 2019. The US raises concerns about the lab's experiments to make coronaviruses more infectious to humans and says it was secretly working with the military. China denies the claims about the sick researchers and military involvement



11
February 2021
 After excluding the lab leak from the terms of reference and choosing a team without the expertise to examine the theory, Tedros arranges for the WHO team to spend a few hours at the Wuhan institute speaking to senior staff. They insist there was no leak, but the team is given no access to records. The WHO team announces that the lab leak theory warrants no further consideration



12
March 2021 onwards
 After the US raises "deep concerns" about the findings, Tedros says all origin theories should remain on the table. China says it will not participate in further inquiries within its borders and is critical of the WHO. Prominent scientists call for a fresh, "transparent and objective" investigation. Joe Biden asks his intelligence services to redouble efforts to uncover the truth

Graphic: The Times and The Sunday Times

The bigger picture was that the WHO study was in disarray. Whether by design or opportunism, China had triumphed. Beijing had never wanted an investigation of the origin of the virus and had used all its considerable influence at the WHO to make sure it was watered down.

“This outbreak was serious enough to potentially damage China’s image, its legitimacy, its interests, its ambitions and the image it was trying to project internationally,” said Fidler, the former lawyer for the health agency. “So that political dynamic led China to control and decide the way in which these investigations were going to happen. And that’s made nobody outside China happy.”

In late May Biden ordered the CIA to redouble its efforts to investigate how the outbreak started, “including whether it emerged from human contact with an infected animal or from a laboratory accident”. When it reports in a few weeks’ time, more may be revealed about the reliability or otherwise of the intelligence on the Wuhan institute.

But China was ready to pull up the drawbridge. When, on July 22, the WHO proposed a new phase two of the investigation, which would include an audit of the Wuhan labs, it was quickly rejected by China. The country’s top health officials held a press conference in Beijing to say the results of the joint team’s work should be accepted and the next phase should look at whether the pandemic had begun in a country outside China.

It means that unless China can be somehow compelled to open itself up to more thorough investigation, which appears unlikely, the world may never get to the bottom of what caused the great pandemic of the 21st century, which has killed four million people and counting.

In preparing this article, we asked to interview the health agency's staff who were part of the investigation as well as Tedros. The WHO press office declined our request. Margaret Chan did not respond to a request for comment.

A WHO spokesperson said this newspaper's article rehashed old events and contained "falsehoods and baseless claims". The agency argues that the director general treats China like any other country as a matter of principle.

"WHO's top priority is ending the acute stage of the Covid-19 pandemic and we are supporting countries to implement comprehensive, evidence based responses, based on the consistent use of public health measures and the equitable use of life-saving tools including vaccines," the spokesperson added.

Meanwhile, Tedros is likely to stand for re-election when his term ends next year and, if he does, will no doubt again seek backing from China.

Cheers,

Peter

Peter Daszak
President

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

From: Morens, David (NIH/NIAID) [E] [b6]
Sent: Sunday, August 15, 2021 1:30 PM
To: Peter Daszak [b6] Robert Kessler [b6] Keusch, Gerald T
[b6]
Subject: RE: Sunday Wash Post editorial

Yes, the shit never ends, it seems. Do you know him well enough to email him and say “wat’s up here?”

David

David M. Morens, M.D.

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From: Peter Daszak [b6]
Sent: Sunday, August 15, 2021 1:23 PM

To: Morens, David (NIH/NIAID) [E] [b6]; Robert Kessler [b6] Keusch,
Gerald T [b6]

Subject: RE: Sunday Wash Post editorial

I don't buy the argument that he simply didn't say anything new. He knowingly gave space for the lab leakers to latch on to the 'field scientist' idea, which is never disprovable of course, but exactly as unlikely as any other lab pathway because 1) they wore PPE, 2) they tested all the samples and none had SARS-CoV-2, and 3) the bat-farmed wildlife-Huanan market is far more likely.

He shouldn't have said what he said to the press, and absolutely knew it would lead to this sort of crap in the US. I think it helps him and WHO look tougher on the lab leak stuff, and helps remove some political heat in the long run.

Very irritating considering the papers are linking and EcoHealth into all this as usual - it's just too easy for them. Sunday Times did another piece today and it's let to more vitriol on social media directly straight at EHA and me.

Cheers,

Peter

Peter Daszak
President

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

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

From: Morens, David (NIH/NIAID) [E] [b6]
Sent: Sunday, August 15, 2021 10:32 AM
To: Peter Daszak [b6]; Robert Kessler

b6

Subject: Sunday Wash Post editorial

Touting Embarek's supposed recantating. d

Sent from my iPhone

David M Morens

OD, NIAID, NIH

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From: Peter Daszak [b6]
Sent: 7/27/2021 6:18:30 PM
To: Morens, David (NIH/NIAID) [E] [b6]; Keusch, Jerry
([b6]);
Subject: RE: Physician-Scientist Steven Quay: Forensic examination of Wuhan Institute of Virology COVID-19 patient specimens from December 2019 reveals extensive laboratory contamination, including evidence of genetic manipulation of the Nipah Viru

No – keep them coming – I miss some of these and I like to be aware.

It's also a chance for me to fill you in on any background if I've heard anything – can be useful given both of your positions...

Cheers,

Peter

Peter Daszak
President

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


From: Morens, David (NIH/NIAID) [E] [b6]
Sent: Tuesday, July 27, 2021 2:16 PM
To: Peter Daszak [b6]; Keusch, Jerry [b6]
Subject: RE: Physician-Scientist Steven Quay: Forensic examination of Wuhan Institute of Virology COVID-19 patient specimens from December 2019 reveals extensive laboratory contamination, including evidence of genetic manipulation of the Nipah Viru

I probably shouldn't even send you this sort of crap, but just want to give you a heads up from a friendly source, before someone blind-sides you. If you have a cat, you can use this paper to line the kitty litter box.....

David

David M. Morens, M.D.

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 301 496 4409

 **b6**

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From: Peter Daszak **b6**

Sent: Tuesday, July 27, 2021 1:42 PM

To: Morens, David (NIH/NIAID) [E] **b6**; Keusch, Jerry **b6**

Subject: RE: Physician-Scientist Steven Quay: Forensic examination of Wuhan Institute of Virology COVID-19 patient specimens from December 2019 reveals extensive laboratory contamination, including evidence of genetic manipulation of the Nipah Viru

This is part of a continuing saga of BS that's something to do with how when you use a certain type of sequencing machine, you get partial bleeds from other samples including previously used. It's extremely common and not at all interesting. It's also not a 'menagerie of viruses' – these are cDNA read outs from a sequencer (or something).

I checked this out previous with Eddie Holmes, Kristian Andersen and a bunch of other well-known virology genetics folks. These people are really scraping the bottom of the barrel!

Worst of all, it's a preprint, which means it might actually get published somewhere and sully the scientific system. It happened with another paper a few weeks ago that was published in American Chemical Society transactions or

something. Zhengli, Linfa, Angela Rasmussen, Bob Garry and me wrote in demanding it be retracted – we'll see how that goes...

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](https://twitter.com/PeterDaszak)

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

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

Sent: Monday, July 26, 2021 5:39 PM

To: Peter Daszak ([b6]); [b6]; Keusch, Jerry ([b6])
[b6]


Subject: FW: Physician-Scientist Steven Quay: Forensic examination of Wuhan Institute of Virology COVID-19 patient specimens from December 2019 reveals extensive laboratory contamination, including evidence of genetic manipulation of the Nipah Viru



David M. Morens, M.D.

CAPT, United States Public Health Service
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 **b6** (assistant: Whitney Robinson)

 301 496 4409

 **b6**

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

b6

Sent: Monday, July 26, 2021 5:37 PM

Subject: Physician-Scientist Steven Quay: Forensic examination of Wuhan Institute of Virology COVID-19 patient specimens from December 2019 reveals extensive laboratory contamination, including evidence of genetic manipulation of the Nipah Virus

Physician-Scientist Steven Quay: Forensic examination of Wuhan Institute of Virology COVID-19 patient specimens from December 2019 reveals extensive laboratory contamination, including evidence of genetic manipulation of the Nipah Virus, a BSL-4 pathogen more lethal than Ebola

News provided by

Dr. Steven Quay

Jul 26, 2021, 09:00 ET

SEATTLE, July 26, 2021 /PRNewswire/ -- Physician-Scientist Steven Quay and a group of international scientists have published a pre-print, available [here](#), entitled, "CONTAMINATION OR VACCINE RESEARCH? RNA Sequencing data of early COVID-19 patient samples show abnormal presence of vectorized H7N9 hemagglutinin segment." In the paper, a forensic examination of the sequencing data from five COVID-19 bronchial lavage patient specimens reveals that the laboratory at the Wuhan Institute of Virology (WIV) was contaminated with a wide range of viruses, including Nipah virus genes in a cloning vector. Nipah is a BSL-4 pathogen with a lethality of 50% to 92%. A video summary of the paper can be found [here](#).

The highlights of the paper are:

- Five patient specimens were sequenced by the WIV in December 2019 and were part of an early report on SARS-CoV-2 published by Dr. Zhengli Shi and colleagues (Nature 579, 270–273 (2020). This paper has been viewed over one million times, making it one of the most highly read papers on the pandemic virus.
- The most abundant contaminant is an undisclosed H7N9 influenza vaccine, which in one specimen is over six-times as abundant as SARS-CoV-2.
- The Nipah virus gene sequences were found in infectious cloning vectors of the type used for genetic manipulation.
- Nineteen other contaminants, including Japanese Encephalitis virus, HIV, human T-cell leukemia virus, and hepatitis delta virus were found.

"It was surprising to find a menagerie of deadly viruses, strange pathogens, and even honeysuckle, plant genes in patient specimens sequenced at the WIV in December 2019, especially since this patient sequencing data has been publicly available to the entire scientific community inside of the US NIH GenBank database since February 2020," stated Dr. Steven Quay, MD, PhD. "The apparent widespread contamination of the laboratory at the very time the pandemic was just beginning is of course worrisome. But more important is getting answers to these questions: Why do these patient specimens contain an unreported influenza vaccine? What was the purpose of creating an undisclosed, apparently infectious clone of the deadly Nipah virus? Is this Nipah research part of another gain-of-function research project at the Wuhan Institute of Virology?"

About the Nipah Virus

Nipah virus, scientific name *Nipah henipavirus*, is a bat-borne virus that causes an infection in humans and other animals, with a high mortality rate. Numerous disease outbreaks caused by Nipah virus have occurred in South and Southeast Asia. Symptoms from infection vary from none to fever, cough, headache, shortness of breath, and confusion. This may worsen into a coma over a day or two, and 50% to 92% of those infected die. Complications can include inflammation of the brain and seizures following recovery. At this time there is no specific treatment for Nipah virus infection nor is there a vaccine..

About Steven Quay, M.D., Ph.D.

Dr. Steven Quay has over 360 published contributions to medicine and has been cited over 10,500 times, placing him in the top 1% of scientists worldwide. He holds 87 US patents and has invented seven FDA-approved pharmaceuticals which have been prescribed to over 80 million people. He is the author of the best-selling book on surviving the pandemic, *Stay Safe: A Physician's Guide to Survive Coronavirus*. He is the CEO of Atossa Therapeutics Inc. (Nasdaq: ATOS), a clinical-stage biopharmaceutical company developing novel therapeutics for oncology and infectious diseases.

He received his M.D. and Ph.D. from The University of Michigan, was a postdoctoral fellow in the Chemistry Department at MIT with Nobel Laureate H. Gobind Khorana, a resident at the Harvard-MGH Hospital, and spent almost a decade on the faculty of Stanford University School of Medicine. A TEDx talk he delivered on breast cancer prevention has been viewed over 220,000 times. His scientific manuscript entitled, "[A Bayesian analysis concludes beyond a reasonable](#)

doubt that SARS-CoV-2 is not a natural zoonosis but instead is laboratory derived," has been viewed over 175,000-times. For more information, visit www.DrQuay.com

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SOURCE Dr. Steven Quay

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From: Morens, David (NIH/NIAID) [E] [b6]
[b6]
Sent: 7/15/2021 2:46:00 PM
To: Peter Daszak [b6]
CC: Keusch, Jerry [b6]
Subject: RE: Science Speaks: Not until June 2021 does China report Wuhan wet markets sold palm civets, racoon dogs and mink from 2017-2019: Where are the SARS-CoV-2 results?

Yes, that's true. But he's a flake not a serious threat...

David

David M. Morens, M.D.

CAPT, United States Public Health Service
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From: Peter Daszak [b6]
Sent: Wednesday, July 14, 2021 9:19 PM
To: Morens, David (NIH/NIAID) [E] [b6]

Cc: Keusch, Jerry [b6]

Subject: RE: Science Speaks: Not until June 2021 does China report Wuhan wet markets sold palm civets, racoon dogs and mink from 2017-2019: Where are the SARS-CoV-2 results?

Yes – exactly. It’s harmless when he’s just writing interesting summaries of outbreaks, but he’s repeatedly supported the lab leak hypothesis and was an ‘early adopter’ of that when he commented about how suspicious he was of China’s outbreak investigation, leading to a piece in NY Times in early summer 2020 that didn’t really help anyone get closer to the truth, but raised his profile, I guess...

<https://www.nytimes.com/2020/07/08/health/coronavirus-origin-china-lucey.html>

Cheers,

Peter

Peter Daszak

President

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New York, NY 10018-6507
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Tel.: [b6]

Website: www.ecohealthalliance.org

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

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

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

Sent: Wednesday, July 14, 2021 8:42 PM

To: Peter Daszak [b6]

Cc: Keusch, Jerry [b6]

Subject: Re: Science Speaks: Not until June 2021 does China report Wuhan wet markets sold palm civets, racoon dogs and mink from 2017-2019: Where are the SARS-CoV-2 results?

I didnt want to say so, but that’s an apt description, or as we would say “gad fly” Without any expertise in anything, he flies off to every epidemic anywhere in the world, and then starts opining on it. Quite an expensive out of pocket but gig, but no one here in town takes him seriously. He’s kind of like a little kid, always trying to get a seat at the grownups table.... d

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

On Jul 14, 2021, at 19:55, Peter Daszak [b6] wrote:

I know him quite well. He's what we'd call in England a 'busy-body'. It's crazy to turn every single paper and event into an attack on China – just because one group was doing studies at a university with the goal of analyzing welfare and ethics at wildlife markets does not mean the China team involved in the WHO mission knew about it.

If China was trying to cover up this, why did they let this group publish a paper on it in Scientific Reviews!

Cheers,

Peter

Peter Daszak

President

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

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

Sent: Wednesday, July 14, 2021 5:23 PM

To: Peter Daszak ([b6]); [b6]; Keusch, Jerry ([b6])

Subject: FW: Science Speaks: Not until June 2021 does China report Wuhan wet markets sold palm civets, racoon dogs and mink from 2017-2019: Where are the SARS-CoV-2 results?

Presumably you guys know Dan Lucey?





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: Wednesday, July 14, 2021 5:01 PM

Subject: Science Speaks: Not until June 2021 does China report Wuhan wet markets sold palm civets, racoon dogs and mink from 2017-2019: Where are the SARS-CoV-2 results?

Not until June 2021 does China report Wuhan wet markets sold palm civets, racoon dogs and mink from 2017-2019: Where are the SARS-CoV-2 results?

By [IDSA Contributor](#) on [July 14, 2021](#).

By **Daniel R. Lucey MD, MPH, FIDSA**

Last month a paper titled "[Animal sales from Wuhan wet markets immediately prior to the COVID-19 pandemic](#)" by Xiao et al., in *Nature Scientific Reports* listed 18 mammalian species sold May 2017 -

November 2019 in Wuhan wet markets (Table 1). These mammalian species included masked palm civets (*Paguma larvata*) and racoon dogs (*Nyctereutes procyonoides*), species linked with SARS-CoV-1 in 2003 and known to be susceptible to SARS-CoV-2. Mink (*neovision vison*) were also sold, and the authors state these mink: . . . originated from fur farms — noting that SARS-CoV-2 has been reported in mink farms in Europe and North America.” (paragraph 3 of the Discussion section).

Notably, Figure 2 shows photos of **caged live mammals in the Huanan seafood market** including a racoon dog, amur hedgehogs, Chinese bamboo rat, marmots and hog badger.

In sharp contrast, the WHO-China joint team report from their work in Wuhan Jan. 14-Feb. 10, 2021 and posted March 30, 2021 (p. 98): “Although there is photographic evidence in a published paper that live mammals were sold at the Huanan market in the past (2014) (36) (date confirmed by author in statement Annex F) and unverified media reports in 2020, **no verified reports of live mammals being sold around 2019 were found.**” (my bolding added for emphasis and contrast with Figure 2 of the paper by Xiao et al. above).

Xiao et al., also state in the next to last paragraph of the Discussion section: “Furthermore, the WHO reports that market authorities claimed all live and frozen animals sold in the Huanan market were acquired from farms officially licensed for breeding and quarantine, as such no illegal wildlife trade was identified. In reality, however, because China has no regulatory authority regulating animal trading conducted by small-scale vendors or individuals it is impossible to make this determination”.

Specific information regarding racoon dogs is provided by Xiao et al:

“Racoon dog fur farming is legal in China; however, due to a drop in fur prices, racoon dogs are now frequently sold off in live animal markets, augmented by wild-caught animals.” (3rd paragraph of the Discussion section).

Xiao et al. state that no pangolins or bats were found in the Wuhan markets.

Memorably, Xiao X. (X.X.) et al. explained how these data were acquired:

“Serendipitously, prior to the COVID-19 outbreak, over the period May 2017-November 2019, we were conducting unrelated routine monthly surveys of all 17 wet market shops selling live wild animals for food and pets across Wuhan City (surveys were conducted by X.X.). This was intended to identify the source of the tick-borne (no human -to-human transmission) Severe Fever with Thrombocytopenia (SFTS), following an outbreak in Hubei province in 2009-2010 . . . these shops selling live, often wild, animals included two at Baishazhou market . . . seven at Huanan seafood market . . . four at Dijiao outdoor pet market . . .and four at Qiyimen live animal market . . .” (1st paragraph of Materials and Methods section).

“As an objective observer unconnected to law enforcement X.X. was granted unique and complete access to trading practices. On each visit, vendors were asked what species they had sold over the preceding month and in what numbers, along with the prices...and origin of these goods (wild caught or captive bred/farmed). Additionally . . . the number of individuals available for sale at the time of each visit was noted, and animals were checked for gunshot wounds . . .” (2nd paragraph of Materials and Methods section).

Even more people than the five co-authors (from China, Canada, and UK), and the multiple market vendors, were well aware of this study and its findings of live mammalian species in Wuhan wet markets, including the Huanan seafood market because:

“All protocols in the market survey were reviewed and approved by the Ethics Committee of Hubei University of Chinese Medicine (no 20161111). All vendors provided written informed consent to participate in these surveys, and all protocols were performed with relevant guidelines and regulations”. (4th paragraph of the Materials and Methods).

Two of the many key questions raised by this June 2021 publication are:

- **Will the WHO Director General, Dr. Tedros, determine from China why the WHO international team in Wuhan Jan-Feb 2021 was not informed of these important data**, especially with regard to the live masked palm civets, racoon dogs, and mink being sold in Wuhan wet markets May 2017 until November 2019 “immediately prior to the COVID-19 pandemic”?
- Will Dr. Tedros determine from China what became of these 18 live mammalian species in Wuhan wet markets in December 2019-January 2020 **and what were the results of (so far undisclosed) testing of these animals for SARS-CoV-2, especially the masked palm civets, the raccoon dogs, and the mink?**



Dr. Daniel Lucey

***Daniel Lucey, M.D. MPH, FIDSA, FACP**, is a Clinical Professor of Medicine at Dartmouth Geisel School of Medicine, Infectious Disease adjunct Professor at Georgetown Medical Center, senior scholar at Georgetown Law, Anthropology Research Associate at the Smithsonian Museum of Natural History and a member of the Infectious Diseases Society of America Global Health Committee. He served as a volunteer to outbreaks overseas including hands-on Ebola patient care in Sierra Leone and Liberia (Doctors without Borders) 2014, MERS 2013, SARS 2003, as well as HIV, H5N1, Zika, yellow Fever, and pneumonic plague 2017 (with WHO/USAID/CDC). Since Jan. 6, 2020 he has contributed more than 100 posts to Science Speaks on COVID-19 and traveled to China in February 2020. He initially proposed, then fundraised and helped design the content for 2018-2022 Smithsonian Exhibition on Epidemics due to zoonotic viruses. From 1982-1988 he trained at University of California San Francisco and Harvard and was an attending physician at the NIH (NIAID) in the 1990s while in the U.S. Public Health Service.*

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