

From: Morens, David (NIH/NIAID) [E] ([b6])
([b6])
Sent: 4/19/2020 6:21:38 PM
To: Akpa, Esther (NIH/NIAID) [E] ([b6]) ([b6]);
([b6]); ([b6]);
[b6]; Babcock Sarah ([b6]) ([b6]);
[b6]; Ellen Carlin ([b6]); Chertow, Jessica (NIH/NHLBI) [E]
([b6]) ([b6]);
([b6]); James T. Douglas ([b6]) ([b6]); Naomi
Gathua ([b6]) ([b6]); Bob Holman ([b6])
([b6]); ([b6]); Reck, Linda ([b6]) ([b6])

From Allison Imrie, 04/19/20:

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

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

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

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

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

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

In the meantime, stay safe, stay healthy, and STAY HOME.
Happy #QuarantineCooking!

1. Allison Imrie

[b6]


2. David Morens

[b6]

David

David M. Morens, M.D.

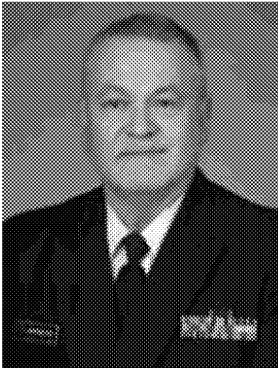
CAPT, United States Public Health Service
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 **b6** (assistants: Kimberly Barasch; Whitney Robinson)

 301 496 4409

 **b6**

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From: Morens, David (NIH/NIAID) [E] [redacted] b6
[redacted] b6
Sent: 8/23/2021 11:36:21 AM
To: Jason Gale [j.gale@bloomberg.net]
CC: [redacted] b6
[redacted] b6 Garry, Robert F [redacted] b6
[redacted] b6 [redacted] b6
BCC: Morens, David (NIH/NIAID) [E] [redacted] b6
[redacted] b6
Subject: Re: Economist - Shared Article 'Putting it all together'

TY, i think this is different from the article in The Economist a week or two ago? That one was interesting as i recall,...

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

On Aug 23, 2021, at 03:08, Jason Gale (BLOOMBERG/ NEWSROOM:) <j.gale@bloomberg.net> wrote:

In case you missed it, FYI.
Seems to lay things out well. I feel sorry for the int'l team. They didn't decide on/agree to the terms of reference, so the response from the DG on the final report (which he waited for until weighing in) seems disingenuous to me.

From: Paul Geitner (BLOOMBERG/ NEWSROOM:) At: 08/23/21 16:40:56 UTC+10:00
To: Jason Gale (BLOOMBERG/ NEWSROOM:)
Subject: Re:Fwd:Economist - Shared Article 'Putting it all together'

“The virus mystery” broadcast on August 12th, drew uncommonly wide attention for a Danish television documentary. That was because it featured Peter Ben Embarek, an expert on food security and zoonotic diseases, casting doubt on the conclusions of a “joint study” on the origins of the covid-19 pandemic carried out earlier this year under the auspices of the World Health Organisation (who). Dr Ben Embarek was the senior who figure who went to China as part of that study.

In March the joint study reported that it was “extremely unlikely” that the virus had been released in a laboratory accident. Dr Ben Embarek revealed that this conclusion did not come from a balanced assessment of all the relevant evidence but from a steadfast refusal by the Chinese members of the joint study to support anything stronger. Indeed they only allowed even that minimal assessment on the condition that the report did not call for further investigation into the question. He also pointed out that the idea that the point of spillover was someone collecting bat samples for research purposes belongs in the “likely” basket, along with other human interactions with wild bats.

Problems in the joint study had long been clear. Within the who one source describes it as “riddled with compromises and sloppiness”. Tedros Adhanom Ghebreyesus, the who’s director-general, was uneasy about the way it was carried out. He pushed back at the marginalisation of the lab-leak hypothesis, particularly when the final report was released in March. He has since called for further investigations into it, as well as into other possibilities.

The further unravelling of the joint study matters because, more than a year and a half after the covid-19 outbreak in Wuhan, a city in Hubei, was first recognised as the work of a new pathogen, there has been nothing like a thorough international investigation of how that pathogen, sars-cov-2, got into humans and spread round the world. The pandemic’s death toll stands at 9m-18m, according to a model which *The Economist* has built on the basis of excess-mortality reports and other indicators. The question of how it started matters both for the relatives of the dead and for those who wish to prevent such an outbreak happening again. China’s efforts to stop the world from answering it are both shabby and, to an extent, self-defeating. The more the truth seems hidden, the more it seems suspicious.

Earnest calls for an international investigation into the origins of covid-19 began in April 2020, voiced most clearly by Scott Morrison, the prime minister of Australia. The next month the World Health Assembly, the gathering of government representatives which serves as the who’s decision-making body, passed a motion calling for a study into the origins of the pandemic. But in order to be acceptable to China—which had reacted furiously to Mr Morrison’s original suggestion—the work was set up as a joint research project between two teams of scientists, one Chinese, one international. And it was to be based on “scientific and collaborative field missions”, rather than a targeted and forensic inquiry into all the relevant circumstances.

The terms of reference, which were subsequently negotiated behind closed doors, allowed the Chinese hosts to frame the joint study’s work in the way which best suited them. The study was set up to build on pre-existing Chinese research, not to delve into unvetted data. Investigating the laboratories that had been working with coronaviruses like sars-cov-2 in Wuhan was not part of its terms of reference.

After a lot of wrangling, the international team got to China in January this year. Data about the first reported covid-19 cases, those from December 2019, were one subject of friction with their hosts. The Chinese had reported 174 such cases, but would not share the underlying data on which those reports were based. Hearing that these vital data were not being made available worried Dr Tedros enough that he lobbied the Chinese government for access. The authorities declined, citing concerns over citizens’ privacy. It could have been anonymised.

Elsewhere the team appears to have been knowingly misled. Take, for example, the live-animal trade at the Huanan seafood and wildlife market, a site associated with a number of Wuhan’s earliest recorded cases of covid-19. In its final report, the study group took at face value claims there was no credible evidence that live mammals were sold there in 2019. A lot of eyewitness accounts gainsay that; so does a study published in *Scientific Reports*, a journal, this summer.

One report and no more

The *Scientific Reports* paper found that 18 species of mammal had been for sale in Wuhan between May 2017 and November 2019; gunshot wounds and trapping injuries suggested that almost a third of them were taken from the wild. Although the paper was published only recently, it was submitted to the journal in October 2020. Chinese law requires that all covid-19 research be reviewed by the government before it is sent to a journal. Some Chinese authorities would have known of its contents before the team arrived.

The market is not the only way for animals and the pathogens they carry to get into Wuhan. The horseshoe bats in which the closest wild relatives to sars-cov-2 have been found do not live anywhere near the city, but the two laboratories there that were known to have engaged in coronavirus research received samples from bat caves around the country. The joint-study team was not allowed to investigate the procedures around, or documentation of, this research; when it visited the laboratories the team was shown presentations on safety procedures but no more.



When the researchers left Wuhan the who

's Geneva headquarters told them that their report needed to be laid out scientifically and could express dissenting opinions; the international members and the Chinese members did not have to reach a consensus. However, according to sources within the who

, the team felt committed to producing a joint report with their Chinese counterparts. Dr Tedros was so unhappy with what finally emerged from the processes that he nobbled the report as it left the starting blocks, rejecting its contention that the possibility of a lab leak needed no further investigation.

On May 26th President Joe Biden ordered America's intelligence services to report on the pandemic's origins in 90 days (time will be up on August 24th). When he and his fellow g7

leaders met in June they joined in calling for a timely, transparent and science-based follow-up study. On July 16th Dr Tedros laid out the next steps which the

who

wants to see taken. They include further work on the Wuhan animal markets, studies of early cases and audits of local laboratories.

The Chinese government has reacted angrily to the idea of further studies on its territory. Zeng Yixin, the vice-minister of China's National Health Commission, said he was "shocked" by the plan to investigate a lab leak, saying it was "impossible" to accept. According to the *Global Times*, a tub-thumping tabloid run by the Communist Party, 55 countries have sent written complaints about the proposal for further investigations to the who

. Dr Tedros, elected director-general with China's support in 2017 and derided by President Donald Trump as China's puppet, may now face a Chinese-backed candidate when he looks for reappointment later this year.

In the absence of any hope that China will co-operate, sources of data beyond its control have become increasingly important. One area of interest is genetic sequence data. Another is early cases exported from China.

See what you did there

An online open-source-intelligence group which calls itself drastic

has been scouring sequencing data to get insight into activities at the Wuhan Institute of Virology (wiv). When researchers publish sequences they typically post the raw data from which those sequences are assembled to public databases such as the sequence-read archive at America's National Centre for Biotechnology Information. Contamination events in the laboratory, or within sequencing machines themselves, mean these data sometimes contain sequences not meant to be there. In theory such evidence could reveal nefarious goings-on.

Such work, while promising, takes a lot of resources. If you have the sort of supercomputers available to America's national labs it gets easier.

Gilles Demaneuf, a data scientist who works with drastic

, says he has a hunch the American intelligence community's 90-day study is working the same angle. It is conceivable that the intelligence services might have been able to filch raw sequence reads directly from Chinese sequencing machines, thus picking up even more data.

Sequencing data only offers a way forward if the virus did indeed leak out of a lab, something which remains a possibility but which is far from proven. The study of early cases should be useful whatever route it took; the closer you get to understanding the when and where of the crossing-over from animal to human, the easier it should be to learn something of the how.

On the basis of information provided by China the joint study concluded it was unlikely for there to have been any substantial transmission in Wuhan before December 2019. That is unlikely to be true. For one thing the *South China Morning Post*, a newspaper based in Hong Kong, obtained government documents in 2020 which showed one to five new cases a day in Wuhan from November 17th 2019 onwards. Further evidence has strengthened the possibility that the virus could have been in circulation much earlier than the official story allows.

That circulation need not have been limited to China. There is increasing evidence suggesting early infections elsewhere. These cases would have been exported from China; no virologists doubt that Hubei was where the virus got going within humans. But if circulation in Hubei goes back further than thought and cannot be directly assessed through studies there, the presence of cases elsewhere offers an alternative way to get an idea of the timing. If a specific travel link were identified, that might help identify a group in Hubei which was infected early on.

A recent study of blood samples from 9,144 adults in 12 different regions of France found seven which contained antibodies against sars-cov-2, all of them taken in November 2019. An Italian lung-cancer screening trial has found samples taken in September 2019 which seem to contain anti-sars-cov-2 antibodies. Another antibody study suggests the virus was circulating at a low level in northern Italy at the same time, notably in

Lombardy, a region which has close connections to Wuhan through the garment trade, and saw Europe's first major outbreak of covid-19 in March 2020.

Antibody tests can give false positives. In a preprint published on August 6th by the *Lancet*, researchers in Lombardy reported on looking instead for sars-cov-2 gene sequences. Examining 289 swabs and urine tests taken from people who had presented with a rash as far back as the second half of 2019, they found

sars-cov-2 sequences in 13, the earliest of which was taken on September 12th.

Sudhir Kumar of Temple University in Philadelphia says the *Lancet* preprint is likely to inspire other investigators to go back and look at retrospective hospital samples. That should help his own research into the origins of the virus. A family tree Dr Kumar and his colleagues have built from vast numbers of published sars-cov-2 genomes allows them to predict the sequence of the progenitor virus from which they are all descended. This sequence differs in three places from that found in the earliest samples taken from patients in Wuhan, meaning there had been enough spread for a certain amount of viral mutation to take place before December. Dr Kumar says that an analysis of the Lombardy sequences suggests that the timeline for the origin of the virus in China might now extend back to the late summer.

More systematic international research into these early infections and their circumstances is needed. Maria Van Kerkhove, head of emerging diseases and zoonoses at the

who, suggests it may be possible to prioritise work in areas which saw the earliest outbreaks in America, France, Italy and Spain. "I think the floodgates will open one day," says Dr Kumar.

A last line of light

An early origin would fit with the timeline that lab-leak proponents tend to favour. Early this August, the minority Republican staff on the House foreign-affairs committee released an 84-page report arguing this case. It makes much of a small but deadly disease outbreak which took place at an abandoned copper mine in Yunnan in 2012. As drastic showed last year, a virus studied at WIV which had been taken from that mine is the closest known relative to sars-cov-2.

The report sees importance in the removal, on September 12th 2019, of a database containing details of sequences and samples from the wiv

. This is read as the beginning of a cover-up, and thus as the point when the authorities first knew something had gone amiss, arguing for a leak in late August or early September. The

wiv

says it was a response to cyber-attacks.

A leak is not the only research-related possibility. The first person infected could have been someone employed by the

wiv

or another lab to collect bats and samples—the prospect to which Dr Ben Embarek pointed in his television interview. And it is important to remember that some other form of spillover outside the lab, either directly from a bat or by way of some other species, may well be to blame.

China clearly does not want lab-leaks investigated; but that does not mean it knows one happened. It is also being misleading about Huanan market, denying access to early-case data and obfuscating in various other non-lab-leak-specific ways. The most obvious explanation is that it does not really want any definitive answer to the question. An unsanitary market, a reckless bat-catcher or a hapless spelunker would not be as bad in terms of blame as a source in a government laboratory. But any definite answer to the origin question probably leaves China looking bad, unless it can find a way to blame someone else. To that end China has called for an investigation of Fort Detrick in Maryland, historically the home of American bioweapons research; state media regularly publish speculations about its involvement.

The possibility of spillover from wild bats does not have to be studied in China. Yunnan abuts onto Laos, Myanmar and Vietnam, and bats are not sticklers in matters of territory. Samples taken outside China could provide a good idea of viral diversity the other side of the border. A thorough evaluation of the existing farm-animal and wildlife trade in the region would also be useful.

Yet there is an inherent risk in such work that needs to be considered.

Efforts to uncover the roots of covid-19 by seeking out a natural reservoir of something very like

sars-cov-2 would, by definition, expose people to the sort of risks that can seed pandemics. Ironically, the very possibility of a lab leak raises questions about how most safely to pursue investigations into other possibilities.

When he called for further inquiries in July, Dr Tedros also announced the formation of a new permanent group of pathogen hunters, the International Scientific Advisory Group for Origins of Novel Pathogens (sago). He wants it to organise further studies of sars-cov-2. But it will also need to look at more general questions for the future—such as how to be sure that, come what may, studies of pathogens involved in past disease outbreaks never create further outbreaks of their own.

From: Jason Gale (BLOOMBERG/ NEWSROOM:) At: 08/23/21 14:34:52 UTC+8:00

To: Paul Geitner (BLOOMBERG/ NEWSROOM:)

Subject: Re:Fwd:Economist - Shared Article 'Putting it all together'

I saw. But it's behind a paywall. U have full access?

From: Paul Geitner (BLOOMBERG/ NEWSROOM:)

At: 08/23/21 16:23:52 UTC+10:00

To: Jason Gale (BLOOMBERG/ NEWSROOM:)

Subject: Fwd:Economist - Shared Article 'Putting it all together'

icymi

From: b6 At:
08/22/21 15:23:17 UTC+8:00
To: Paul Geitner (BLOOMBERG/
NEWSROOM:)
Subject: Economist - Shared
Article 'Putting it all together'

The Economist | Putting
it all together
[https://www.economist.co
m/international/2021/08/
19/the-world-needs-a-
proper-inve
stigation-into-how-
covid-19-
started?frsc=dg%7Ce](https://www.economist.com/international/2021/08/19/the-world-needs-a-proper-investigation-into-how-covid-19-started?frsc=dg%7Ce)


From: Morens, David (NIH/NIAID) [E]
Sent: Wed, 22 Sep 2021 16:40:14 +0000
To: Jason Gale; (b)(6);
(b)(6); Garry, Robert F; (b)(6)
Subject: RE: (TEL) Wuhan Scientists Planned to Release coronaviruses Into


If I read it correctly, these are inert nanopartricles to which are affixed proteins of interest, like a spike protein, so they wouldn't replicate but might be used as vaccines. The later part of the article describes so-called potential GoF experiments with live viruses.


David

David M. Morens, M.D.

CAPT, United States Public Health Service
Senior Advisor to the Director
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 (b)(6) (assistant: Whitney Robinson)

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 (b)(6)

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From: Jason Gale (BLOOMBERG/ NEWSROOM:) <j.gale@bloomberg.net>

Sent: Wednesday, September 22, 2021 12:28 PM

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

(b)(6); Garry, Robert F

Subject: RE: (TEL) Wuhan Scientists Planned to Release coronaviruses Into

I have no idea, David. It's the first time I've heard of this and it seemed too ridiculous to be true.

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

From: David Morens (b)(6)

To: JASON GALE, (b)(6)

(b)(6)

At: 09/23/21 00:27:24 UTC+10:00

Jason et al, these are just inert protein nanoparticles, correct, not live viruses as it might imply at the top?

David M. Morens, M.D.

CAPT, United States Public Health Service

Senior Advisor to the Director

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From: Jason Gale (BLOOMBERG/ NEWSROOM:) <j.gale@bloomberg.net>

Sent: Wednesday, September 22, 2021 3:09 AM

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

(b)(6);

Garry, Robert F (b)(6)

Subject: (TEL) Wuhan Scientists Planned to Release coronaviruses Into

The latest installment, jfyi

Wuhan Scientists Planned to Release coronaviruses Into Cave Bats 18 Months Before Outbreak
2021-09-21 17:14:22.531 GMT

By Sarah Knapton, Science Editor

(Telegraph) -- Wuhan scientists were planning to release enhanced airborne coronaviruses into Chinese bat populations to inoculate them against diseases that could jump to humans, leaked grant proposals dating from 2018 show.

New documents show that just 18 months before the first Covid-19 cases appeared, researchers had submitted plans to release skin-penetrating nanoparticles containing “novel chimeric spike proteins” of bat coronaviruses into cave bats in Yunnan, China.

They also planned to create chimeric viruses, genetically enhanced to infect humans more easily, and requested \$14million from the Defense Advanced Research Projects Agency (Darpa) to fund the work.

Papers, confirmed as genuine by a former member of the Trump administration, show they were hoping to introduce “human-specific cleavage sites” to bat coronaviruses which would make it easier for the virus to enter human cells.

When Covid-19 was first genetically sequenced, scientists were puzzled about how the virus had evolved such a human-specific adaptation at the cleavage site on the spike protein, which is the reason it is so infectious.

The documents were released by Drastic, the web-based investigations team set up by scientists from across the world to look into the origins of Covid-19.

In a statement, Drastic said: “Given that we find in this proposal a discussion of the planned introduction of human-specific cleavage sites, a review by the wider scientific community of the plausibility of artificial insertion is warranted.”

The proposal also included plans to mix high-risk natural coronavirus strains with more infectious but less dangerous varieties.

The bid was submitted by British zoologist Peter Daszak of EcoHealth Alliance, the US-based organisation, which has worked closely with the Wuhan Institute of Virology (WIV) researching bat coronaviruses.

Team members included Dr Shi Zhengli, the WIV researcher dubbed “bat woman”, pictured below, as well as US researchers from the University of North Carolina and the United States Geological Survey National Wildlife Health Centre.

Darpa refused to fund the work, saying: “It is clear that the proposed project led by Peter Daszak could have put local communities at risk”, and warned that the team had not properly considered the dangers of enhancing the virus (gain of function research) or releasing a vaccine by air.

Grant documents show that the team also had some concerns about the vaccine programme and said they would “conduct educational outreach ... so that there is a public understanding of what we are doing and why we are doing it, particularly because of the practice of bat-consumption in the region”.

Angus Dalglish, Professor of Oncology at St Georges, University of London, who struggled to get work published showing that the Wuhan Institute of Virology (WIV) had been carrying out “gain of function” work for years before the pandemic, said the research may have gone ahead even without the funding.

“This is clearly a gain of function, engineering the cleavage site and polishing the new viruses to enhance human cell infectibility in more than one cell line,” he said.

Daszak was also behind a letter published in The Lancet last year which effectively shut down scientific debate into the origins of Covid-19.

Viscount Ridley, who has co-authored a book on the origin of Covid-19, due for release in November, and who has frequently called for a further investigation into what caused the pandemic in the House of Lords, said: “For more than a

year I tried repeatedly to ask questions of Peter Daszak with no response.

“Now it turns out he had authored this vital piece of information about virus work in Wuhan but refused to share it with the world. I am furious. So should the world be.

“Peter Daszak and the EcoHealth Alliance (EHA) proposed injecting deadly chimeric bat coronaviruses collected by the Wuhan Institute of Virology into humanised and ‘batified’ mice, and much, much more.”

A Covid-19 researcher from the World Health Organisation (WHO), who wished to remain anonymous, said it was alarming that the grant proposal included plans to enhance the more deadly disease of Middle-East Respiratory Syndrome (Mers).

“The scary part is they were making infectious chimeric Mers viruses,” the source said.

“These viruses have a fatality rate over 30 per cent, which is at least an order of magnitude more deadly than Sars-CoV-2.

“If one of their receptor replacements made Mers spread similarly, while maintaining its lethality, this pandemic would be nearly apocalyptic.”

EcoHealth Alliance and the Wuhan Institute of Virology have been approached for comment.

-0- Sep/21/2021 17:14 GMT

To view this story in Bloomberg click here:


<https://blinks.bloomberg.com/news/stories/QZSNVY33O5C1>

From: Morens, David (NIH/NIAID) [E]
Sent: Tue, 5 Oct 2021 11:34:58 +0000
To: Taubenberger, Jeffery (NIH/NIAID) [E] ((b)(6)); Peter Daszak ((b)(6)); Keusch, Jerry ((b)(6))
Subject: FW: Wpost: NIH Director Francis S. Collins will step down by year's end


David

David M. Morens, M.D.

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

Sent: Monday, October 4, 2021 11:00 PM

Subject: Wpost: NIH Director Francis S. Collins will step down by year's end

NIH Director Francis S. Collins will step down by year's end

By

Lenny Bernstein

and

Carolyn Y. Johnson

Today at 10:21 p.m. EDT

National Institutes of Health Director Francis S. Collins, who headed the government's effort to map the entire human genetic code and two decades later became one of the most recognizable leaders in the battle against the coronavirus pandemic, will leave his post by the end of this year, NIH will announce Tuesday.

After more than 12 years directing the nation's premier biomedical research center, Collins, a 71-year-old physician-geneticist, will return to his lab at the National Human Genome Research Institute, part of NIH. He is the longest-tenured director of the Bethesda, Md.,-based NIH, which he ran through the Obama and Trump administrations and into the first year of the Biden presidency.

No decision has been made on an interim director, an NIH official said. In the midst of the pandemic, Biden will nominate a new director who must be confirmed by the evenly divided Senate.

In an interview, Collins said he went on a retreat by himself in May to assess the pros and cons of stepping down and eventually concluded that this was the year to do it. He said he did not want to get too far into the Biden administration before making the move and was confident NIH's role in developing therapeutics, tests and vaccines for the coronavirus had reached "a pretty stable place." The NIH partnered with Moderna to produce a highly effective coronavirus vaccine with stunning speed. "There comes a time where an institution like NIH really benefits from new vision, new leadership," he said. "This was the right timing."

A born-again Christian who wrote a book about reconciling science and religion, Collins came into his job in 2009 facing many questions — and some sharp criticism — about whether a man of faith should lead a data-driven research institution that includes world-renowned scientists among its 18,000 employees. How NIH chief Francis Collins is trying to get people of faith to wake up to coronavirus realities

He will step down at a time when such questions have given way to the politicization of science and sometimes violent disagreement about even well-proved medical facts.

"Every issue, the polarization gets deeper and deeper, the tribes have formed their views and it's very hard to see how we step back from that," he said.

Over the 12 years of Collins's tenure, NIH budget has risen from \$30 billion to \$41.3 billion and support from Congress has mostly remained steady. He has appointed most of the current heads of NIH's 27 institutes and centers.

Along the way, Collins, who still sometimes rides a Harley-Davidson motorcycle and breaks into song for occasions large and small, became one of the more public faces of science in the United States, especially as the pandemic continued. Collins plays an acoustic guitar decorated with a double-helix and sang the national anthem at Nationals Park in 2016.

“Francis Collins is a brilliant scientist and an amazing administrator, and a real humanist and a pretty good guitar player and singer too,” said Eric Lander, who worked with Collins on the Human Genome Project, which finished identifying and mapping all 20,000 human genes in 2000.

“Time after time, Francis was able to bring a vision to his institute at NIH, and then the whole NIH, to see what the next challenges would be that the scientific community could rally around. It was a huge thing,” Lander said.

But early in Collins’s tenure a deadly infection killed six people at NIH Clinical Center, the hospital where patients come for cutting edge treatments as part of clinical trials. In 2016, Collins was forced to replace the leadership of the Clinical Center after an independent review determined that patient safety had become “subservient to research demands.” And NIH has struggled to substantially add more people of color among the scientists who receive its grants.

The NIH passes out about 80 percent of its money to researchers at academic institutions around the U.S. and internationally, spending about 20 percent for the work conducted in its own labs.

“We have increased modestly the number of NIH grantees who are people of color, but it’s still well below” their proportion in the general population, Collins said. NIH has done a better job of bringing women into leadership positions, he said. In 2019, Collins said he would no longer appear on all-male panels at scientific meetings.

Born in Staunton, Va., and home-schooled through the sixth grade, Collins became one of the world’s top genetic researchers, helping to discover the genes responsible for cystic fibrosis and neurofibromatosis, a condition that causes tumors to form in the spine and brain.

Under Collins, NIH launched ambitious projects that took advantage of the scientific expertise he was able to tap, his experience leading the genome project — which involved scientists in six nations — and the money at his command.

They include the Cancer Moonshot championed by then vice president Biden in 2016; a large initiative to study the human brain; the All of Us Research Program that is enrolling 1 million Americans in a gigantic database to help examine a wide range of factors that affect health; a precision medicine project that would use the information from those research studies to better treat cancer and other diseases by targeting patients’ individual characteristics; a project to strengthen genomic research in Africa; and most recently an effort to understand long-haul covid-19 symptoms that plague 10 percent to 30 percent of people who develop the infection.

“As NIH director, you get to help coordinate that kind of high risk, as well as high reward, program,” Collins said.

Then came the pandemic, which would thrust Collins into his most public role as a communicator, force him to accelerate scientific research with sometimes breathtaking results and deliver a few of the lowest moments of his career.

“He has a knack for taking very complex topics and breaking them down in a way that people can understand,” said Jeff Zients, the White House Coronavirus Response Coordinator. “I think that’s very underappreciated in public health.

“I do think he is a force for good. And that he always leads with the data and the science and the facts and brings tremendous credibility to the public health arena.”

NIH’s best-known triumph of the pandemic is its work with the company Moderna to develop one of the three coronavirus vaccines in less than a year. The timeline and effectiveness of the vaccine were beyond what most thought possible when the effort began.

NIH also has worked with drug companies to develop therapeutics and at-home testing after the Centers for Disease Control and Prevention initially botched the rollout of the U.S. coronavirus testing program. Anthony S. Fauci, director of the National Institute of Allergy and Infectious Diseases, who has known Collins for decades, now interacts with him every day as part of the pandemic response.

He said one of the most important contributions Collins has made during the pandemic was his presence on Saturday morning calls with pharmaceutical companies, in an effort to persuade them to recruit Black and Hispanic people into vaccine trials.

“That is extremely noteworthy — that the director of NIH would join me and my programmatic colleagues on the nuts and bolts of what you need to do to get more African Americans and Hispanics involved in the clinical trials. He didn’t have to do that.”

But as President Trump veered from scientific fact in 2020, Collins considered stepping down. Collins came to Fauci’s office after hours on a winter evening to tell his friend that he was thinking of moving on.

“I said, ‘Please don’t do this,’” Fauci recalled in a conversation that Collins acknowledged in the interview. “I was pleading with him. For the good of NIH, he stayed on.”

Nor did Collins envision the culture war over vaccines and mask-wearing that has plagued the U.S. coronavirus response, a situation he called a “major heartbreak.

“I did not dream that we would end up with fantastic, historic [vaccine test] results and here we are in October 2021 with 70 million” people unvaccinated and hundreds of thousands dead “as a result of a culture war,” Collins said.

“I did not imagine that possible in the United States of America.”

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From: Morens, David (NIH/NIAID) [E]
Sent: Thu, 14 Oct 2021 20:52:22 +0000
To: Keusch, Gerald T; Peter Daszak ((b)(6)); Kessler, Robert ((b)(6)); Peter Hotez ((b)(6)); Gale, Jason
Subject: RE: Nature: 'I hope you die': how the COVID pandemic unleashed attacks on scientists/Dozens of researchers tell Nature they have received death threats, or threats of physical or sexual violence.

I called (b)(6) and told him I would speak to him either off the record or on.


He immediately called our NIH folks and asked to speak to me on the record, but so far HHS hasn't cleared it.

I am going to check again today. I am still on leave with (b)(6) and not checking things closely.


David

David M. Morens, M.D.

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

 301 496 4409

 (b)(6)

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From: Keusch, Gerald T (b)(6)
Sent: Thursday, October 14, 2021 4:47 PM
To: Morens, David (NIH/NIAID) [E] (b)(6); Peter Daszak
(b)(6); (b)(6); Kessler, Robert
(b)(6); (b)(6); Peter Hotez (b)(6)
(b)(6) Gale, Jason <j.gale@bloomberg.net>
Subject: RE: Nature: 'I hope you die': how the COVID pandemic unleashed attacks on scientists/Dozens of researchers tell Nature they have received death threats, or threats of physical or sexual violence.

Shameful. I saw Peter Hotez sitting there in the photo, and I know about his experiences too antedating CoV-2 because he is a proponent of vaccines and immunization programs.

We need more and more pushback. I know that (b)(6) is planning to write about the disbanding of our Lancet Task Force, having spoken to him at length, and while I have no idea how he will put it together I am pretty sure he will include comments from me that push back on Sachs "holier than thou" stance, as I provided information on all the other non-negotiable demands he made that seriously infringed on the integrity of the Task Force's work and the necessary fire wall that must be in place between an expert evaluation panel and the sponsor of the panel to maximize objective assessment.

Jerry

From: Morens, David (NIH/NIAID) [E] (b)(6)
Sent: Thursday, October 14, 2021 3:17 PM
To: Peter Daszak (b)(6); (b)(6); Keusch, Gerald T
(b)(6); Kessler, Robert (b)(6); (b)(6)
Peter Hotez (b)(6); (b)(6); Gale, Jason <j.gale@bloomberg.net>
Subject: FW: Nature: 'I hope you die': how the COVID pandemic unleashed attacks on scientists/Dozens of researchers tell Nature they have received death threats, or threats of physical or sexual violence.

Does this ring any bells?


David

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

Sent: Thursday, October 14, 2021 3:08 PM

Subject: Nature: 'I hope you die': how the COVID pandemic unleashed attacks on scientists/Dozens of researchers tell Nature they have received death threats, or threats of physical or sexual violence.

- NEWS FEATURE
- 13 October 2021

‘I hope you die’: how the COVID pandemic unleashed attacks on scientists

Dozens of researchers tell *Nature* they have received death threats, or threats of physical or sexual violence.

- [Bianca Nogrady](#)



Public-health researcher Tara Kirk Sell (centre) experienced online and e-mail attacks after talking about COVID-19 in the media. Credit: US House of Representatives’ Committee on Science, Space, and Technology

Infectious-diseases physician Krutika Kuppalli had been in her new job for barely a week in September 2020, when someone phoned her at home and threatened to kill her.

Kuppalli, who had just moved from California to the Medical University of South Carolina in Charleston, had been dealing with online abuse for months after she’d given high-profile media interviews on COVID-19, and had recently testified to a US congressional committee on how to hold safe elections during the pandemic. But the phone call was a scary escalation. “It made me very anxious, nervous and upset,” says Kuppalli, who now works at the World Health Organization (WHO) in Geneva, Switzerland. She called the police, but didn’t hear that they took any action. The threatening e-mails, calls and online comments continued. The police officer who visited Kuppalli after a second death-threat call suggested she should get herself a gun.

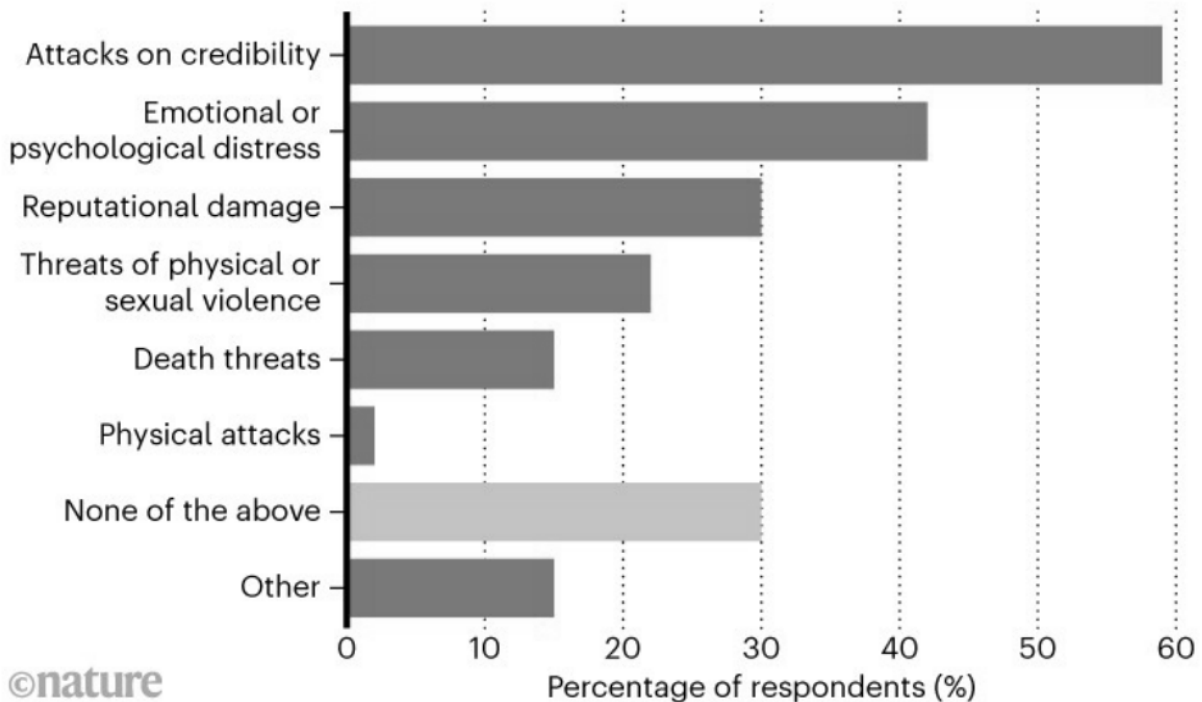
Kuppalli’s experience during the pandemic is not uncommon. A survey by *Nature* of more than 300 scientists who have given media interviews about COVID-19 — many of whom had also commented

about the pandemic on social media — has found wide experience of harassment or abuse; 15% said they had received death threats (see ‘Negative impacts’).

NEGATIVE IMPACTS

In a *Nature* survey of scientists who have commented about COVID-19, 15% of 321 respondents said they had received death threats.

Question: Have you experienced any of the following negative impacts after speaking about COVID-19 to the media, or posting on social media? (You may select multiple options.)



Source: *Nature* analysis

Some high-profile examples of harassment have been well documented. Anthony Fauci, head of the US National Institute of Allergy and Infectious Diseases, was assigned personal security guards after he and his family received death threats; UK chief medical adviser Chris Whitty was grabbed and shoved in the street; and German virologist Christian Drosten received a parcel with a vial of liquid labelled ‘positive’ and a note telling him to drink it. In one extraordinary case, Belgian virologist Marc Van Ranst and his family were placed in a safe house when a military sniper went on the run after leaving a note outlining his intentions to target virologists.

These examples are extreme. But in *Nature’s* survey, more than two-thirds of researchers reported negative experiences as a result of their media appearances or their social media comments, and 22% had received threats of physical or sexual violence. Some scientists said that their employer had received complaints about them, or that their home address had been revealed online. Six scientists said they were physically attacked (see Supplementary information for survey data tables).

Coordinated social-media campaigns and threatening e-mails or phone calls to scientists are not new: topics such as climate change, vaccination and the effects of gun violence have drawn similar attacks in the past. But even scientists who had a high profile before COVID-19 told *Nature* that the abuse was a new and unwelcome phenomenon tied to the pandemic. Many wanted the extent of the

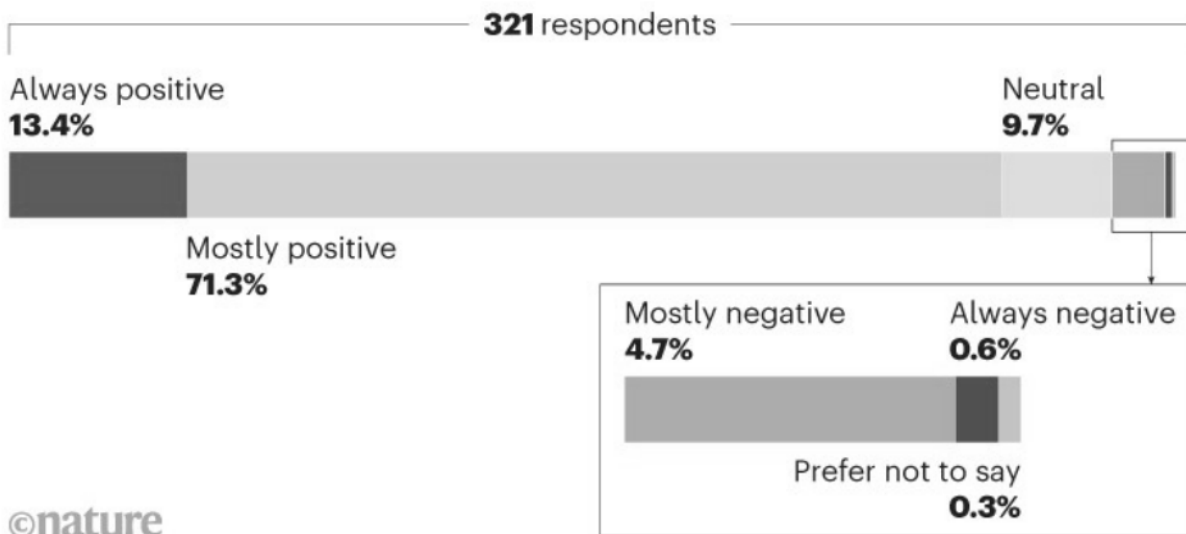
problem discussed more openly. “I believe national governments, funding agencies and scientific societies have not done enough to publicly defend scientists,” one researcher wrote in their survey response.

Some researchers say that they have learnt to cope with the harassment, accepting it as an unpleasant but expected side effect of getting information to the public. And 85% of survey respondents said that their experiences of engaging with the media were always or mostly positive, even if they were harassed afterwards (see ‘Media experiences’). “I think scientists need training for how to engage with the media and also about what to expect from trolls — it’s just a part of digital communication,” one wrote.

MEDIA EXPERIENCES

In *Nature*’s survey, scientists mostly reported positive experiences with the media during COVID-19.

Question: How would you rate your experiences with the media during the pandemic?



Source: *Nature* analysis

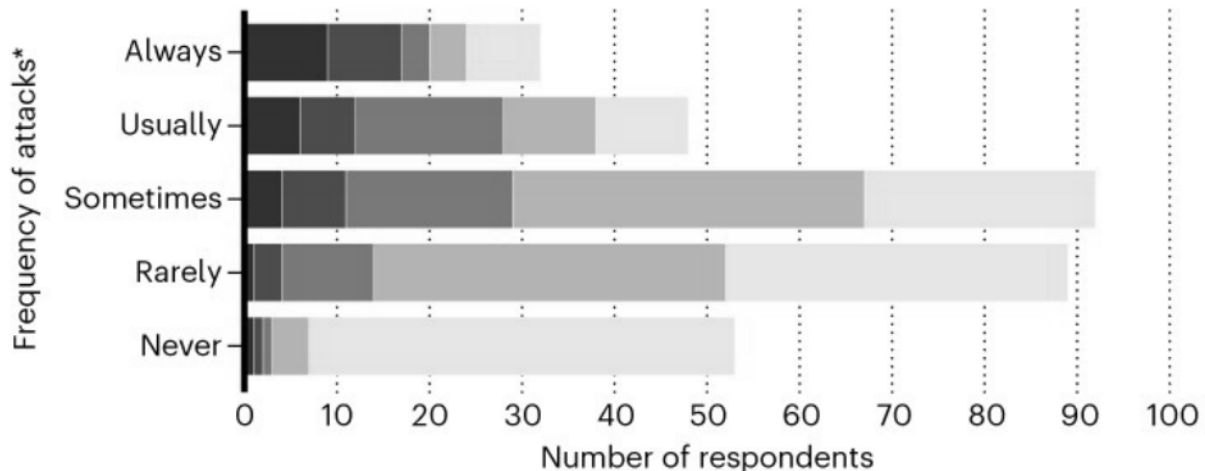
But *Nature*’s survey suggests that even though researchers try to shrug off abuse, it might already have had a chilling effect on scientific communication. Those scientists who reported higher frequencies of trolling or personal attacks were also most likely to say that their experiences had greatly affected their willingness to speak to the media in the future (see ‘Chilling effect?’).

CHILLING EFFECT?

In *Nature's* survey, scientists who reported the highest frequency of trolling or personal attacks* were also most likely to say that their experiences had greatly affected their readiness to give future media interviews.

Question: How much have your experiences with trolls and personal attacks affected your willingness to speak to the media in the future?

■ An enormous amount ■ A lot ■ A moderate amount ■ A little ■ Not at all



*Respondents who answered the question: Have you experienced trolling or personal attacks after speaking about COVID-19 in the media?

©nature

Source: *Nature* analysis

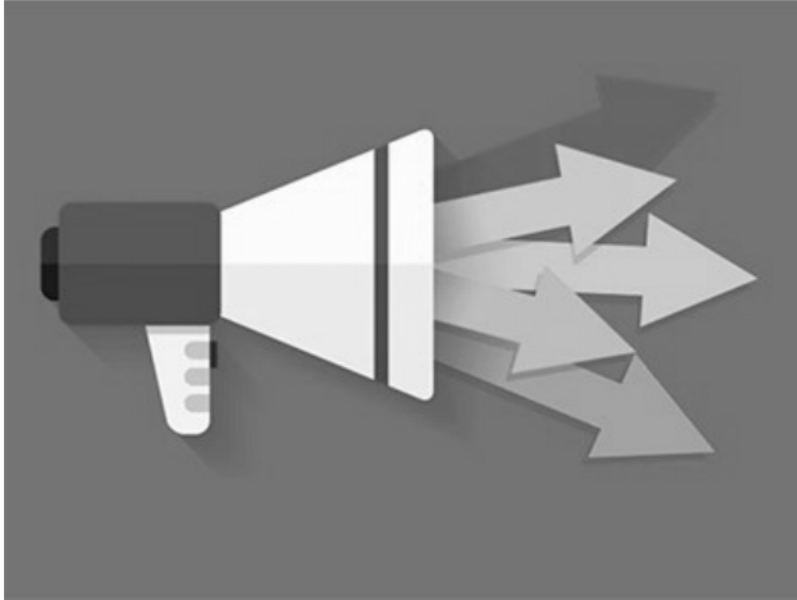
That is concerning during a global pandemic which has been accompanied by a battery of disinformation and misinformation, says Fiona Fox, chief executive of the UK Science Media Centre (SMC) in London — an organization that collates scientific comment and organizes press briefings for journalists. “It’s a great loss if a scientist who was engaging with the media, sharing their expertise, is taken out of a public debate at a time when we’ve never needed them so badly,” she says.

Tracking harassment

In June, the Australian SMC in Adelaide asked researchers on its COVID-19 media lists about their experiences. The centre had been alerted to online bullying and hate campaigns directed at scientists, and wanted to know whether it was a broader problem, says Lyndal Byford, the centre’s director of news and partnerships.

Byford shared the results with *Nature*. Fifty researchers answered the SMC’s informal survey. Nearly one-third reported experiencing emotional or psychological distress after talking about COVID-19; 6 people (12%) reported receiving death threats, and 6 said they had received threats of physical or sexual violence. “I think any organization involved in helping scientists communicate would find that quite disturbing,” Byford says.

To get a broader sense of the scale of harassment, *Nature* adapted the Australian SMC’s survey, and asked science media centres in the United Kingdom, Canada, Taiwan, New Zealand and Germany to send it to scientists on their COVID-19 media lists. *Nature* also e-mailed researchers in the United States and Brazil who had been prominently quoted in the media.



“I had to be with bodyguards with guns” — attacks on scientists during the pandemic

The results are not a random sample of researchers who have given media interviews on COVID-19, because they represent only the experiences of the 321 scientists who chose to respond (predominantly in the United Kingdom, Germany and the United States). But the numbers reveal that researchers in many countries are facing abuse related to the pandemic, and the proportions reported were higher than in the Australian survey. More than one-quarter of respondents to the *Nature* survey said they always or usually received comments from trolls or were personally attacked after speaking in the media about COVID-19. And more than 40% reported experiencing emotional or psychological distress after making media or social media comments.

Politicized science

To some extent, this harassment of scientists reflects their rising status as public figures. “The more prominent you are, the more abuse you’re going to get,” says historian Heidi Tworek at the University of British Columbia in Vancouver, Canada, who is studying online abuse of health communicators in the pandemic. Most US public-health departments have also received harassment directed at staff and officials, adds Beth Resnick, a public-health researcher at Johns Hopkins Bloomberg School of Public Health in Baltimore, Maryland, who has surveyed 580 departments in a study that is not yet published. And such attacks might have little to do with the science itself and more to do with who’s talking. “If you’re a woman, or a person of colour from a marginalized group, that abuse will probably include abuse of your personal characteristics,” says Tworek. For instance, Canada’s chief public-health officer Theresa Tam is Asian Canadian, and abuse levelled against her included a layer of racism, Tworek says. Kuppalli, a female scientist of colour, says she also experienced this. Abusers told her she “needs to go back where she came from”.



Krutika Kuppalli. Credit: Kathryn Van Aernum

Both the Australian SMC and *Nature's* survey, however, found no clear difference between the proportions of violent threats received by men and women. "We were surprised," Byford says. "We really felt women would be bearing more of a brunt in terms of the abuse that they got."

Some aspects of COVID-19 science have become so politicized that it is hard to mention them without attracting a storm of abuse. Epidemiologist Gideon Meyerowitz-Katz at the University of Wollongong in Australia, who has gained a following on Twitter for his detailed dissection of research papers, says that two major triggers are vaccines and the anti-parasite drug ivermectin — controversially promoted as a potential COVID-19 treatment without evidence it was effective. "Any time you write about vaccines — anyone in the vaccine world can tell you the same story — you get vague death threats, or even sometimes more specific death threats and endless hatred," he says. But he's found the passionate defence of ivermectin surprising. "I think I've received more death threats due to ivermectin, in fact, than anything I've done before," he says. "It's anonymous people e-mailing me from weird accounts saying 'I hope you die' or 'if you were near me I would shoot you'."



Gideon Meyerowitz-Katz. Credit: Daniel Naidel

Andrew Hill, a pharmacologist at the University of Liverpool's Institute of Translational Medicine, received vitriolic abuse after he and his colleagues published a meta-analysis in July. It suggested ivermectin showed a benefit, but Hill and his co-authors then decided to retract and revise the analysis when one of the largest studies they included was withdrawn because of ethical concerns about its data (A. Hill *et al.* *Open Forum Inf. Dis.* **8**, ofab394; 2021). After that, Hill was besieged with images of hanged people and coffins, with attackers saying he would be subject to 'Nuremberg trials', and that he and his children would 'burn in hell'. He has since closed his Twitter account.

In Brazil, microbiologist-turned-science-communicator Natalia Pasternak also noticed online attacks against her increasing when she spoke about the unproven COVID-19 treatments being promoted by the Brazilian government, which include ivermectin, the antimalarial drug hydroxychloroquine and the antibiotic azithromycin. In 2018, Pasternak founded the *Instituto Questão de Ciência* — the Question of Science Institute — with the aim of promoting the use of scientific evidence in policymaking and discourse. When COVID-19 happened, Brazil "became the first country in the world to actually promote pseudoscience as a public policy, because we promote the use of unproven medications for COVID-19", Pasternak says.

She appeared on major television stations and produced her own YouTube show, called the Plague Diary. Commenters criticized her voice and appearance, or argued that she wasn't a real scientist. But, Pasternak says, the attacks rarely challenged what she was saying.

Some attackers have also tried to use the law to silence their targets. A group of supporters of Brazilian president Jair Bolsonaro tried to sue Pasternak for defaming him when she likened Bolsonaro to a plague on her YouTube show; the lawsuit was dismissed. And Van Ranst has been sued for defamation

by a Dutch protester who opposes vaccination and public-health measures such as lockdowns in Belgium and the Netherlands.

Another topic that attracts high volumes of abuse is the question of SARS-CoV-2's origins. Both the Australian and UK SMCs say they have struggled to find scientists who are willing to comment publicly on the issue for fear of getting attacked. Fox says the UK SMC has approached more than 20 scientists to participate in a briefing on this question, but all declined.

Virologist Danielle Anderson, now at the Peter Doherty Institute for Infection and Immunity at the University of Melbourne in Australia, received intense, coordinated online and e-mail abuse after writing a fact-checking critique in early 2020 of an article suggesting that SARS-CoV-2 might have leaked from China's Wuhan Institute of Virology (WIV). At the time, she was based at the Duke–National University of Singapore Medical School in Singapore, but had collaborated with the WIV since the epidemic of severe acute respiratory syndrome (SARS) in 2002–04. "Eat a bat and die, bitch," one e-mail read.



Virologist Danielle Anderson received abuse after critiquing an article on SARS-CoV-2's origins. Credit: James Bugg

Another researcher with a long-standing WIV collaboration, Peter Daszak, president of EcoHealth Alliance in New York City, has also received abuse. Daszak, who travelled to Wuhan in January as part of a WHO-coordinated inquiry into the origins of SARS-CoV-2, says he's had a letter containing white powder sent to his home, had his address posted online and regularly receives death threats. Harassment has cut both ways when it comes to SARS-CoV-2's origins. Alina Chan, a postdoctoral researcher at the Broad Institute of MIT and Harvard in Cambridge, Massachusetts, has received abuse for her work on the idea that the pandemic might have resulted from exposure to a virus at a laboratory or research site (sometimes also called the 'lab leak' hypothesis). Ultimately, she says, abusive attacks

are counterproductive to the people making them. “They make the people on their own side appear unreasonable and dangerous,” she says. “Second, they make it difficult to hold people accountable because now everyone is distracted by having to address the excessively abusive attacks.”

Coping strategies

For researchers who receive online abuse, individual coping strategies include trying to ignore it; filtering and blocking e-mails and social-media trolls; or, for abuse on specific social-media platforms, deleting their accounts. But it’s not easy.

“It is very harrowing if every day, you open up your e-mails, your Twitter, you get the death threats, you get abuse every single day, undermining your work,” says Hill. It also takes time to go through messages and filter out abusers, he says. That led to his decision to delete his Twitter account.

Kuppalli has kept her social-media presence, but is more careful about how she uses it. Her rule is now not to respond to comments or posts when she is upset or angry or, in some cases, not to reply at all. “I just don’t read the comments and I don’t engage.”

Trish Greenhalgh, a health researcher and doctor at the University of Oxford, UK, said on Twitter in March that she had received “malicious abuse” from another academic and was blocking her abuser’s followers to make it harder for them to target her. She had previously tweeted that if anyone abused her PhD students, she would try to identify the abuser and report them to their employer.

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From: Morens, David (NIH/NIAID) [E]
Sent: Tue, 19 Oct 2021 17:14:03 +0000
To: Peter Daszak ((b)(6)); Keusch, Jerry ((b)(6));
Kessler, Robert ((b)(6)); Rich Roberts ((b)(6)); Taubenberger,
Jeffery (NIH/NIAID) [E] ((b)(6)); Eddie Holmes ((b)(6))
Attachments: mBio.01864-21.pdf


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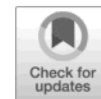
 ((b)(6)) (assistants: Kimberly Barasch; Whitney Robinson)

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Rapid Proliferation of Pandemic Research: Implications for Dual-Use Risks

 Sriharshita Musunuri,^a  Jonas B. Sandbrink,^{b,c}  Joshua Teperowski Monrad,^{b,d,e}  Megan J. Palmer,^{f,g}  Gregory D. Koblentz^h

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Sriharshita Musunuri, Jonas B. Sandbrink, and Joshua Teperowski Monrad made equal contributions. Author order was decided arbitrarily.

ABSTRACT The COVID-19 pandemic has demonstrated the world's vulnerability to biological catastrophe and elicited unprecedented scientific efforts. Some of this work and its derivatives, however, present dual-use risks (i.e., potential harm from misapplication of beneficial research) that have largely gone unaddressed. For instance, gain-of-function studies and reverse genetics protocols may facilitate the engineering of concerning SARS-CoV-2 variants and other pathogens. The risk of accidental or deliberate release of dangerous pathogens may be increased by large-scale collection and characterization of zoonotic viruses undertaken in an effort to understand what enables animal-to-human transmission. These concerns are exacerbated by the rise of preprint publishing that circumvents a late-stage opportunity for dual-use oversight. To prevent the next global health emergency, we must avoid inadvertently increasing the threat of future biological events. This requires a nuanced and proactive approach to dual-use evaluation throughout the research life cycle, including the conception, funding, conduct, and dissemination of research.

KEYWORDS COVID-19, dual-use research, biosecurity, biosafety, pandemic preparedness, preprints, zoonotic risk

The COVID-19 pandemic has revealed the world's vulnerability to biological threats and will shape pandemic preparedness efforts for decades to come. Recent discussions have particularly emphasized biosafety risks associated with gain-of-function experiments and accidental pathogen release (1). However, global health security leaders have also cautioned that the COVID-19 pandemic may increase the threat from deliberate biological events, i.e., biosecurity risks, by potentially inspiring malicious actors (2–4). These warnings come against the backdrop of existing global vulnerabilities to potential biosecurity risks, as both the WHO Joint External Evaluations and the inaugural 2019 Global Health Security Index have identified inadequate capacity and policies for biosecurity in the vast majority of countries (5, 6).

Additionally, biosecurity threats may be particularly concerning given that pathogens engineered for transmissibility or virulence may cause biological events of the largest magnitude, including global catastrophic biological risks (GCBRs) (7). Such engineering may be enabled by the misapplication of publicly available insights and tools from certain “dual-use” life sciences research, even when this research was conceived

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Editor Paul Keim, Northern Arizona University

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Published 19 October 2021

TABLE 1 Journal articles on SARS-CoV-2 published between 1 January 2020 and 5 July 2021 and GHS Index Dual-Use Indicator by country on a scale of 0 to 100 (low to high preparedness)^a

Country	Research output (no. of articles)	GHS Index Dual-Use Indicator score (0–100)
United States	52,281	50
United Kingdom	21,600	33.3
China	19,389	0
Italy	15,093	0
India	12,896	0
Spain	8,862	0
Canada	8,203	33.3
Germany	7,977	0
France	7,410	0
Australia	7,039	33.3

^aArticles were counted if they included “SARS-CoV-2” OR “COVID-19” OR “Coronavirus 2019” OR “novel coronavirus” OR “2019-nCoV,” in title or abstract. The Indicator is determined by whether countries have (a) active oversight of potential dual-use research of concern and (b) screening of genetic synthesis orders against lists of known pathogens and toxins.

with beneficial intent. Research associated with the greatest misuse potential constitutes “dual-use research of concern” (DURC), which the U.S. National Institutes of Health defines as “life sciences research that, based on current understanding, can be reasonably anticipated to provide knowledge, information, products or technologies that could be directly misapplied to pose a significant threat with broad potential consequences to public health and safety” (8).

Determining what research exhibits dual-use risks is an ongoing challenge, and if national policies on this exist, they frequently fall short of establishing comprehensive, flexible, and nuanced oversight. In the United States, in addition to the review of risks from public funding of the enhancement of potential pandemic pathogens under the P3CO framework, federally funded institutions are required to assess dual-use risks for only research involving 7 classes of experiments on 15 biological agents, and individual investigators are encouraged to voluntarily raise concerns about research that falls outside these categories (8, 9). Currently, SARS and SARS-CoV-2 are not considered Select Agents under this classification. In contrast, in Canada all institutions working with pathogens and toxins, regardless of funding source, are required to assess dual-use risks of any conducted research (10). According to the Global Health Security Index (GHSI), only 1% of countries worldwide are equipped with adequate review processes for research with especially dangerous pathogens (11). This means that almost all research carried out in the wake of the pandemic will be both conducted and published without adequate dual-use oversight, underscoring the importance of improved guidance globally (Table 1). Moreover, even when review processes are nominally in place, worrying research may nevertheless be conducted in the absence of robust efforts to implement and evaluate the effectiveness of existing policies (12, 13).

The COVID-19 pandemic may exacerbate biological risks stemming from the misapplication of research. We highlight several types of research with dual-use potential associated with pandemic response and preparedness efforts and emphasize how changes to the life science research enterprise complicate oversight of research with dual-use potential. We then describe the need for dual-use frameworks suited for application in the midst of emergency situations, as well as the need to consider dual-use risks associated with pandemic countermeasures. Ongoing dual-use review throughout the research life cycle is necessary to address increasingly common dissemination of research before peer review.

COVID-19 RESPONSE EFFORTS HAVE CREATED DUAL-USE INSIGHTS

The vast majority of research that is being conducted and published related to the development of countermeasures against SARS-CoV-2 aims to contribute to global

pandemic response efforts. This research includes advances such as the identification of neutralizing monoclonal antibodies as therapeutics, genetic surveillance to rapidly characterize variants of concern, and immunogens that aim to elicit lasting protection against the disease (14, 15). However, some work may have dual-use potential that increases the risk of deliberate misuse alongside the potential for accidents, thereby endangering not only the current response but also preparedness efforts for future outbreaks.

For instance, certain research may inform the explicit identification of mutations to the genome of the virus to enhance its resistance to existing countermeasures (16), replicative fitness, or transmissibility. While such studies are often done to pinpoint exactly how current countermeasures, such as convalescent patient sera or monoclonal antibody therapeutics, are insufficient to address potential emerging variants of concern, they also offer a blueprint of changes to be made that could increase the virulence of the virus. Thus, a few of these studies constitute “gain-of-function” (GOF) experiments that have the potential to enhance the lethality and/or transmissibility of a virus. These types of experiments deserve additional review given the associated dual-use risks but may have received less scrutiny due to the urgency of the pandemic and already widespread circulation of the pathogen in question. Some of this information has been rapidly incorporated into countermeasures upon publication and dissemination, such as modification of vaccine formulations to reflect circulating variants (17, 18). However, we must still be wary of the risk that the availability of granular mutational data linked to viral phenotype poses in the long term. This is especially important if it enables the engineering of more concerning strains of SARS-CoV-2, or other viruses, by malicious actors for deliberate release or strategic stockpiling as a biological weapon. While accidental and intentional misuse scenarios may be associated with the same lines of research, the latter could be more catastrophic.

Instructions for the *de novo* reconstruction of replication-competent SARS-CoV-2 virus are another example of dual-use knowledge that has been created and disseminated as a result of the pandemic (19, 20), as they may lower tacit knowledge barriers to conducting risky research. While methods such as restriction enzyme digestion, cDNA fragment assembly, and polymerase chain reaction are staple biochemistry techniques, detailed protocols regarding the assembly of functional virus and its derivative mutants may increase the number of researchers capable of using reverse genetics, regardless of prior training. Therefore, the likelihood that a bad actor acquires the practical knowledge necessary to culture recombinant viruses without safeguards, including those engineered for properties such as immune evasion, increases.

It is important to recognize that transparent dissemination of protocols and reagents is a crucial aspect of accelerating pandemic response research among the scientific community. However, there may be specific tools or insights that pose greater risks than benefits and should require an additional screening step before being shared or should be replaced by a safer alternative. Similar to the practical use of pseudotyped viruses wherever possible to reduce biosafety risks, we should adopt approaches that minimize biosecurity risks. For instance, there are a number of available methods to obtain replication-competent virus other than through synthesis. Extraction of live virus from clinical isolates is not accompanied by straightforward methods of introducing mutations that accentuate certain viral properties in the way that reverse genetics approaches are (21). Another viable alternative may be the use of a transcomplementation system producing nonvirulent SARS-CoV-2 that is infectious for only a single round of replication (22). This approach is also attractive given that it duplicates authentic viral replication, can be implemented in biosafety level 2 (BSL-2) containment, and facilitates the development of countermeasures with fewer risks.

Evidently, only a small fraction of response efforts is associated with dual-use risks. However, we must ensure that such studies do not endanger the overall response and preparedness effort. While an ongoing pandemic warrants rapid dissemination and collaboration to develop countermeasures, maintenance and consideration of dual-use

concerns cannot be neglected either in order to avoid the possibility of an even larger crisis in the future.

COUNTERMEASURE RESEARCH IN THE WAKE OF THE PANDEMIC CAN POSE DUAL-USE RISKS

In addition to the potential dissemination of security-relevant insights during the direct pandemic response, increased infectious disease countermeasure research over the coming years may raise risks from deliberate and accidental biological events. To minimize biosecurity risks from deliberate events, conception and funding decisions regarding infectious disease countermeasure research need to consider how associated insights may inform pathogen engineering by malicious actors. For instance, research on viral vector platform-based vaccines may be associated with generating insights on engineering immune evasion could be translated to pathogens of concern (23). Previous natural exposure to the virus utilized as a vaccine vector may result in preexisting immunity that can limit the effectiveness of vaccination in certain individuals, and induction of antivector immunity through vaccine administration limits the reusability of a given vector platform (24). To overcome this limitation, chimeric vector viruses have been created which evade neutralization by preexisting antibodies (25). While most vaccine-related work focuses on less concerning viral families, such as *Adenoviridae*, researchers have also explored and engineered orthopoxviruses—related to variola virus, the agent that causes smallpox—like vaccinia virus. Less risky alternatives to solving antivector immunity include expanding the vector portfolio to include nonhuman viruses and focusing efforts on nongenetic modifications which are not passed onto viral progeny, such as PEGylation (26, 27). Especially promising may be preferential investment into mRNA-based vaccines which both exhibit excellent properties as fast response platforms and are associated with few dual-use risks (23, 28, 29).

Another example of potentially concerning countermeasure research is the creation of transmissible vaccines for eradicating zoonotic pathogens, which has been advocated for with increased urgency in the wake of the pandemic (30, 31). Despite some potentially useful applications, such research would be associated with substantial safety risks as well as ecological and ethical concerns about introducing a new transmissible agent into animal populations. Importantly, such research would also create unique incentives for engineering the transmissibility, genetic stability, and immune evasion of viruses and hence be associated with significant dual-use risks (32).

SAFETY AND SECURITY RISKS FROM EFFORTS TO UNDERSTAND ZOOONOTIC SPILLOVER EVENTS

Beyond specific countermeasure research leading to dual-use insights on viral engineering, research conducted to investigate and predict zoonotic spillover events may also increase biosafety and biosecurity risks. Experiments that use a “gain-of-function” approach to determine the contribution of genotypic changes to the transmissibility or virulence of a virus could create enhanced potential pandemic pathogens (33), such as the controversial generation of mammalian transmissible H5N1 avian influenza virus (34, 35) as well as more recent work on coronaviruses (36). While this type of research should be conducted at facilities with the appropriate level of safety and security measures, even high-containment labs have an appreciable accident rate (33, 37). Moreover, making specific insights on concerning mutations publicly available can pose information hazards if this enables malicious actors to reconstruct or enhance pandemic pathogens (38, 39).

Systematic approaches to the characterization of viruses with potential for zoonotic spillover bear particular biosecurity risks. Large-scale efforts with the aim to collect hundreds of thousands of samples of viruses and investigate them in laboratories have been proposed and initiated (40). Such efforts are associated not only with accidental exposure and release risks (41) but also the potential of generating dual-use insights. Large-scale characterization of animal viruses may enable computational viral

engineering capabilities by creating large data sets which link genetic sequence and function for thousands of viruses. This may be leveraged to create more transmissible and virulent pathogens (42). In addition, broad genomic surveys and characterization of animal viruses have been suggested to be of little practical use to mitigate the emergence of biological events (43). Therefore, preferential investment into approaches which are associated with little biosecurity risk may more robustly reduce overall health security risk. For instance, the real-time surveillance of human populations for emerging pathogens does not involve large-scale collection and characterization of zoonotic viruses and has been highlighted as an effective approach to mitigating outbreaks (44).

Transmissible vaccine research, specific GOF experiments, and large-scale efforts to characterize animal viruses are examples of research aimed at reducing zoonotic risks that at the same time may increase the biological risk from other sources, including deliberate and accidental release. Table 2 summarizes the potential dual-use nature of research across pandemic response and preparedness efforts. Assessing pandemic preparedness research for associated risks should be of particular importance during the coming years, given increased funding for necessary efforts to prevent future pandemics as well as potentially heightened interest in weaponizing viruses by malicious actors, inspired by the havoc caused by the COVID-19 pandemic.

A CHANGING LANDSCAPE FOR DURC REVIEW

Changes to how scientific information is disseminated also pose new challenges for managing dual-use risks. From the rapid sharing of the SARS-CoV-2 genome by Chinese researchers (45) to the internationally coordinated vaccine development process, the swift dissemination of knowledge has been a cornerstone of the groundbreaking scientific advances since the beginning of the pandemic. Although this spread of information has been vital for efforts to curtail global outbreaks, the emergency conditions of the pandemic pose distinct challenges from the perspective of managing any emerging dual-use research of concern.

Though dual-use concerns are ideally identified earlier in the research life cycle, in practice many concerns arise or are made apparent when insights are codified for wider release via publication. Only a minority of life science research journals have written policies for assessing dual-use risks (46–48), but the role of journal review has featured prominently in historical controversies over DURC. In cases involving the reconstruction of the 1918 pandemic influenza virus (49), GOF research on avian influenza A/H5N1 (50–52) and A/H7N1 (53, 54) viruses, and the synthesis of horsepox virus (39, 55, 56), editors, journal DURC committees, and external bodies such as the U.S. National Science Advisory Board for Biosecurity (NSABB) ultimately decided in favor of publication of the manuscripts in question. In contrast, the *Journal of Infectious Diseases* decided in 2014 to redact information on key gene sequences from two manuscripts on the molecular characterization of a novel *Clostridium botulinum* toxin, following consultation between editors, authors, and various U.S. government agencies (57, 58), while another journal previously rejected manuscripts on smallpox and anthrax out of security concerns (59). Irrespective of each specific outcome, the discussions around these cases have emphasized the role of journal review in biosecurity. However, recent developments in publication practices as well as the unique circumstances of public health emergencies pose distinct challenges for this approach to managing dual-use risks.

One such challenge relates to the use of preprint servers such as bioRxiv, medRxiv, and SSRN, which has been steadily increasing in recent years and surged as the COVID-19 pandemic unfolded. Clearly, preprint publishing provides many benefits, including the rapid dissemination, evaluation, and discussion of academic work; open-access research; the facilitation of interdisciplinary collaborations; and benefits for early-career researchers (60–62). However, the discussion around preprints has primarily focused on scientific integrity (63), and scant attention has been given to the implications of preprint publishing for research with dual-use potential (64). While the effectiveness of

TABLE 2 Pandemic response and preparedness research related to SARS-CoV-2 associated with dual-use potential

Work	Proposed benefits	Potential risks	Reference(s)
Identification of mutations that make SARS-CoV-2 more transmissible, virulent, and immune evasive	Informing genomic surveillance and countermeasure design such as vaccines or monoclonal antibodies	May enable engineering of more concerning variants of SARS-CoV-2 or other viruses	Starr et al. (2021) (16)
Publication of detailed SARS-CoV-2 engineering protocols	Increased access to recombinant SARS-CoV-2 for response research	May inform malicious or careless actors on how to create SARS-CoV-2 variants	Xie et al. (2021) (20)
Engineering immune evasion for viral vectors	Improve effectiveness and reusability of viral vector vaccines	Can create transferable insights on engineering immune evasion for pathogens	Sandbrink and Koblentz (2021) (23), Roberts et al. (2006) (25)
Creation of transmissible vaccines	Use for vaccination of animal reservoirs for eradication of zoonotic viruses at risk of spillover	Safety risks; ethical and ecological concerns; may create insights on engineering transmissibility, genetic stability, and immune evasion	Nuismer et al. (2018) (31), Nuismer and Bull (2020) (30), Sandbrink et al. (2021) (32)
Increased gain-of-function work on future potential pandemic pathogens, not limited to coronaviruses	Prediction of zoonotic epidemics, possibility to inform biosurveillance targeting, and design of countermeasures	Risk of accidental exposure and lab release of engineered pathogens; risk of informing the creation of pathogens with enhanced lethality and transmissibility	Herfst et al. (2012) (34), Imai et al. (2012) (35), Casadevall and Imperiale (2014) (74)
Large-scale viral collection and characterization	Prediction of zoonotic epidemics, possibility to inform biosurveillance targeting, and design of countermeasures	Risk of accidental exposure and release; risk of informing viral engineering by creating large-scale data sets connecting sequence and function	Carroll et al. (2018) (40), Monrad and Katz (2020) (41), Carlsson et al. (2021) (42)

any peer review, with or without guidance, to reliably identify and resolve dual-use risks remains uncertain, preprint publishing removes a safeguard against the dissemination of potential biosecurity information hazards that cannot be redacted once published on public servers. Therefore, scientists who choose to publish research with dual-use implications must assume a greater responsibility for reviewing the benefits and risks of their work before publication, including consulting with appropriate experts and authorities, and take measures as relevant to minimize the information hazards posed by their research.

Even when manuscripts are not posted to preprint servers, a public health emergency could influence the extent of scrutiny for dual-use risks, either due to accelerated review (65) or because the presence of a significant health threat—rather than a hypothetical or minor one—leads to a higher tolerance for potential risks than under usual circumstances. Consequently, it is critical that scientific journals and external committees are equipped to evaluate dual-use considerations swiftly and in a way that considers how the risks posed by some information hazards may persist longer than any given public health emergency (38).

THE PATH FORWARD

To safeguard global pandemic response and preparedness efforts, we need to proactively address dual-use risks. Certain elements of a pandemic response, such as the publication of detailed protocols or insights on immune evasion engineering, bear dual-use potential and may increase the risk from deliberate biological events for the foreseeable future alongside accidents in the near term. Therefore, despite the importance of a fast pandemic response, scientists, funders, and publishers should not blindly conduct or publish any and all research that might help with these efforts but still pause and examine individual approaches for risks and benefits. Importantly, deliberative frameworks must be established and incorporated in the life science research cycle now, so as to avoid becoming an unwelcome burden during the next public health emergency and as the life science enterprise grows. Moreover, steps must be taken to ensure that established guidance has the intended effects on shaping scientific efforts. Specifically, it is vital that implementation of the guidelines is continually evaluated in terms of whether the assumptions embedded in their design hold true in practice, including whether they are correctly interpreted and adhered to by laboratory scientists and where ambiguities arise. Realizing the full potential of dual-use policies requires a strong feedback loop between implementation, evaluation, and review (12, 13).

Pandemic preparedness efforts directed at mitigating risks from different sources of biological risks may interfere with each other (66). For instance, large-scale collection of viruses, GOF experiments, and research into acquisition of human transmissibility that is conducted to assess the risk of zoonotic spillovers may increase the pandemic risk from accidental or deliberate releases (67). Consequences of actions by individuals in this space may have global repercussions, necessitating a global dialogue on how to manage tradeoffs from different lines of preparedness. Key drivers of such a global dialogue should be international organizations and scientific bodies including the World Health Organization, the Biological Weapons Convention, and the InterAcademy Partnership. Moreover, commercial, philanthropic, and public funders will need to play a more active role in incentivizing researchers to consider dual-use tradeoffs. To withstand the test of time and future emergencies, such evaluation must consider dual-use risks beyond lists of specific pathogens and existing technologies (68).

The changing landscape for how scientific information is disseminated necessitates a modern approach to managing dual-use research. The growing role of preprint publishing accentuates the disadvantage of relying exclusively on the academic review stage as a filter for biosecurity risks and the importance of evaluating research early on and throughout its life cycle (56, 69). Enabling stakeholders to manage dual-use concerns in a rapidly evolving landscape will require strategies and incentives to increase

transparency, information sharing, and education about risk management (70). At the same time, scientific journals continue to have a critical role in shaping norms and incentives in the life sciences, as research typically receives considerably more attention once it is published in prestigious outlets. Consequently, more publishers should follow the example of pioneering journals in the field that already have robust policies for dual-use review (68). Successful efforts from academic journals will also influence the norms governing preprint servers, which could advance innovative practices. At the minimum, these may include providing guidance and conditions for submission of manuscripts including attesting to and disclosing reviews and moving toward implementing screening for biosecurity and biosafety risks in submitted manuscripts where needed. Given that a few prominent servers host the majority of life science preprints, such screening may be a high-leverage avenue for identifying and mitigating potentially concerning research.

Adequately addressing dual-use risks will require updating assessment frameworks, strengthening oversight of life science research from proposal to publication, educating scientists and other stakeholders who shape the scientific landscape about the importance of this topic, and further developing a culture of responsible science (71). The biosecurity community should also recognize that dual-use oversight is not just a scientific and technical matter but also has political and social dimensions, which must be taken into account when designing processes and systems designed to address dual-use concerns (72). Many of the assumptions underlying the effectiveness of our governance strategies for risk management remain untested, and despite calls for applied biosafety and biosecurity research, this work has received little support (9). In particular the social sciences can make an important contribution to designing institutions necessary to monitor, evaluate, and learn from dual-use governance measures (11). Moreover, oversight is only part of what must be a more comprehensive approach that addresses incentives for proactive risk management—including rewarding innovations and highlighting best practices and champions (73). COVID-19 continues to demonstrate the grave costs of pandemic events and that we cannot afford to wait to address dual-use risks until an inevitable, avoidable disaster strikes. The aftermath of this pandemic is an opportunity to proactively increase preparedness for a wide range of potential global catastrophic biological risks.

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From: Morens, David (NIH/NIAID) [E]
Sent: Thu, 21 Oct 2021 14:17:02 +0000
To: Peter Daszak ((b)(6)); Keusch, Jerry ((b)(6));
Kessler, Robert ((b)(6))
Subject: FW: SARS-CoV-2 and NIAID-supported Bat Coronavirus Research
<https://bit.ly/3n6kojC>


Fom NIH website


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

Sent: Wednesday, October 20, 2021 5:16 PM

Subject: SARS-CoV-2 and NIAID-supported Bat Coronavirus Research <https://bit.ly/3n6kojC>

SARS-CoV-2 and NIAID-supported Bat Coronavirus Research

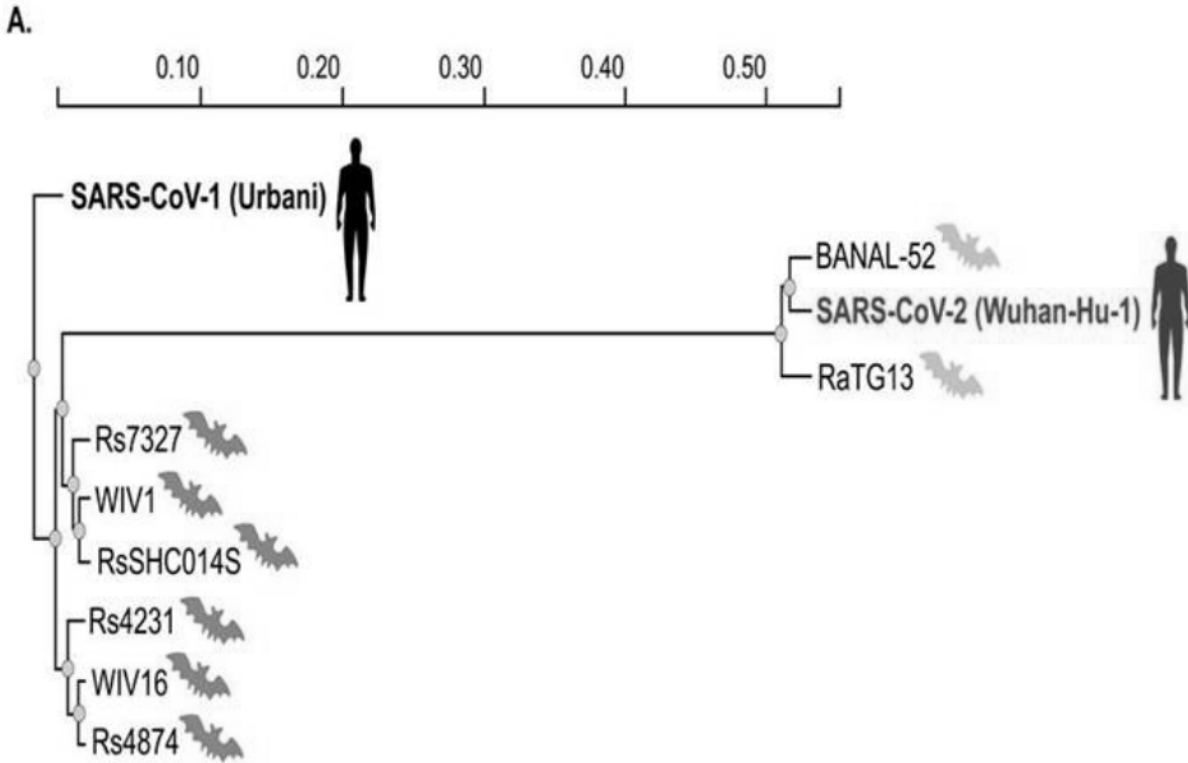
An Analysis: Evolutionary Distance of SARS-CoV-2 and Bat Coronaviruses Studied Under the NIH-supported Research Grant to EcoHealth Alliance

The research that NIH approved under the grant to EcoHealth Alliance with a subaward to the Wuhan Institute of Virology in Wuhan, China sought to understand how animal coronaviruses, especially bat coronaviruses, evolve naturally in the environment and have the potential to become transmissible to the human population. This research included studying viral diversity in bat reservoirs, surveying people who work in live animal markets or other occupations with high exposure to wildlife for evidence of bat coronavirus infection and analyzing data to predict which newly discovered viruses pose the greatest threat to human health.

Coronaviruses use a protein called spike to bind to a protein on the surface of a host cell to facilitate infection. Some coronaviruses, including SARS-CoV-1 (the cause of the SARS outbreak in 2003) and SARS-CoV-2 (the cause of the COVID-19 pandemic), use the angiotensin converting enzyme-2 (ACE2) protein to help enter and infect host cells. In order to study animal coronaviruses circulating in nature, the investigators replaced the spike protein from a well-characterized bat coronavirus, WIV1-CoV, with the spike protein of animal coronaviruses recently discovered in bats in China. Using techniques common in virology, experiments involved a single round of infection in several cell lines, and in some cases, in mice that were genetically modified to express the human version of ACE2. All other aspects of the mice, including the immune system, remained unchanged. The ACE2 transgenic mice were used to determine if spike proteins from bat coronaviruses discovered in China were capable of binding human ACE2, and therefore, whether the bat coronaviruses themselves, which were already present in the environment, could potentially infect humans and cause disease. WIV1-CoV is not known to cause infection in humans but has been shown in the laboratory to infect both human cells and ACE2 transgenic mice ([ref](#)), making it an ideal tool to use for these studies. Several of the bat coronaviruses used in these experiments were also found to be capable of replicating in ACE2 transgenic mice, indicating that the spike protein from the naturally occurring bat coronaviruses from which they were made could bind ACE2 in vivo.

Questions have been raised about whether this NIH-funded research had a role in the emergence of SARS-CoV-2. In this regard, the chimeric viruses that were studied (i.e., the WIV-1 virus with the various spike proteins obtained from bat viruses found in nature) were so far distant from an evolutionary standpoint from SARS-CoV-2 (Figure 1) that they could not have possibly been the source of SARS-CoV-2 or the COVID-19 pandemic. The body of the scientific data from this award including the bat coronavirus sequences published in the scientific literature and public databases makes this conclusion readily apparent to anyone with experience in and knowledge of virus phylogeny and evolutionary biology.

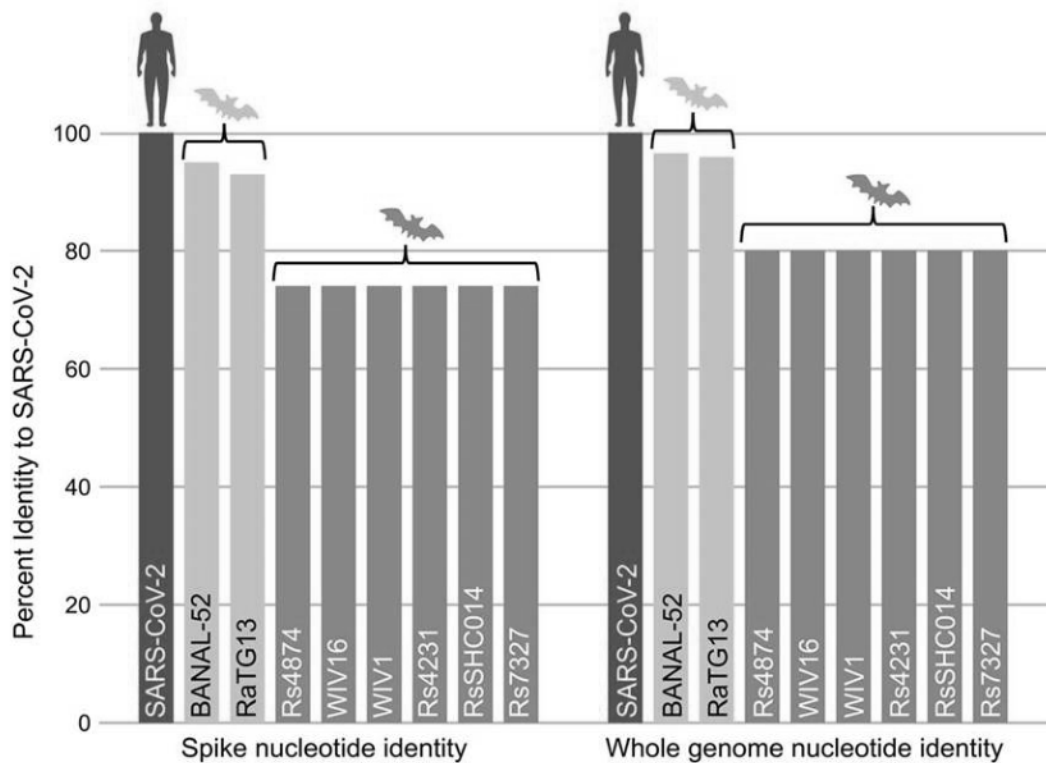
Figure 1. Relationship of bat coronaviruses to SARS-CoV-1 and SARS-CoV-2.



A) A phylogenetic tree based on nucleotide sequences of indicated coronavirus spike proteins demonstrating the evolutionary distance of SARS-CoV-2 with the bat coronaviruses experimentally studied under the NIH grant to EcoHealth Alliance (blue bat icons). Bat coronaviruses most closely related to SARS-CoV-2, none of which were studied in the EcoHealth grant, are denoted with orange bat icons. The scale bar represents the number of nucleotide substitutions per site.

Credit
NIAID

B.



B) Comparison of the nucleotide sequence identity of indicated coronaviruses to SARS-CoV-2. The left panel shows the percent identity of indicated coronavirus spike nucleotide sequences to SARS-CoV-2. The right panel shows the percent nucleotide identity of the indicated full coronavirus genomes to SARS-CoV-2.

Despite the similarity of RaTG13 and BANAL-52 bat coronaviruses (orange bars) to SARS-CoV-2 (red bars), experts agree that even these viruses are far too divergent to have been the progenitor of SARS-CoV-2, further highlighting that the bat coronaviruses studied under the EcoHealth Alliance grant (blue bars) could not have been the source of SARS-CoV-2 and the COVID-19 pandemic. Several other similarly divergent viruses that failed to replicate in cells are not shown ([ref](#)).

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The above figure shows the sequence relationships between SARS-CoV-1, SARS-CoV-2 and the naturally occurring bat coronaviruses used in experiments under the NIH grant to EcoHealth Alliance and reported in the scientific literature ([ref](#)) or annual progress reports. From this analysis, it is evident that the viruses studied under the EcoHealth Alliance grant are very far distant from SARS-CoV-2. Included for comparison is RaTG13, one of the closest bat coronavirus relatives to SARS-CoV-2 collected by the Wuhan Institute of Virology ([ref](#)) and BANAL-52, one of several bat coronaviruses recently identified from bats living in caves in Laos ([ref](#)). Although RaTG13 and BANAL-52 are 96-97% identical to SARS-CoV-2 at the nucleotide level (>900 nucleotide differences across the entire genome), the difference actually represents decades of evolutionary divergence from SARS-CoV-2. Experts in evolutionary biology and virology have made it clear that even the closest known relatives of SARS-CoV-2, which were not studied under the EcoHealth Alliance grant, are evolutionarily too distant from SARS-CoV-2 to have been the progenitor of the COVID-19 pandemic ([ref](#), [ref](#)). Field studies continue the search for more proximate progenitors.

Content last reviewed on October 20, 2021


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From: Morens, David (NIH/NIAID) [E]
Sent: Thu, 21 Oct 2021 13:26:42 +0000
To: Peter Daszak ((b)(6)); Kessler, Robert
((b)(6)); Keusch, Jerry ((b)(6))
Subject: FW: House Energy & Commerce GOP Leaders Statement on Documents
Released by the NIH


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

Sent: Thursday, October 21, 2021 9:24 AM

Subject: House Energy & Commerce GOP Leaders Statement on Documents Released by the NIH

Energy & Commerce GOP Leaders Statement on Documents Released by the NIH

10.20.21

Washington, D.C. — House Energy and Commerce Committee Republican Leader Cathy McMorris Rodgers (R-WA), Subcommittee on Health Republican Leader Brett Guthrie (R-KY), and Subcommittee on Oversight and Investigations Republican Leader Morgan Griffith (R-VA), released a statement in response to the National Institutes of Health (NIH) turning over a limited number of previously requested documents related to the origins of the COVID-19 pandemic.

As leaders of the House committee with jurisdiction over public health, the leaders have sent four letters to the NIH since March 18, 2021, asking the NIH to help inform a complete, scientific investigation into the COVID-19 pandemic.

Their statement:

“We are reviewing these documents sent to us by the NIH, including EcoHealth Alliance’s Year Five progress report, which should have been submitted to the NIH two years earlier. We now know for certain that EcoHealth Alliance violated the terms of one of their grants that funded research in China.

“We are glad that the NIH is finally pursuing unpublished data from EcoHealth Alliance as we have urged for months, and as we pressed the NIH to do in June. However, it’s unacceptable that the NIH delayed asking EcoHealth Alliance to submit unpublished data about risky research that they were required to do under the terms of their grant.

“The NIH has acknowledged that EcoHealth violated the terms of its grant and has been non-compliant. Yet, at the same time, NIH takes the word of this grant policy violator

that EcoHealth is fully accounting for its research and that none of it had anything to do with the pandemic.

“We need full compliance with Congressional oversight. These documents are only the first step from the NIH in rebuilding public trust. They must be fully transparent about any research they have funded in China and how they will ensure proper oversight of risky research in the future. They owe it to the American people to be a better partner in revealing how this pandemic started. Every day that goes by, it will be harder to get answers to best prepare us in preventing future pandemics.”

[CLICK HERE](#) to read the NIH’s letter to the Energy and Commerce Committee Republican leaders.

[CLICK HERE](#) to read the EcoHealth Alliance Year Five progress report.


[CLICK HERE](#) to read the NIH genetic analysis document.


From: Morens, David (NIH/NIAID) [E]
Sent: Thu, 21 Oct 2021 18:33:08 +0000
To: Peter Daszak ((b)(6)); Keusch, Jerry ((b)(6));
Kessler, Robert ((b)(6))
Subject: FW: New letter to F Collins


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From: Folkers, Greg (NIH/NIAID) [E] (b)(6)
Sent: Thursday, October 21, 2021 2:17 PM
To: NIAID OD AM <NIAIDODAM@niaid.nih.gov>
Subject: New letter to F Collins

<https://twitter.com/GPOversight/status/1451249202714054657?s=20>

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From: Morens, David (NIH/NIAID) [E]
Sent: Thu, 24 Jun 2021 16:45:56 +0000
To: Peter Daszak ((b)(6)); Rich Roberts ((b)(6));
Keusch, Jerry ((b)(6)); Taubenberger, Jeffery (NIH/NIAID) [E] ((b)(6));
Bremner, Joel (NIH/FIC) [V] ((b)(6))
Subject: FW: Nautilus: When a Good Scientist Is the Wrong Source/How a bad "fact"
helped the lab-leak hypothesis go viral.

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

Sent: Thursday, June 24, 2021 12:18 PM

Subject: Nautilus: When a Good Scientist Is the Wrong Source/How a bad “fact” helped the lab-leak hypothesis go viral.

When a Good Scientist Is the Wrong Source How a bad “fact” helped the lab-leak hypothesis go viral.

By Thomas Levenson June 23, 2021

Six weeks ago, a reporter, Nicholas Wade, published what seemed to be a blockbuster story, one that, if true, would expose the greatest scandal in recent history. SARS-CoV-2, he wrote, or SARS2 for short, the virus that has driven the global COVID-19 pandemic, had likely been modified in a lab at the Wuhan Institute of Virology, from which it then escaped into the wild. “Neither the natural emergence nor the lab escape hypothesis can yet be ruled out,” Wade wrote. “But it seems to me that proponents of lab escape can explain all the available facts about SARS2 considerably more easily than can those who favor natural emergence.”

Wade, a former *New York Times* science reporter, best known for promoting a genetic basis to racial hierarchies, first placed his piece at the self-publishing site Medium on May 2. The story really took wing when it was reposted three days later at the *Bulletin of the Atomic Scientists*. It was an extraordinary assertion, and as the saying goes, such claims need extraordinary proof.

Validation came from one of the most prominent biologists of the last half century.

That validation came, it seemed, from one of the most prominent biologists of the last half century, the Nobel laureate David Baltimore, who confirmed one of the key pillars of the argument. Some features in a brief genetic sequence in the virus seemed to suggest that a human, in a lab experiment, had put it there. When he first saw the sequence, Baltimore is quoted as saying, “I said to my wife it was the smoking gun for the origin of the virus.”

With that a bad “fact” was born: a seemingly simple statement about reality that turns out to be not so simple—and deeply misleading. The Baltimore quote sealed the deal, not just because of what was said, but who was saying it.

It’s standard practice in science journalism to seek confirmation of key facts from experts who are not directly involved in the research that lies at the center of any given story, the reporter’s equivalent of peer review. That’s what Wade needed, a source that could transform his long chain of inference, his series of ifs and assertions about what evolution can and cannot do, into a statement that (to use Isaac Newton’s phrase) “cannot fail but to be true.”

That’s what Baltimore provided. “Smoking gun” is the critical phrase; it leaves no room for doubt. It confirmed, or seemed to, that the 4 million and counting who have died of COVID were victims of human choices and mistakes.

Baltimore’s picture could appear in the dictionary next to “authority.” He won his Nobel Prize for work on the molecular genetics of tumor viruses. He has run a trio of the world’s most important research institutions, as director of the Whitehead Institute at MIT, then as president first at Rockefeller University, and then at Caltech. After stepping down, he continued to run an active lab, investigating basic questions about gene regulation and expression. If there were anyone whose word one could accept on a question of who did what to a virus it would seem to be Baltimore.

And yet Baltimore got this one wrong—and has retreated from his earlier emphatic support for Wade’s claims. But like most retractions in media stories, Baltimore’s admission has made little impact, and the originally reported “fact” has continued to feed the ongoing promotion of the lab-escape hypothesis.

Wade asserted that a particular arrangement of a specific sequence in the viral genome, called a codon, was unlikely to have gotten there naturally. There are actually six different codons for arginine, and the one found in a particular region of the SARS-CoV-2 genome called the furin cleavage site does occur less frequently in viruses than it does in the human genome. An even more telling detail to Wade is that this uncommon arginine codon shows up twice in that small segment of the virus’s genome. For that to occur naturally, Wade wrote, “a chain of events has to happen, each of which is quite unlikely.”

That’s what Baltimore assented to. But scientists say Wade misdescribed critical links in his chain. Scripps Research virologist Kristian Andersen led an early inquiry into the possible role of a lab escape in the origin of the virus, which concluded that it “is not a laboratory construct,” a finding that Wade termed “poor science” in his article. After Baltimore’s quote became public, Andersen re-entered the argument, and became one of a number of researchers to challenge many of the details Wade relied on. Andersen told *Nature* that Wade’s claim that steps in the emergence of the virus were too improbable to have occurred is not true. Rather, the pandemic virus uses that codon about 3 percent of the time that its genome calls for arginine—not common, but not impossibly scarce either—and, importantly, that other coronaviruses make use of it too, at similar or greater frequency.

This is a phenomenon that few outside science and journalism fully grasp.

Columbia University virologist Vincent Racaniello says the unusual pairing of a particular codon that Wade saw as decisive actually points *away* from laboratory manipulation. “We have some idea why this codon is rare in RNA viruses,” Racaniello says. Selection pressures have been identified that would discourage its use in viral genomes. But, he says, “We don’t know why it’s not zero. The fact that it is conserved in many viruses means that it’s beneficial in some way we don’t understand.” This is the kind of mystery that evolution throws at researchers all the time. Racaniello adds that if a lab researcher was trying to modify a virus to measure its effect, the researcher wouldn’t use the codon pairing identified by Wade because its effect would be too unpredictable.

As Wade’s claims attracted more media interest, seemingly validated by Baltimore’s seal of approval, similar critiques began to appear, pointing out how Wade shaded his interpretation of the details toward one conclusion—lab escape—and away from a natural origin. In a *New York Times* interview, Andersen said while both lab and natural scenarios are possible, “they are not equally likely—precedence, data and other evidence strongly favor natural emergence as a highly likely scientific theory for the emergence of SARS-CoV-2, while the lab leak remains a speculative hypothesis based on conjecture.”

It may seem surprising that Andersen, a well-regarded biologist, could correct Baltimore, a legend. It’s not. This is an example of a phenomenon that few outside science, and especially journalists inexperienced in covering cutting-edge research, fully grasp. Biology is a discipline in which the details make all the difference; there are more of them than seems possible; and if a given expert is not expert in the right domain, their answers are not that useful. Baltimore certainly is *an* authority, but his jurisdiction does not extend to all the complexity that nature displays.

Baltimore has mostly accepted such corrections. In an email to *Nature*, he said that Andersen could be correct that evolution produced SARS-CoV-2, but adds that “there are other possibilities and they need careful consideration, which is all I meant to be saying.” He walked his quote further back in an interview with *Los Angeles Times* columnist Michael Hiltzik, saying that he “should have softened the phrase ‘smoking gun’ because I don’t believe that it proves the origin of the furin cleavage site but it does sound that way.”

And yet the “fact” of a smoking gun lives on. Donald G. McNeil Jr., a former colleague of Wade’s who covered the pandemic at *The New York Times* until he recently resigned, posted a [long essay](#) on Medium endorsing Wade’s conclusions, a piece that was cited by David Leonhardt in a *Times* “explainer” on the state of the debate. Leonhardt concluded that dismissing the lab escape possibility “appears to be a classic example of groupthink, exacerbated by partisan polarization.” The issue, as Leonhardt saw it, turns on America’s political conflicts, and not the strength or weakness of the specific scientific evidence available. A reporter whose career has centered on Washington and economic coverage would find this plausible; it is not, however, a judgment based on the expertise needed to assess competing scientific arguments.

Wade has not backed off his claim that the pandemic was probably caused by a lab-engineered virus that escaped. Baltimore’s recant hasn’t changed a thing, Wade argues, writing to the *Los Angeles Times*’ Hiltzik that he believes “the totality of the quote” still supports his case.

Bad “facts” have played an indispensable role in advancing the lab-escape allegation to its current prominence. In the past week, lab-escape speculation with little or no critical scrutiny reached into entertainment media. NPR’s *Fresh Air* aired an episode featuring a reporter, not a scientist, advancing the lab allegation, with no expert on zoonosis in sight, while Jon Stewart retailed Wuhan lab conspiracy theories on *The Late Show with Stephen Colbert*, riffing, “I think we owe a great debt of gratitude to science. Science has, in many ways, helped ease the suffering of this pandemic,” pausing for a beat, and then going for the rimshot: “which was more than likely caused by science.”

Meanwhile, the research seeking to trace the origins of SARS-CoV-2 continues. Identifying the specific animal origins for human diseases is difficult at the best of time—it took well over a decade to track down the source for the first SARS epidemic, and the complete sequence of transmission behind the Ebola outbreaks is still being pursued. Even so, evidence is trickling in, like a recent survey of bat populations in Southeast Asia turned up a number of newly identified viruses related to the one causing the human pandemic.¹ That study is itself no smoking gun, but it is a reminder: the investigation into the most likely origin of the SARS-CoV-2 is ongoing, and may take a very long time, given the space and near-infinite variety of the natural world that must be explored.

In the meantime, the true scandal of the COVID years continues to unfold. It’s not breathless speculation on the origins of the virus, but rather that the United States and many other nations failed to prepare for the pandemic. Everywhere but China had months to anticipate its arrival, come up with strategies to limit transmission, and to ready their public health and medical systems to take care of those who did get sick. Six hundred thousand dead in the US and nearly 4 million worldwide are the brutal measure of that failure—and a reminder. It was human errors and choices that enabled a virus of still-uncertain origin to spark a global disaster.

Thomas Levenson is Professor of Science Writing at the Massachusetts Institute of Technology. He is the author, most recently, of Money for Nothing: The Scientists, Fraudsters and Corrupt Politicians Who Reinvented Money, Panicked a Nation, and Made the World Rich. Follow him on Twitter@TomLevenson.

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From: Morens, David (NIH/NIAID) [E]
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Rich Roberts ((b)(6)); Peter Hotez ((b)(6))
Subject: FW: Global Times, China -- Suspect No.1: Why Fort Detrick lab should be investigated for global COVID-19 origins tracing

You can't make this stuff up.... Oops.... I guess you CAN...

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

Sent: Monday, June 28, 2021 7:13 PM

Subject: Global Times, China -- Suspect No.1: Why Fort Detrick lab should be investigated for global COVID-19 origins tracing

Suspect No.1: Why Fort Detrick lab should be investigated for global COVID-19 origins tracing

Why US labs need to be investigated for COVID-19 origins

By Fan Lingzhi, Huang Lanlan and Zhang Hui Published: 2021/06/28 01:30:00

The lab-leak theory, that COVID-19 was leaked from a laboratory, has once again caused a clamor since the beginning of this year, months after the argument was thrown into the trash can of conspiracy theories by an overwhelming number of scientists.

Observers found that things only get more complicated when the origins of the coronavirus - an already difficult scientific issue - is entangled in political manipulation tricks. Combing through more than 8,000 pieces of news reports related to the lab-leak theory, the Global Times found that as many as 60 percent of the coverage was from the US alone.

It is worth noting that many media outlets in the US-led Western world, which hyped the lab-leak theory, are only willing to focus on the Chinese labs though they have been thoroughly investigated by the World Health Organization (WHO), while turning a blind eye to the more suspicious American biological research institutions, such as the infamous US Army Medical Research Institute of Infectious Diseases (USAMRIID) at Fort Detrick, Maryland.

The USAMRIID was temporarily shut down in 2019 after a Centers for Disease Control and Prevention (CDC) inspection. Although this mysterious lab reported the reason for the closure as "ongoing infrastructure issues with wastewater decontamination," the explanation was not persuasive enough. The Global Times found that the lab's failure to control toxins seemed to have alarmed the Countering Weapons of Mass Destruction related institutions in the US.

Resurgence of lab-leak theory

A joint study into the origins of COVID-19 by Chinese experts and the WHO in March dismissed the "lab-leak" conspiracy theory. More evidence pointed to the fact that the virus had probably jumped from bats to humans via another intermediary animal, and it was "extremely unlikely" that it leaked from a lab, the study report said.

Nonetheless, the lab-leak theory has not disappeared; instead, especially from the beginning of May, it has been largely promoted by some US politicians and media outlets as a "plausible science." In an article published on Bulletin of the Atomic Scientists on May 5, without any evidence, science writer Nicholas Wade claimed that "proponents of lab escape can explain all the available facts about SARS2 considerably more easily than can those who favor natural emergence."

Days later, The Wall Street Journal reported on May 23 that three researchers at Wuhan Institute of Virology (WIV) "became sick enough in November 2019 that they sought hospital care," and they had "symptoms consistent with both Covid-19 and common seasonal illness." The WSJ report quoted a "previously undisclosed US intelligence report."

On May 26, President Biden stated that he had ordered the US intelligence community to "redouble" its efforts to investigate the origins of COVID-19. The US national security adviser Jake Sullivan even claimed on June 20 that China will face "isolation in the international community" if it doesn't cooperate with a further probe into the origin of the COVID-19 pandemic, Bloomberg reported that day.



Research personnel work inside the bio-level 4 lab at the USAMRIID at Fort Detrick on September 26, 2002. Photo: AFP

Pressure from politicians and the media seems to have affected some authoritative medical scientists in the US, including Director of the US National Institute of Allergy and Infectious Diseases (NIAID), Anthony Fauci. On May 11, after Rand Paul, a Republican to the Senate, accused Fauci of helping the Wuhan lab "create" the virus, Fauci strongly denied the accusation but said he is "fully in favor of any further investigation of what went on in China."

This sudden change in attitude of some US experts is due to the political pressure they have received, a Chinese virologist told the Global Times. "Western media like to ask the experts misleading questions, like, 'is (lab leak) absolutely impossible?'" said the virologist who requested anonymity.

It's very difficult for experts to answer a question like that, as the possibility, although very little, still exists, the virologist said. "All they can say is, 'it's possible,'" he told the Global Times. Actually, most experts usually add "but it's highly unlikely" after "it's possible," but the media only presents the part which confirms their own bias, he said.

Big data shows the US is pushing the narrative of the COVID-19 lab-leak theory. Among the 8,594 pieces of news report related to "lab leak" that database GDELT collected since 2020, 5,079 were from the US, accounting for 59 percent. Following the US was the UK (611 pieces) and Australia (597 pieces). Almost all the coverage targeted the WIV lab.

While the US is solely focused on Chinese labs, the US seldom pays attention to the fault in its own domestic labs, some of which have even triggered virus-related accidents before. According to an August 2020 article by ProPublica, an independent newsroom that produces investigative journalism, the University of North Carolina at Chapel Hill reported 28 lab incidents involving genetically engineered organisms to safety officials at the National Institutes of Health between January 2015 and June 2020. "Six of the incidents involved various types of lab-created coronaviruses," ProPublica said in the article. "Many were engineered to allow the study of the virus in mice."

Weirdly, very few US mainstream media outlets have raised the question whether there is the possibility that COVID-19 was leaked from US labs, said the Chinese virologist. "They dare not ask that," he said.

In an article published on the independent political blog site Moon of Alabama on May 27, the author pointed out that some Westerners' hyping of the Wuhan lab leak conspiracy is similar to the trick the US played in pushing the Iraq War in 2002 - the US claimed "Saddam Hussein will soon have nuclear weapon," which was "obvious nonsense," the author said.

"The 'lab leak' theory is similar to the WMD claim - evidence-free speculation long promoted by a neoconservative leaning administration that was extremely hostile to the 'guilty' country in question," said the author.

The lab-leak theory, therefore, "isn't just about an implausible, evidence free tale of a SARS-CoV-2 lab escape," the author noted. "It is a campaign launched to depict China as an enemy of humankind."

Intl concerns on US bio-labs

The US has many bio-labs in 25 countries and regions across the Middle East, Africa, Southeast Asia and the former Soviet Union states, with 16 in Ukraine alone. Some of these labs have seen large-scale outbreaks of measles and other dangerous infectious diseases, according to media reports.



Outside view of the bio-level 3 and 4 lab at the USAMRIID at Fort Detrick on September 26, 2002. Photo: AFP

The international community has frequently expressed concern over US' biological militarization activities in other countries.

In October 2020, Deputy Chairman of the Security Council of Russia, Dmitry Medvedev, said that the US research activities in bio-labs in members of the Commonwealth of the Independent States have caused grave concern. The US not only builds bio-labs in these countries, but also tries to do so in other places across the world. However, its research lacks transparency and runs counter to the rules of the international community and international organizations.

Anatoly Tsyganok, a corresponding member of the Russian Academy of Military Sciences and associate professor of Faculty of World Politics at Lomonosov Moscow State University, told the Global Times that biological and bacteriological weapons tests on US territory are prohibited by the US Congress. He said that the US military has been and is still carrying out tests of biological and bacteriological weapons in Georgia.

This is done under the guise of providing sick people with various therapeutic vaccines conducted by the US military and American private contractors at the Richard Lugar Center for Public Health Research, Tsyganok said. Related tests have been exposed by various media outlets.

In December 2015, 30 patients at the research center who were being treated for hepatitis C died. Twenty-four of them died on the same day, and their cause of death was listed as "unknown," according to Tsyganok and Russia news outlet.

Residents of neighborhoods around these labs often complain about health problems.

Bulgarian journalist Dilyana Gaytandzhieva published a story about the Lugar center in early 2018. In her interviews for the report, most residents who lived nearby the labs complained of headaches, nausea and high blood pressure. They also said there was black smoke coming from the lab.

USA Today reported that since 2003, hundreds of incidents involving accidental contact with deadly pathogens occurred in US bio-labs at home and abroad. This may cause the direct contacts to be infected, who can then spread the virus to communities and start an epidemic.

A member of the Russian Academy of Sciences, Armais Kamalov said in an interview with TASS in early June that development of genetically-engineered viruses as biological weapons should be subject to the same worldwide ban as the testing of nuclear weapons. He mentioned US labs in Georgia and Armenia as reference.

"There are a lot of labs, which are bankrolled today by the United States Department of Defense. It's no secret that they are in Georgia, Armenia and other republics. It's surprising that access to such labs is off-limits, and we don't understand what they are doing there," he said.

What had happened in July 2019?

The terrible safety records of American biological labs around the world shows a possibility of a virus escaping from an American lab. Many point to the shutdown of Fort Detrick lab in July 2019.

In July 2019, six months before the US reported its first COVID-19 case, Army laboratory at Fort Detrick that studies deadly infectious material like Ebola and smallpox was shut down after the US Centers for Disease Control and Prevention issued a cease-and-desist order. CDC officials refused to release further information after citing "national security reasons."

The USAMRIID in Fort Detrick said in August 2019 that the shutdown was because the center did not have "sufficient systems in place to decontaminate wastewater" from its highest-security labs, the New York Times reported.

What exactly happened at Fort Detrick in the summer of 2019? Some US media previously turned to CDC to get answers, but many key contents in the report had been redacted.

In early June, a Virginia-based Twitter user got the CDC documents on the inspection of the Fort Detrick under The Freedom of Information Act (FOIA). Global Times found that most of the documents were emails between CDC officials at various departments and USAMRIID from 2018 to 2019. Although some of the emails were covered by an ABC-affiliated television station in Washington, the report did not catch much attention.

The emails revealed several violations at the Fort Detrick lab during CDC's inspections in 2019. Four of which were labeled serious violations.

One of these serious violations, the CDC said, was one inspector who entered a room multiple times without the required respiratory protection while other people in that room were performing procedures with a non-human primate on a necropsy table.

This deviation from entity procedures resulted in a respiratory occupational exposure to select agent aerosols, the CDC said.

In another serious violation, the CDC said the USAMRIID had "systematically failed to ensure implementation of biosafety and containment procedures commensurate with the risks associated with working with select agents and toxins."

Other violations included lack of proper waste management where waste wasn't transported in a durable leak proof container, which creates the potential for spills or leaks.

The CDC documents show that it sent a letter of concern to USAMRIID, which resulted in a temporary shutdown of the Fort Detrick lab in 2019.

In an email on July 12, 2019, the CDC said the USAMRIID reported two breaches of containment on July 1 and July 11, 2019, and this demonstrated a "failure of USAMRIID to implement and maintain containment procedures sufficient to contain select agents or toxin generated by BSL-3 and BSL-4 laboratory operations."

"Effective immediately, USAMRIID must cease all work involving select agents and toxins in registered laboratory areas until the root cause investigation has been conducted for each incident and the results have been submitted to FSAP for review," the CDC said.

The FSAP (Federal Select Agent Program) is jointly comprised of the Centers for Disease Control and Prevention's Division of Select Agents and Toxins and the Animal and Plant Health Inspection Service's Division of Agricultural Select Agents and Toxins. The program oversees the possession, use and transfer of biological select agents and toxins, which have the potential to cause a severe threat to the public, animal or plant health or to animal or plant products. Common examples of select agents and toxins include the organisms that cause anthrax, smallpox, and the bubonic plague.

Three days later, the Fort Detrick replied the email by saying that it had submitted messages in response to the immediate action, but the messages were deliberately blotted out.

The message was submitted by a director for Strategic Studies (Countering Weapons of Mass Destruction) at the USAMRIID whose name was also blotted out.

The Fort Detrick's public statement released in August 2019 said the shutdown was due to problems in decontaminating wastewater. But it's not clear whether the statement was consistent with CDC's inspection results.

The management of such high-level labs in general must be very strict with regular inspections. Various systems should be able to ensure that no potential risks can occur, and equipment failure and wastewater leakage certainly should not occur, a Chinese scientist from the WHO-China virus origins tracing team who requested anonymity told the Global Times.

The wastewater problems revealed major loopholes in the management at the Fort Detrick lab, and one has to wonder what else was leaked with the mismanaged wastewater.

"Some highly pathogenic pathogens in the laboratory were likely released. And the US military never told the public about what they were doing," the scientist said.

It is highly likely that researchers at Fort Detrick may have been infected accidentally but showed no obvious symptoms. In this way they could have brought the virus to the outside world, the scientist said.

"Under the circumstances of no obvious symptoms, 9 of the 10 individuals may not have known that they were infected and it's possible that more than 90 percent of the transmission routes had been lost when the virus was finally detected. This is also why the tracing of virus origins is difficult to conduct," he said, noting only serological survey on a large scale could find some of the early infections.

Why not open Fort Detrick lab

Several virologists and analysts interviewed by the Global Times urged the Fort Detrick lab to open its doors for an international investigation, since international experts have already visited the Wuhan Institute of Virology.

Many Western politicians and media outlets pinned the blame of the pandemic on Wuhan, saying that Wuhan was where the virus was first detected and where the virus came from despite mounting evidence that it's not the case.

In a recent example in June, a research study run by the National Institutes of Health's All of Us Research Program found evidence of COVID-19 infections in the US as early as December 2019, weeks before the first documented infection in the country.

Wuhan recorded the earliest COVID-19 symptoms from a patient on December 8, 2019.

When asked to give more details on the study, a media person with the All of Us Research Program told the Global Times that the program "has nothing further to add" from the information it had already released.

As for why the virus was first detected in Wuhan, the anonymous scientist said that the virus was difficult to be detected at an early stage, especially in autumn and winter with more cold cases. And it would not attract attention until a large number of people were infected. That's what happened in densely populated Wuhan, the scientist said.

China's public health system is very sensitive especially after the SARS outbreak in 2003, but this is not always the case abroad, especially when the population density is low and the virus does not spread so fast, the expert said.

"The novel coronavirus was first discovered by three Chinese companies at the same time. It is very simple to detect these things, and China has lots of such third-party companies with strong medical detection ability," he said.

Without going back to earlier serum samples elsewhere now, it is going to be difficult to find the source of the virus. The retrospective studies that have been done in China have not found any evidence. It's important for the world to work together now to sort through the evidence and do early serological investigations where necessary, he said.

Zeng Guang, former chief epidemiologist of the Chinese Center for Disease Control and Prevention, told the Global Times that laboratory leak is easy to identify, as infections are bound to show signs, whether it is an operational problem or an infection of a lab staff.

The WHO experts assessed the lab-leak hypothesis when they visited Wuhan and found no evidence, and the speculation on its possibility in a Wuhan lab should have ended by now. In the meantime, we should put a question mark on other hypotheses, such as other labs around the world, Zeng said.

Zeng said the US is afraid of WHO's inspection in the same way it was done in China, Zeng said.

The US, the only country obstructing the establishment of a Biological Weapons Convention (BWC) verification mechanism, has systematic problems, Zeng said, adding that the US is afraid that the investigation into its labs would lead to more of its dirt being dug out.

Xia Wenxin contributed to this story

CHINA


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From: Morens, David (NIH/NIAID) [E]
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Subject: FW: Wash Examiner: Trump COVID testing czar testifies coronavirus most likely originated in Wuhan lab


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From: Folkers, Greg (NIH/NIAID) [E] ((b)(6))
Sent: Tuesday, June 29, 2021 3:58 PM
Subject: Wash Examiner: Trump COVID testing czar testifies coronavirus most likely originated in Wuhan lab

Trump COVID testing czar testifies coronavirus most likely originated in Wuhan lab

by [Jerry Dunleavy, Justice Department Reporter](#) |
| June 29, 2021 02:37 PM

The [COVID-19](#) testing czar for former President [Donald Trump](#) says the “most likely” origin for the pandemic was an accidental escape from a [Wuhan lab](#), testifying Tuesday as one of four expert witnesses during a House Republican effort to get to the bottom of how the coronavirus emerged. [Brett Giroir](#), an assistant secretary of health and a member of Trump’s White House Coronavirus Task Force, [said](#): “I assess that the most likely origin was an accidental infection of laboratory personnel from the Wuhan Institute of Virology, with secondary transmission to the local population and subsequent spread to hundreds of millions of people around the world.”

Giroir, a former four-star admiral in the U.S. Public Health Service Commissioned Corps, spoke Tuesday as part of a panel [organized](#) by House Republicans on the Select Subcommittee on the Coronavirus Crisis.

“There is now an increasing body of circumstantial evidence pointing to a lab leak origin of the virus,” Giroir said. “The bottom line is: I believe it’s just too much of a coincidence that a worldwide pandemic caused by a novel bat coronavirus that cannot be found in nature started just a few miles away from a secretive laboratory doing potentially dangerous research on bat coronaviruses. Sometimes, the most obvious explanation is indeed the correct one.”

A State Department [fact sheet](#) released in January contended Wuhan lab researchers “conducted experiments involving the bat coronavirus identified by Wuhan virologists in January 2020 as its closest sample to COVID-19” and that the lab “has a published record of conducting ‘gain-of-function’ research to engineer chimeric viruses.” The fact sheet also asserted the lab “engaged in classified research, including laboratory animal experiments, on behalf of the Chinese military” and that lab workers became sick with coronavirus-like symptoms in autumn 2019.

The National Institutes of Health’s [RePORTER website](#) said the agency provided \$15.2 million to Peter Daszak’s New York-based EcoHealth Alliance over the years, with \$3.74 million [toward](#) understanding bat coronavirus emergence. Daszak, a key member of the World Health Organization-[China](#) joint study team earlier this year, maintained a working relationship with Wuhan lab “bat lady” Shi Zhengli, sending at least \$600,000 in NIH funding for bat coronavirus research.

Giroir said: “It is essential that Congress provides leadership for a comprehensive, transparent, and unbiased investigation to determine the most likely origin of the virus, whether the NIH funded, directly or indirectly, or approved of, explicitly or tacitly, potentially dangerous research within the Wuhan lab, and what the U.S. can do to minimize the possibility of future pandemics and enable rapid global containment of any suspicious infectious outbreak.”

He added that the WHO couldn’t be relied upon for an investigation because it has no authority to do anything in [China](#) without direct approval from the Communist Party.

[NIH DEFENDS DELETING GENETIC SEQUENCES OF COVID-19](#)

The Biden administration and the United States’s allies are largely pinning hopes for a second COVID-19 [origins investigation](#) in [China](#) on the WHO, despite the WHO-[China](#) joint study team’s visit to Wuhan earlier this year that essentially dismissed the lab leak hypothesis.

David Asher, who [led](#) the Trump State Department’s Bureau of Arms Control, Verification, and Compliance investigation into COVID-19’s origins, said China should be punished for its role in the pandemic.

"We should stop funding the Chinese Communist research into biology. This dangerous gain-of-function collaboration with China has to end ... We've gotta enforce our treaty compliance, that should be a focus across the board," Asher said, adding, "Sanctions — China needs to be coerced. They need to feel the pain."

Asher added: "Whether the Chinese did this deliberately or not in terms of creating this pathogen — I think the chances are they were working on it and it was funded by the military, I'm very confident of that — but whether they released it or not deliberately or just had an accident, I think the answer is they probably had an accident, but that doesn't matter, because they allowed it to be weaponized in the wake of its release."

The State Department concluded in April that China has "engaged in activities with dual-use applications, which raise concerns regarding its compliance with Article I of the Biological Weapons Convention" and that "the United States does not have sufficient information to determine whether China eliminated its assessed historical biological warfare program, as required under Article II of the Convention."

Asher said: "What we found truly disturbed us: that the Chinese were working on a military-supported program, which they did not declare under the Biological Weapons Convention — so they lied. It involved coronaviruses, which they said they weren't working on at the Wuhan institute."

The former State Department official called for a 9/11-like commission to investigate COVID-19's origins.

Dr. Steven Quay and Richard Muller, scientists who earlier this month wrote a piece for the *Wall Street Journal* which contended that "the most compelling reason to favor the lab leak hypothesis is firmly based in science," also testified on Tuesday.

Quay, the founder of Atossa Therapeutics, said Tuesday: "I believe the evidence conclusively establishes that the COVID pandemic was not a natural process but instead came from a laboratory in Wuhan, China, and that it has the fingerprints of genetic manipulation through a process called 'gain-of-function' research."

Muller, an emeritus professor of physics at the University of California, Berkeley, said: "Some people say we will never know, not until China confesses or unless there is a whistleblower."

"Well, we have a whistleblower. It was the virus itself. It came here, it came out of China, it came to us, and it carried with it genetic information."

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To: Peter Daszak ((b)(6))
Cc: Taubenberger, Jeffery (NIH/NIAID) [E] ((b)(6))
Subject: Peter, I am curious to know what you think of these data and conclusions. TY, David
Attachments: 2021.07.05.451089v1.full.pdf

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Mutation signatures inform the natural host of SARS-CoV-2

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Abstract

The before-outbreak evolutionary history of SARS-CoV-2 is enigmatic because it shares only ~96% genomic similarity with RaTG13, the closest relative so far found in wild animals (horseshoe bats). Since mutations on single-stranded viral RNA are heavily shaped by host factors, the viral mutation signatures can in turn inform the host. By comparing publically available viral genomes we here inferred the mutations SARS-CoV-2 accumulated before the outbreak and after the split from RaTG13. We found the mutation spectrum of SARS-CoV-2, which measures the relative rates of 12 mutation types, is 99.9% identical to that of RaTG13. It is also similar to that of two other bat coronaviruses but distinct from that evolved in non-bat hosts. The viral mutation spectrum informed the activities of a variety of mutation-associated host factors, which were found almost identical between SARS-CoV-2 and RaTG13, a pattern

difficult to create in laboratory. All the findings are robust after replacing RaTG13 with RshSTT182, another coronavirus found in horseshoe bats with ~93% similarity to SARS-CoV-2. Our analyses suggest SARS-CoV-2 shared almost the same host environment with RaTG13 and RshSTT182 before the outbreak.

Introduction

Darwin's evolutionary theory has been challenged ever since it was proposed by the unavailability of some key intermediates between extant species¹. Importantly, the growing understanding of life in the past one and half century, particularly since the time of molecular biology, provided indisputable intermediate-free supports to Darwin's theory. When we examine the genomes of current human and, say, chimpanzee, mouse, fish and fly, it's clear that the delicate principles operating in the non-human species apply to humans as well. There is simply no need to call for a special creator or designer to explain the origin of human beings.

Today we are facing a similar scenario Darwin used to face. The debate on the natural or unnatural origin of SARS-CoV-2, the causative virus of COVID-19, has existed since the beginning of the outbreak² and surged lately^{3,4}. One of the main reasons is that RaTG13, the closest relative so far found⁵ (in horseshoe bats *Rhinolophus affinis*), has only ~96% nucleotide similarities to SARS-CoV-2 (with ~1,200 nucleotide differences). The situation is distinct from the two previous coronavirus outbreaks happened this century (SARS at 2003 and MERS at 2012); in both cases, a closely related virus with over 99% nucleotide similarities to the causative virus was found in wild animals shortly after the start of each outbreak^{6,7}. The missing intermediates between RaTG13 and SARS-CoV-2 prevent a better understanding of the

spillover. Fortunately, the signatures left on the available viral genomes would inform the before-outbreak history of SARS-CoV-2.

SARS-CoV-2 belongs to the Betacoronavirus genus, with a single-stranded positive-sense RNA genome of ~30 thousand nucleotides⁸. There are 12 types of substitution mutations on the viral genome: C>U, C>A, C>G, G>U, G>A, G>C, A>U, A>G, A>C, U>A, U>G, and U>C. The genome-wide mutation spectrum, which measures the relative rates of the 12 mutation types, comprises a set of summary statistics with little functional relevance. More importantly, the viral mutation spectrum is expected to be heavily shaped by host factors⁹. For example, the large number of RNA-binding proteins in mammalian cells would necessarily interact with the single-stranded RNA genome¹⁰, which is critical for preventing the hydrolytic deamination of cytosines (leading to C>U) and the reactive oxygen species (ROS) induced oxidation of guanines (leading to G>U)¹¹. Also, the two key RNA editing protein families, ADAR¹² (adenosine deaminase acting on RNA) and APOBEC¹³ (apolipoprotein B mRNA editing enzyme catalytic polypeptide-like), would cause A>G and C>U mutations, respectively. In addition, when the host immunity failed to prevent high virion production, the cellular supply of dATP, dUTP, dCTP, and dGTP would modulate the viral mutations during genome replication¹⁴. The activities of the host factors often vary substantially among different species or even among different tissues of the same species¹⁵, and their interplay would be even more complex. Hence, the viral mutation spectrum as a 12-dimension signature vector would be a powerful tool for tracking the hosts.

Results

Evolution of mutation spectrum in the SARS-CoV-2 lineage

We included SARS-CoV-2 and six related viruses in the analysis (Fig. 1a). The six related viruses were chosen because they are evolutionarily close enough for reliable mutation inferences while distant enough for observing plenty of mutations. At least three different hosts, bat, pangolin and human, are involved, highlighting a complex host history of this viral lineage^{16,17}. Two separate phylogenetic trees were constructed to avoid the phylogeny confusions caused by recombination (Fig. S1), which results in different genealogical histories at different genomic regions in the ancestor of Bat-Cov-ZXC21 and Bat-Cov-ZC45 (both found in horseshoe bats *Rhinolophus sinicus*¹⁸). The branch X, which represents the before-outbreak history of SARS-Cov-2, and the B1, which represents the history of RaTG13 after it split from SARS-Cov-2, are present in both phylogenetic trees. Using conventional molecular evolutionary methods¹¹, we compared the viral genomes to infer the substitution mutations occurred on the evolutionary branches as marked in Fig. 1a (Methods). We considered only the third codon positions such that the obtained mutation spectra are less shaped by selection¹⁹ (Fig. 1b and Table S1). Because the mutations on different evolutionary branches occurred independently, the derived mutation spectra of the branches are independent. To quantify the similarity between two mutation spectra we computed an identity score (i-score), which is the proportion of the total rate variation explained by the x=y dimension in a two-dimensional plot of the two spectra as in Fig. 1c (Methods). An i-score equal to 100% means the two mutation spectra are 100% identical.

The mutation spectra calculated separately in the two phylogenetic trees are nearly identical for the same branches (i-score = 99.9% for X versus X' and 99.4% for B1 versus B1'; Fig. S2), suggesting the results of the two trees comparable. There are three notable features

regarding the obtained spectra (Fig. 1b-c). First, the branch X is nearly identical to B1, with an i-score = 99.9%. Second, the branch X is distinct from the after-outbreak branch of SARS-CoV-2 (i.e, the Human branch), with an i-score = 83.9%. The obtained spectrum of the Human branch is consistent with a previous study⁹. Compared to branch X, the Human branch has a lot more G>U and C>U mutations, suggesting much stronger mutational pressures imposed by ROS and APOBEC family, respectively, to the SARS-CoV-2 genome in infected human cells. Meanwhile, the rates of A>G/U>C mutations reduce substantially, suggesting weaker activity of the ADAR family. Third, the branch X is in general highly similar to the branches with bats as the putative hosts (B1, B6 and B7) while less similar to the branches with non-bat hosts involved. These results, in particular, the 99.9% identify of X and B1, suggest SARS-CoV-2 not be artificially synthesized for gain-of-function research, because mutation spectrum is of little functional relevance and a synthesized genome is unlikely to show such a similar mutation spectrum to a naturally evolved viral genome (RaTG13). Notably, making comparably similar mutation spectra is doable by nature for close sister lineages like B6 and B7 (Fig. S2)

Host signatures inferred from viral mutations

The viral mutations are caused by both replication errors and replication-independent lesions or editing. The former is mostly associated with the viral self-encoded replication-transcription complex (RTC) and the latter would be mostly explained by host factors²⁰ (Fig. 2a). The coronavirus positive-sense RNA genome is replicated first by forming a negative-sense RNA intermediate, which then serves as template for both transcription and replication⁸. The same replication errors occurred in producing negative-sense strand and in producing positive-sense strand would result in different mutation types. For example, the two steps for replicating a

nucleotide C (C-to-G followed by G-to-C) are the same, but in an opposite order, as the two steps of replicating a G (G-to-C followed by C-to-G). Then, the same replication error of, say, C-to-A, in the C-to-G step would cause a C>U mutation in the replication of C but a G>A mutation in the replication of G (Fig. 2a). Other types of replication errors have the same feature. As a result, the 12 mutation types would form six complementary pairs: C>A/G>U, C>U/G>A, C>G/G>C, A>U/U>A, A>C/U>G, and A>G/U>C; in each pair the two complementary mutation types would have the same rate if all mutations were due to replication errors. Hence, the different mutation rate observed in each complementary pair would be ascribed to replication-independent factors, which are associated in a large part with host. For example, the preferential binding of the host APOBEC family to the single-stranded positive-sense RNA would lead to more C>U mutations than G>A mutations²¹. The host ADAR family would preferentially edit the negative-sense strand that are often in a double-stranded form, resulting in more U>C mutations than A>G mutations²². In addition, the damage effects of ROS primarily on single-stranded RNA would cause a higher rate of G>U mutations over C>A mutations²³. The direction and magnitude of the rate difference in each complementary pair then constitute a signature of host factors, which informs the identity of hosts.

To obtain the host signatures we calculated the rate difference in each complementary pair. The six host signatures (S1-S6), each corresponding to a complementary pair, are indeed informative (Fig. 2b). For example, S1, the rate of C>U minus the rate of G>A, ranges from 0.06 to 0.42 among the different evolutionary branches. This may represent the different activities of the APOBEC family in different hosts. S2, the rate of U>C minus the rate of A>G, ranges from -0.03 to 0.1. This is likely associated with the relative activity of the ADAR family. S3, the rate of G>U minus the rate of C>A, ranges from -0.03 to 0.23 and appeared unusually

strong in the Human branch. This could be related to ROS that may preferentially target the single-stranded positive-sense RNA and have a strong induction in the infected human cells. Notably, the mentioned genes/pathways are just putatively associated with the observed host signatures. We found branch X has nearly identical host signatures to B1, with an i-score = 99.5%, despite substantial deviations from the human or pangolin associated branches (Fig. 2c). A multidimensional scaling plot shows that X is almost perfectly overlapping with B1, close to B6 and B7, and distant from the other branches (Fig. 2d). These results suggest that SARS-CoV-2 shared almost the same host environment with RaTG13 before the outbreak.

To gauge the probability that an arbitrary cell culture condition in laboratory matches the natural host environment of RaTG13, we estimated the size of the space formed by the host signatures, each of which has an empirical range according to the nine branches presented in Fig. 2b. We considered S1, S2 and S3 because their empirical ranges are the largest and their associated genes/pathways (APOBEC, ADAR and ROS) appear independent. As shown in Fig. 2e, the probability of approaching, as closely as SARS-CoV-2, the host environment of RaTG13 is ~2.0%, if S1 and S2 are considered. The number would be 0.02% if S3 is also considered (Fig. 2f). The estimations are conservative because the other three signatures (S4-S6) were not considered and also the real ranges of the signatures would be larger than the empirical ranges based on the nine evolutionary branches. We cautioned that the calculations assumed the associated gene/pathway activities are uniformly distributed within the empirical ranges. Nevertheless, the results are helpful for thinking of the likelihood that an arbitrary cell culture condition set in laboratory happens to duplicate a defined natural host environment.

Robust signals after replacing RaTG13 with RshSTT182

Because there are concerns on the quality of the assembled genome of RaTG13²⁴, we reproduced the above analyses after replacing RaTG13 with another bat coronavirus RshSTT182.

RshSTT182 was isolated from Shamel's horseshoe bats (*Rhinolophus shameli*), being the first close relative of SARS-CoV-2 found in Southeast Asia (Cambodia) and with 92.6% genomic identity to SARS-CoV-2²⁵. The whole-genome phylogeny of the involved viruses is (((((SARS-CoV-2, RaTG13), RshSTT182), Pangolin-CoV-GD), Pangolin-CoV-GX), Rc-o319). Hence, replacing RaTG13 with RshSTT182 would affect mainly the branches X, B1, and B2 in our analyses. Using the same procedure we obtained the mutation spectra and derived the host signatures for each of the evolutionary branches. The findings remain qualitatively the same (Fig. S3-S4 and Table S2). In brief, the mutation spectrum of SARS-CoV-2 is 99.3% identical to that of RshSTT182 (99.9% in the case of RaTG13). The slight reduction of the similarity may reflect the fact that the host of RaTG13 is *Rhinolophus affinis* but the host of RshSTT181 is another horseshoe bat species *Rhinolophus shameli*. Taken together, our analyses suggest the host environment of SARS-CoV-2 before the outbreak be fully compatible with horseshoe bats.

Discussion

It should be emphasized that this study is to address the evolution of the SARS-CoV-2 genome but nothing else. Using mutational signatures inferred from the available viral genomes we probed the evolutionary time window (branch X) SARS-CoV-2 spent before the outbreak and after the split from bat coronavirus RaTG13. The missing intermediates within this time window that presumably spans a few tens of years²⁶ prevents a better understanding of the spillover. Our analyses based on public data provide compelling evidence that during this time window SARS-CoV-2 evolved in a host environment highly similar, if not identical, to RaTG13. The host

environment is also similar to that of the three bat coronaviruses RshSTT182, ZXC21 and ZC45, and difficult to duplicate by an arbitrary cell culture condition set in laboratory. One may argue that, while the branch X as a whole is compatible with natural laws, it may not be at a few key sites. Such an argument presumes that there are intermediates with over 99% similarity to SARS-CoV-2 to be found in nature. Notably, claiming such natural intermediates would leave little room for speculations, as in the cases of SARS⁶ and MERS⁷. The mission of the scientific community is then to find them in nature to better understand the spillover.

Methods

Genomic Data

The SARS-CoV-2 related bat and pangolin coronavirus genomic sequences were obtained from NCBI GenBank (<https://www.ncbi.nlm.nih.gov/genbank>). For genomes without accurate annotations of ORFs, we re-annotated these genomes with CDSs annotated in SARS-CoV-2 by Exonerate2 (`-model protein2genome: bestfit -score 5 -g y`)²⁷. The complete genomic sequences and metadata of SARS-CoV-2 were retrieved from Global Initiative on Sharing All Influenza Data (GISAID; <https://www.gisaid.org/>; accessed on 19 March 2021)²⁸. Gap-containing genomes in examined regions were removed, and only genomes from Dec. 2019 to Dec. 2020 were chosen for analysis. All available genomes submitted to GISAID from Dec. 2019 to Feb. 2020 were included, and, among the too many submitted genomes from Mar. to Dec. 2020, 2,000 genomes were randomly selected for each month. Finally, a total of 214,32 SARS-CoV-2 genomes were included. Following GISAID we used SARS-CoV-2 WIV04 (EPI_ISL_402124)

as the reference genome. The detailed information of SARS-CoV-2 and the related coronaviruses included in this analysis is summarized in Supplementary Dataset I.

Phylogenetic analysis and mutation spectra calculation

The codon alignments of ORFs were performed based on amino acid sequences translated by TranslatorX²⁹ and MAFFT v7.471³⁰, and further concatenated by AMAS³¹ and refined with visual check. Only ORFs with consistent annotations in the examined viruses were included. Maximum likelihood phylogenetic analysis based on the whole coding regions was conducted by using IQ-TREE v2.0.3³² with GTR+FO+R10 substitution model and 1,000 bootstrap replicates. The ancestral sequences of the internal nodes were inferred in IQ-TREE with an *-asr* parameter, and mutations on each branch were derived by comparing the ancestral sequence to the descendant sequence. To avoid the confounding effects of potential recombination and convergent evolution, the region covering the receptor binding domain and the furin-like cleavage site (319th-770th codons) of the spike protein was removed from the analysis. Only the third codon positions were considered in calculation of the mutation spectra. The aligned sequences can be found in Supplementary Dataset II-V.

To obtain the after-outbreak mutations of SARS-CoV-2, 59 separate main clades each containing more than 100 sequences and supported by a bootstrap value >90 were selected from the phylogenetic tree. Mutations were inferred by comparing each individual sequences to the corresponding common ancestral sequences of each clade, respectively. To avoid redundancy, recurrent mutations within a clade were counted once. Then, the 59 clade-specific ancestral sequences were compared to the earliest common ancestral sequence of SARS-CoV-2.

Mutations obtained from the two steps were pooled to derive the mutation spectrum of the Human branch.

For a specific mutation type, say C>A, the rate was calculated as the number of C>A mutations divided by the total number of C nucleotides in the ancestral sequence of the given branch (third codon positions). The mutation rates of the 12 mutation types were then each divided by their sum to obtain the relative mutation rates (i.e., mutation spectrum). The i-score of two mutation spectra is the proportion of variance explained by the x=y dimension in a two-dimensional plot of the two spectra. Specifically, let $A = [S_1, S_2]^T$, where S_1 and S_2 are the two mutation spectra under examination, and $B = [D_1, D_2]^T$, where D_1 is the projection of A onto the x=y dimension and D_2 onto the x= -y dimension. Then, the i-score = $\text{cov}(D_1) / (\text{cov}(S_1) + \text{cov}(S_2))$.

To verify the whole-genome-based evolutionary branches at different genomic regions a sliding window analysis through the viral genomes was conducted. Specifically, each window covers 500 codons (or 1500 nucleotides, ~5% of the viral genome) and the step size is a half window. For each window we constructed the phylogeny of the viruses using synonymous sites, and then checked if the whole-genome-based branches exist in the window. Neighbor-Joining phylogeny was obtained in MEGA X³³, which allows such analysis on synonymous sites, with 1,000 bootstrap replicates.

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Figure legends

Fig. 1. Evolution of mutation spectrum in the SARS-CoV-2 lineage. **a.** The phylogenetic relationships of the seven coronaviruses included in the analysis. Two separate phylogenetic trees are considered to resolve the confusions caused by recombination, which results in different genealogical histories at different genomic regions in the ancestral branch of Bat-CoV-ZXC21 and Bat-CoV-ZC45. Nine major evolutionary branches examined in this study, X, B1-B7, and the Human branch, are shown. The branch X and B1 are also present (as X' and B1') in the tree with B6 and B7 to help infer the ancestor of B6 and B7. The Bat-CoV-Rc-o319 is used as outgroup in both trees. **b.** The relative mutation rate of the 12 mutation types on each of the nine evolutionary branches. **c.** The similarity of mutation spectrum between branch X and each of the other eight branches. The similarity of two branches is measured by identity score (i-score), which is the proportion of total rate variation explained by the $x=y$ dimension in the plot of the two spectra.

Fig. 2. Host signatures inferred from viral mutation spectrum. **a.** A diagram showing the major sources of viral mutations, which include the replication errors (by the viral replication-transcription complex RTC) and the lesions caused by host factors. Because replication processes are the same, despite in the opposite order, for nucleotides G and C (or A and T), replication errors would result in equal rates of complementary mutations such as $C>A$ and $G>T$. However, host factors would distort the equal-rate pattern of complementary mutation pairs. The positive-sense RNA is often in a single-stranded form, sensitive to ROS and the APOBEC family, while the negative-sense RNA tends to be in a double-stranded form, thus more affected by the ADAR family. **b.** The rate difference of each complementary mutation pair serves as a signature of host factors. There are thus six host signatures, each corresponding to a complementary mutation pair, inferred from the viral mutation spectrum. Among the three major host signatures, S1 is likely associated with the APOBEC family, S2 the ADAR family, and S3 the ROS. **c.** The similarity of host signatures between branch X and each of the other eight branches. Branch X is highly similar to B1, B6 and B7, the three branches of bat coronavirus. **d.** A multidimensional scaling (MDS) plot of the host signatures reveals nearly the same positions of branch X and B1. **e.** Estimation of the likelihood that an arbitrary laboratory condition happens to match the host signatures of B1 (the branch of RaTG13). The grey rectangle area is defined by the empirical ranges of S1 (APOBEC-associated) and S2 (ADAR-associated) that are based on the data of panel b. The probability of approaching B1 as closely as X is the area of the circle divided by the whole rectangle area, which is $\sim 2.0\%$. The positions of the other seven branches are also shown in the rectangle area. **f.** The probability that an arbitrary condition approaches B1 as closely as X is given, by considering the different combinations of S1, S2, and S3, respectively.

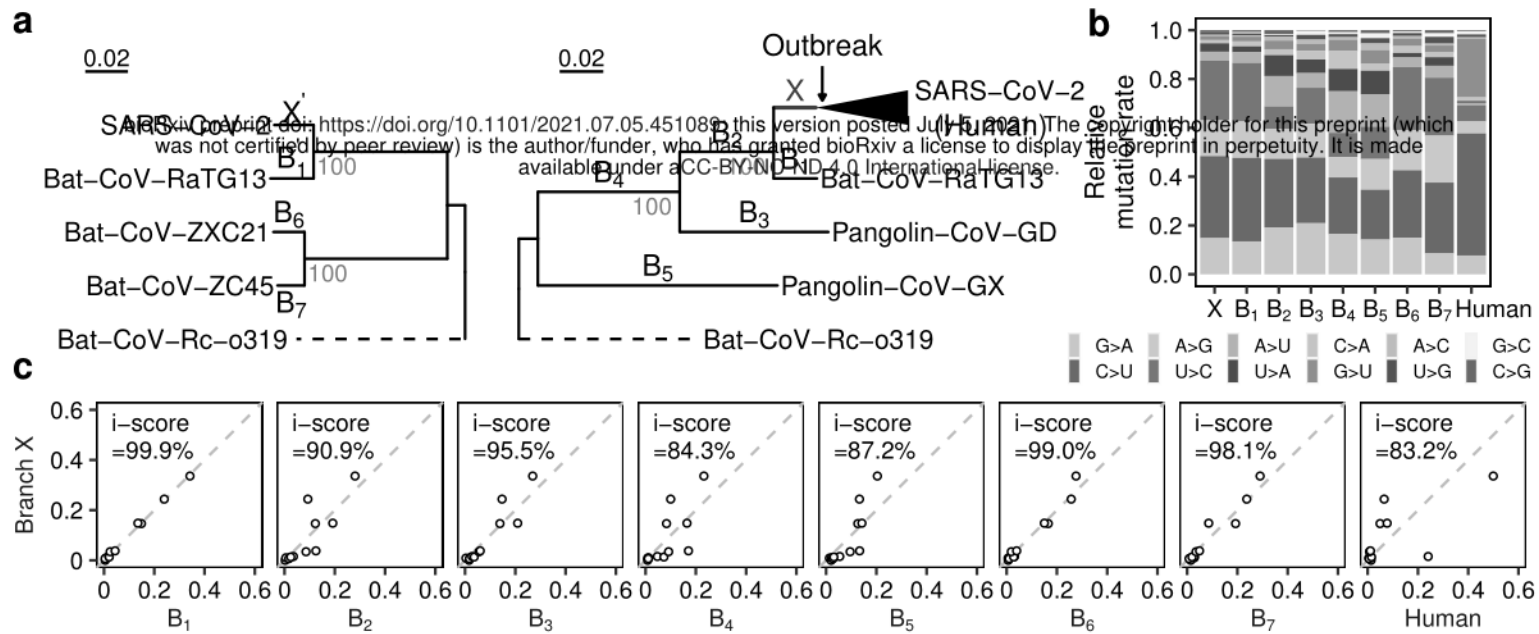


Fig. 1. Evolution of mutation spectrum in the SARS-CoV-2 lineage. **a.** The phylogenetic relationships of the seven coronaviruses included in the analysis. Two separate phylogenetic trees are considered to resolve the confusions caused by recombination, which results in different genealogical histories at different genomic regions in the ancestral branch of Bat-CoV-ZXC21 and Bat-CoV-ZC45. Nine major evolutionary branches examined in this study, X, B1-B7, and the Human branch, are shown. The branch X and B1 are also present (as X' and B1') in the tree with B6 and B7 to help infer the ancestor of B6 and B7. The Bat-CoV-Rc-o319 is used as outgroup in both trees. **b.** The relative mutation rate of the 12 mutation types on each of the nine evolutionary branches. **c.** The similarity of mutation spectrum between branch X and each of the other eight branches. The similarity of two branches is measured by identity score (i-score), which is the proportion of total rate variation explained by the $x=y$ dimension in the plot of the two spectra.

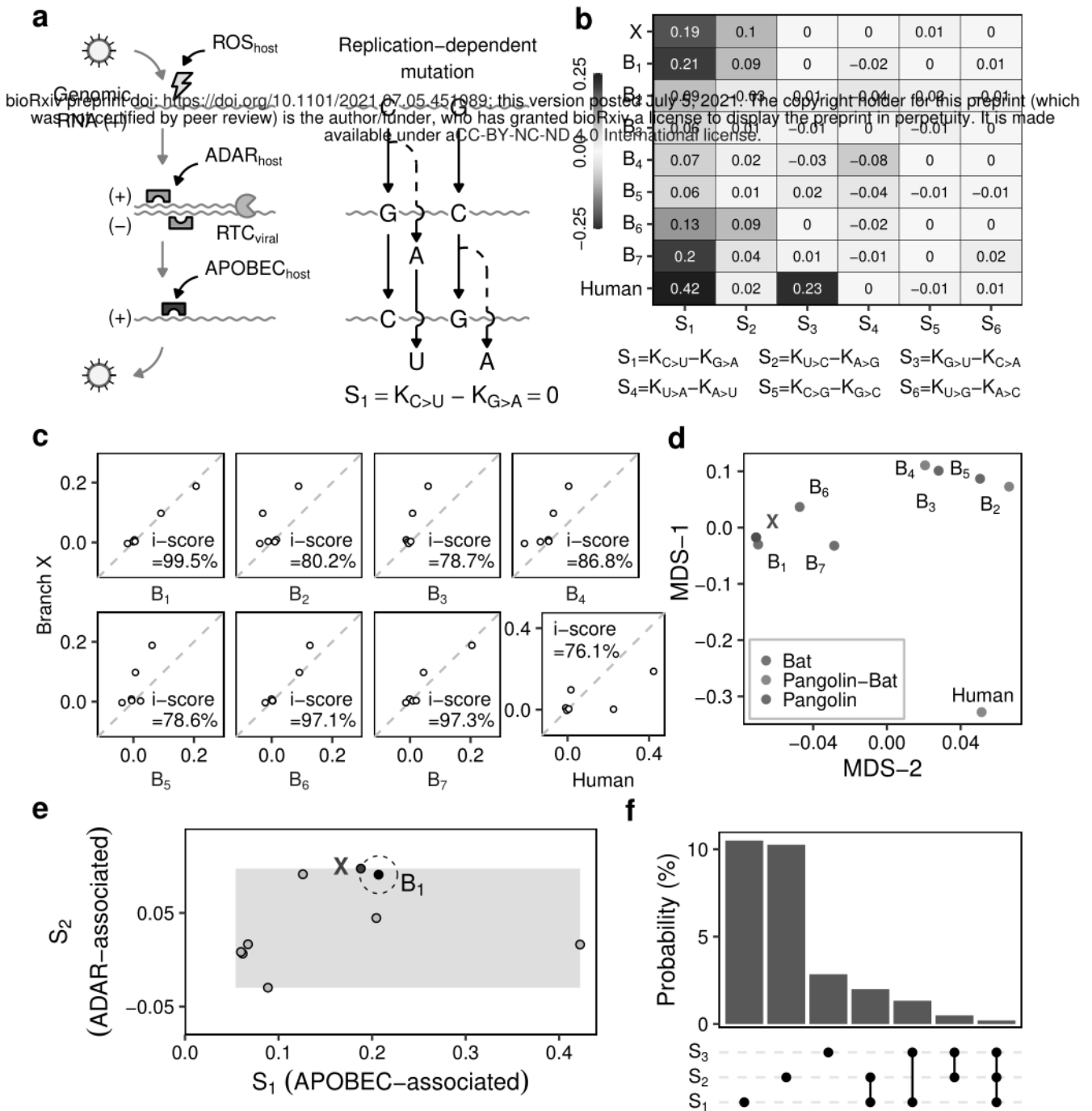


Fig. 2. Host signatures inferred from viral mutation spectrum. **a.** A diagram showing the major sources of viral mutations, which include the replication errors (by the viral replication-transcription complex RTC) and the lesions caused by host factors. Because replication processes are the same, despite in the opposite order, for nucleotides G and C (or A and T), replication errors would result in equal rates of complementary mutations such as C>U and G>A. However, host factors would distort the equal-rate pattern of complementary mutation pairs. The positive-sense RNA is often in a single-stranded form, sensitive to ROS and the APOBEC family, while the negative-sense RNA tends to be in a double-stranded form, thus more affected by the ADAR family. **b.** The rate difference of each complementary mutation pair serves as a signature of host factors. There are thus six host signatures, each corresponding to a complementary mutation pair, inferred from the viral mutation spectrum. Among the three major host signatures, S₁ is likely associated with the APOBEC family, S₂ the ADAR family, and S₃ the ROS. **c.** The similarity of host signatures between branch X and each of the other eight branches. Branch X is highly similar to B₁, B₆ and B₇, the three branches of bat coronavirus. **d.** A multidimensional scaling (MDS) plot of the host signatures reveals nearly the same positions of branch X and B₁. **e.** Estimation of the likelihood that an arbitrary laboratory condition happens to match the host signatures of B₁ (the branch of RaTG13). The grey rectangle area is defined by the empirical ranges of S₁ (APOBEC-associated) and S₂ (ADAR-associated) that are based on the data of panel b. The probability of approaching B₁ as closely as X is the area of the circle divided by the whole rectangle area, which is ~2.0%. The positions of the other seven branches are also shown in the rectangle area. **f.** The probability that an arbitrary condition approaches B₁ as closely as X is given, by considering the different combinations of S₁, S₂, and S₃, respectively.

From: Morens, David (NIH/NIAID) [E]
Sent: Tue, 29 Jun 2021 20:46:55 +0000
To: Peter Daszak ((b)(6)); Keusch, Jerry ((b)(6));
Rich Roberts ((b)(6))
Subject: FW: Webcast -- GOP Oversight committee hearing 6/29/2021: Led By Science:
The COVID-19 Origin Story <https://bit.ly/3jns1lz>


Giroir testifying before the Republicans today, this may be where he said that covid was man made.


David

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From: Folkers, Greg (NIH/NIAID) [E] ((b)(6))
Sent: Tuesday, June 29, 2021 2:19 PM

Subject: Webcast -- GOP Oversight committee hearing 6/29/2021: Led By Science: The COVID-19 Origin Story <https://bit.ly/3jns1lz>




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From: Morens, David (NIH/NIAID) [E]
Sent: Thu, 1 Jul 2021 16:21:40 +0000
To: Peter Daszak ((b)(6)); Keusch, Jerry ((b)(6))
Subject: FW: Fox News: Columbia professor who thanked Fauci for Wuhan lab messaging maintains close ties to China


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

Sent: Thursday, July 1, 2021 12:17 PM

Subject: Fox News: Columbia professor who thanked Fauci for Wuhan lab messaging maintains close ties to China

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

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

By [Joe Schoffstall](#) | [Fox News](#)

Published 37 mins ago



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

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

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

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

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

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

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



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

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

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

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

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

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

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

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

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

Lipkin has also praised China's response and transparency early on in the coronavirus pandemic, despite indications that the Chinese government engaged in a cover-up.

Lipkin did not respond to a request for comment.

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

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

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

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

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

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

Columbia has received millions in foreign funding from China. According to the College Foreign Gift and Contract Report database, which relies on universities self-reporting their foreign cash, the university has raked in at least \$17.7 million from China for research, facilities and professorships. Columbia did not provide a comment on the funding.

China conducts numerous influence campaigns within the United States, including targeting institutes of higher learning.

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

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

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

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

"One of the things we're concerned about is the Chinese trying to make American students believe that the communists in China are good people," Foxx said. "They want them to believe that the culture in China is good, and we know the culture of

China is controlled by the Chinese Communist Party - and that is definitely not good for Americans."

Columbia University was the only Ivy League school to host a Confucius Institute, which it has since quietly dissolved.

But while the institute was in operation, the university had failed to disclose at least \$1 million in Chinese government funding towards it, the Washington Free Beacon reported. Part of that money was used for professor Dedong Wei, an adviser to the Chinese regime's propaganda department, to lead the institute.

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

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


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

From: Morens, David (NIH/NIAID) [E]
Sent: Mon, 5 Jul 2021 16:08:56 +0000
To: Peter Daszak ((b)(6)); Keusch, Jerry ((b)(6))
Subject: FW: Global Times, China: Western scientists face government probe, death threats for opposing COVID-19 lab-leak theory: source


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

Sent: Monday, July 5, 2021 11:50 AM

Subject: Global Times, China: Western scientists face government probe, death threats for opposing COVID-19 lab-leak theory: source

Western scientists face government probe, death threats for opposing COVID-19 lab-leak theory: source

By GT staff reporters Published: Jul 05, 2021 02:18 PM



Peter Ben Embarek (center) talks with Liang Wannian (left) and Marion Koopmans (right) after a press conference to wrap up a visit by an international team of experts from the World Health Organization (WHO) in the city of Wuhan, in Central China's Hubei Province on Tuesday. Photo: AFP

Prominent US and Australian scientists focused on the COVID-19 origins tracing are now facing tremendous political pressure, and some have been sidelined for not yielding to politicians-driven conspiracy theory on the matter and received anonymous threatening letters with bullets, the Global Times learned from people familiar with the matter. Chinese experts have urged the US to stop politicizing the origin-tracing research and conduct a comprehensive investigation in the US.

Since the Biden administration ordered in May US intelligence agencies to report on COVID-19 origins within 90 days, several US scientists have been put at the center of the political storm. These scientists have been facing the suppression of Republicans. For example, Anthony Fauci, who advises US President Joe Biden and leads National Institute of Allergy and Infectious Diseases, has been a target of the GOP. Elise Stefanik, the House Republicans conference chair, sent a fundraising email recently with the subject "Fire Fauci" and senator Josh Hawley also tweeted that Fauci's recently released emails and investigative reporting about COVID-19 origins are shocking. The time has come for him to resign and for a full congressional investigation into the origins to take place, according to US media reports.

Under such growing political pressure, Fauci has been increasingly ambiguous on his rhetoric. Another US scientist, who also took part in the WHO-China joint team on the origins research, has also been a target of such attacks, the Global Times learned. After collaborating in the project with China, Peter

Daszak, president of EcoHealth Alliance, was recused from the UN-backed commission work on the origins of the epidemic.

A source close to the matter told the Global Times earlier that the US scientist is being personally threatened by emails, phone calls and messages on social media, and people who attacked him generally have far-right and even white supremacism leanings. GOP members of Congress are whipping those extremists up now.

"There is a coordinated political campaign to undermine anyone involved in the origins work if they do not fit the lab leak narrative. This is coming mainly from the right wing circles in the US, Australia, and in Europe, mainly the UK," the source said.

In the meantime, some so-called "international scientists" seeking attention have been making grandstanding campaigns by issuing open letters to call for an investigation into the COVID-19 origins.

It's revealing that some so-called "international scientists" who recently called for a COVID-19 origins inquiry were politicians with political agendas. But many scientists who truly uphold the spirit of science - objectivity and impartiality - have been attacked by some governments and extremists, or even received death threats, Chinese Foreign Ministry spokesperson Wang Wenbin said at Monday's routine press conference. Wang said that the right idea was to carry out more in-depth and detailed scientific studies in a wider range.

Death threats, unable to continue work

Letting politics to override science is not only prevailing in the US but also in Australia. Evolutionary biologist Edward Holmes at the University of Sydney, who released an open letter back in last April, is being probed by the Australian government. In the letter, Holmes claimed that there was no evidence that SARS-CoV-2, the virus that causes COVID-19 in humans, originated in a lab in Wuhan, Central China's Hubei Province. Like many others who oppose the lab-leak theory, Edward Holmes has received a number of threatening letters with real bullets, the Global Times learned from the people familiar with the matter.

He was threatened that if he continued expressing opinions on the origins of the virus, he may face even further crackdown, a source close to the matter said. Due to the tremendous pressure Holmes faces, he is undergoing psychotherapy and is unable to carry out normal scientific research work, the source said.

According to a Sydney Morning Herald report in October, 2020, Holmes became the target of online harassment after he co-authored a paper in Nature Medicine debunking the pervading conspiracy theory that the virus was engineered in or escaped from a laboratory in Wuhan. He also received "death threats" from conspiracy theorists, the report said.

Though the US government and politicians have been pushing forward their political agenda in bashing China with the lab-leak theory, targeting a number of global scientists and the Wuhan Institute of Virology (WIV), most scientists spoke out and dismissed the theory, reiterating that the most likely scenario is that the virus has a natural origin.

For instance, Danielle Anderson, the only foreign scientist who once worked at the WIV, was quoted as saying in a Bloomberg report on June 28 that no one she knew at the Wuhan institute was ill toward the

end of 2019. Recently the Wall Street Journal falsely claimed three researchers from the lab were hospitalized with flu-like symptoms in November 2019. She also described the place as having the highest biosafety designation with very strict procedures.

After she told Health Feedback that it's "simply false" to label the WIV as a bioweapons research lab, she had her name "trashed so viciously by extremists she had to call in police," the Sydney Morning Herald reported on Sunday.

"I really find it hard to think that if something escaped from a laboratory it would be this difficult to prove that concept. Among other things, it is an unknown virus that has no signs of genetic engineering inside," said Massimo Galli, director of Infectious Diseases at Milan's Luigi Sacco Hospital, the Adnkronos reported on June 22.

He said that there is a 99-percentage chance that the spread of the virus is a natural event. "This story of the laboratory virus does not have the slightest basis from a scientific point of view to be carried forward," added Galli.

Next country for tracing virus origins: the US

The US National Institute of Health issued a new antibody testing study that suggested the virus was present in some states in late December 2019, earlier than the first case reported in the country in January 2020. With some US scientists reporting more earlier cases, Chinese scientists have urged that these cases should serve as evidence for the next-stage virus-tracing investigations in the US.

In the All of Us study, by the US institutes released on June 15, researchers analyzed more than 24,000 stored blood samples contributed by program participants across all 50 states between January 2 and March 18, 2020. "In this study, the first positive samples came from participants in Illinois and Massachusetts on January 7 and 8, 2020, respectively, suggesting that the virus was present in those states in late December," it said.

However, the study authors noted several limitations to their study. While the study included samples from across the US, the number of samples from many states was low.

Yang Zhanqiu, a virologist from Wuhan University, told the Global Times on Monday that the research has shown the epidemic in the US probably emerged earlier than in Wuhan. In other words, the epidemic in the US was probably caused by a domestic virus rather than one transmitted from Wuhan.

But more large-scale epidemiological surveys are needed in the US to identify the relationship between these cases and those in other countries and regions, including Wuhan, to determine the origin and transmission route of the virus.

Yang mentioned the outbreaks of flu and pneumonia related to the use of E-cigarette in the US prior to the COVID-19 pandemic, calling for the US to release epidemiological surveys into these outbreaks, if they did any, to find out if they were COVID-19 cases.

The US has nearly all the variants spreading around the world, based on this, the virus most likely originated in the US rather than the Wuhan lab, according to Yang.


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From: Morens, David (NIH/NIAID) [E]
Sent: Wed, 28 Jul 2021 13:51:52 +0000
To: Peter Daszak ((b)(6)); Keusch, Jerry ((b)(6))
Subject: FW: Senate Committee on Foreign Relations: Risch, Menendez, Rubio, Warner
Stress Importance of Pursuing COVID Origins


David

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

Sent: Wednesday, July 28, 2021 8:15 AM

Subject: Senate Committee on Foreign Relations: Risch, Menendez, Rubio, Warner Stress Importance of Pursuing COVID Origins

July 27, 2021

Risch, Menendez, Rubio, Warner Stress Importance of Pursuing COVID Origins

WASHINGTON – U.S. Senators Jim Risch (R-Idaho) and Bob Menendez (D-N.J.), ranking member and chairman of the Senate Foreign Relations Committee, along with U.S. Senators Marco Rubio (R-Fla.) and Mark Warner (D-Va.), vice chairman and chairman of the Senate Select Committee on Intelligence, today sent a [letter](#) to President Biden asking the administration to take three crucial steps to get to the bottom of the origins of the COVID-19 pandemic in order to prevent a similar calamity in the future.

“The PRC’s refusal to cooperate with the World Health Organization (WHO) investigation into COVID-19 origins, the gag order it imposed on Chinese scientists and medical personnel, and its ongoing obfuscation and disinformation campaign regarding the pandemic have caused severe hardship worldwide,” **wrote the senators.** “As the United States emerges from the pandemic, we believe that, in addition to addressing gaps in international pandemic prevention, preparedness, and response, including within our own government, three crucial steps are necessary to prevent a similar calamity in the future.”

These steps include:

- Directing the intelligence community to continue prioritizing a thorough investigation into the origins of COVID-19 until there is a conclusion in which the United States has a high degree of confidence;
- Working with allies and partners to use all available resources and tools to pressure Beijing into permitting a transparent forensic investigation in the People’s Republic of China; and
- Completing a thorough review of existing and prior U.S. government support or funding for research collaboration with the PRC related to gain-of-function, synthetic biology, biotechnology, or other research areas that pose dual-use concerns.

“We expect that Congress will remain fully informed of and consulted on your efforts to reach definitive conclusions regarding the origins of this pandemic, as well as any concrete policy recommendations,” **concluded the senators.** “We stand ready to work with your administration in a bipartisan manner to seek answers to these important questions.”

Full text of the letter can be found [here](#) and below:

Dear Mr. President:

The threat to international health and security posed by the Chinese Communist Party’s (CCP) repressive and opaque governance of the People’s Republic of China (PRC) has become glaringly apparent over the past eighteen months, particularly given the PRC’s efforts to conceal the severity and scope of the outbreak of the SARS-CoV-2 virus that caused the COVID-19 pandemic. The PRC’s refusal to cooperate with the World Health Organization (WHO) investigation into COVID-19 origins, the gag order it imposed on Chinese scientists and medical personnel, and its ongoing obfuscation and disinformation campaign regarding the pandemic have caused severe hardship worldwide.

We were therefore glad to see your May 26, 2021, statement directing the intelligence community to “redouble their efforts to collect and analyze information that could bring us closer to a definitive

conclusion” with regard to the pandemic’s origin. As the United States emerges from the pandemic, we believe that, in addition to addressing gaps in international pandemic prevention, preparedness, and response, including within our own government, three crucial steps are necessary to prevent a similar calamity in the future.

First, we agree that the intelligence community must lead a thorough investigation into the origins of COVID-19. Identifying where the virus originated and how it first spread will be critical to preventing future pandemics. If the 90-day effort you have announced does not yield conclusions in which the United States has a high degree of confidence, we urge you to direct the intelligence community to continue prioritizing this inquiry until such conclusions are possible.

A full and impartial investigation that carefully considers all credible theories, backed by all available evidence, is critical. This includes theories suggested in an open letter by 18 distinguished experts to *Science Magazine* on May 14, 2021, which argued that “theories of accidental release from a lab and zoonotic spillover both remain viable.”

We believe the intelligence community should examine relevant research at the Wuhan Institute of Virology (WIV) and associated facilities, such as the Wuhan Center for Disease Prevention and Control and the Wuhan Institute of Biological Products. This investigation must evaluate evidence regarding WIV researchers who fell ill in the fall of 2019. It should identify other details of any researchers at the WIV who were working on coronavirus projects, and attempts by the PRC government to silence or disappear them; details of any WIV gain-of-function research specific to coronaviruses or other potential human pathogens; laboratory safety standards and practices for such research; and details of any research in synthetic biology and biotechnology connected to the Military-Civil Fusion strategy, and other military work or funding at the WIV.

Additionally, this investigation must examine any evidence pointing to the possible transmission of SARS-CoV-2 from animals to humans, including specific zoonotic transmission chains, and the most probable timing, location, and contributing factors of any zoonotic spillover events.

We also believe that the investigation should address PRC efforts to prevent international inquiries into the origins of SARS-CoV-2, and other actions PRC authorities have taken to obscure the nature of the virus and its transmission. The U.S. government should examine the international agreements to which the PRC is a party that require disclosure and cooperation in the event of a viral outbreak like SARS-CoV-2, assess whether the PRC violated any of these agreements, and analyze its motivations for doing so. The investigation should also include details on the collection and analytic guidance the Intelligence Community used from the start of the SARS-CoV-2 pandemic to the present to support policy and programmatic requirements.

Second, the U.S. government should lead efforts by the international community and the WHO to seek a transparent forensic investigation in the PRC. The PRC has an obligation to the international community to allow a full, unfettered, impartial, and scientific investigation into COVID-19 origins. In light of the PRC’s continued stonewalling of WHO efforts, the U.S. government should work with our allies and partners to use all available resources and tools to pressure Beijing to permit a serious investigation. Third, the United States must complete a thorough review of existing and prior U.S. government support or funding for research collaboration with the PRC related to gain-of-function, synthetic biology, biotechnology, or other research areas that pose dual-use concerns. U.S. taxpayer funding should not support any collaboration with PRC entities that pose health, economic or security risks for the United States. The PRC has demonstrated lax biosecurity standards, violated the International Health Regulations (2005), attempted to steal intellectual property related to COVID-19 vaccines, and may be in violation of the Biological Weapons Convention. The United States should not be partnering with or funding any country that exhibits these risk factors.

As part of a formal review, we therefore urge you to analyze the following: any direct or indirect U.S. taxpayer funding or engagement with entities in China, including the WIV, regarding gain-of-function

research or other forms of research related to viruses, pathogens, and toxins; whether any such research for civilian purposes was diverted for military research; any U.S. taxpayer funding that was used to support gain-of-function research in China during the U.S. moratorium on such research from 2014-2017; and steps taken, if any, to apply additional scrutiny to direct or indirect U.S. government funding, including sub-grants, to support gain-of-function studies in China, including at WIV, after the U.S. government lifted the moratorium on gain-of-function research in 2017.

We expect that Congress will remain fully informed of and consulted on your efforts to reach definitive conclusions regarding the origins of this pandemic, as well as any concrete policy recommendations. *The U.S. Innovation and Competition Act (S. 1260)*, which recently passed the U.S. Senate, requires a report to Congress on many of the matters described in this letter. We stand ready to work with your administration in a bipartisan manner to seek answers to these important questions.

Thank you for your attention to and cooperation on these important issues.

Sincerely,

###

From: Morens, David (NIH/NIAID) [E]
Sent: Thu, 22 Jul 2021 22:26:06 +0000
To: Peter Daszak; Gerald Keusch

From Scalise presser: every single expert we have identified tells us the virus was released from the Wuhan lab. This is the BS that 50-100 million Americans hear every day. d


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

From: Morens, David (NIH/NIAID) [E]
Sent: Fri, 30 Jul 2021 19:55:20 +0000
To: Peter Daszak ((b)(6)); Keusch, Jerry ((b)(6))
Subject: FW: Fox: Fauci, top scientist called to brief House committees; phone call questioned


David

David M. Morens, M.D.

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Senior Advisor to the Director
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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: Friday, July 30, 2021 3:11 PM

To: NIAID COGCORE <COGCORE@mail.nih.gov>; NIAID OCGR Leg <NIAIDOCGRLeg@mail.nih.gov>; NIAID OD AM <NIAIDODAM@niaid.nih.gov>

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

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

Edmund DeMarche

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

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

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

NYT WRITER HITS FAUCI IN SCATHING OP-ED

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

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

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

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

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

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

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

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

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

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

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

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


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From: Morens, David (NIH/NIAID) [E]
Sent: Mon, 2 Aug 2021 15:09:24 +0000
To: Peter Daszak ((b)(6)); Keusch, Jerry ((b)(6))
Subject: FW: Republican report says coronavirus leaked from China lab; scientists still probing origins


David

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

Sent: Monday, August 2, 2021 11:01 AM

Subject: Republican report says coronavirus leaked from China lab; scientists still probing origins

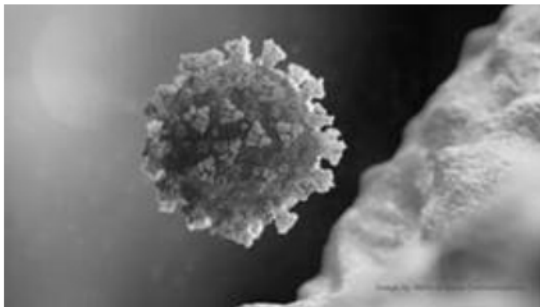
August 2, 2021 12:37 AM EDT Last Updated 11 minutes ago

United States

Republican report says coronavirus leaked from China lab; scientists still probing origins

Reuters

•
• • • 2 minute read



A computer image created by Nexu Science Communication together with Trinity College in Dublin, shows a model structurally representative of a betacoronavirus which is the type of virus linked to COVID-19, shared with Reuters on February 18, 2020. NEXU Science Communication/via REUTERS WASHINGTON, Aug 2 (Reuters) - A preponderance of evidence proves the virus that caused the COVID-19 pandemic leaked from a Chinese research facility, said a report by U.S. Republicans released on Monday, a conclusion that U.S. intelligence agencies have not reached.

The report also cited "ample evidence" that Wuhan Institute of Virology (WIV) scientists - aided by U.S. experts and Chinese and U.S. government funds - were working to modify coronaviruses to infect humans and such manipulation could be hidden.

Representative Mike McCaul, the top Republican on the House Foreign Affairs Committee, released the report by the panel's Republican staff. It urged a bipartisan investigation into the origins of the COVID-19 coronavirus pandemic [that has killed 4.4 million people worldwide](#).

China denies a genetically modified coronavirus leaked from the facility in Wuhan - where the first COVID-19 cases were detected in 2019 - a leading but unproven theory among some experts. Beijing also denies allegations of a cover-up.

Other experts suspect the pandemic was caused by an animal virus likely transmitted to humans at a seafood market near the WIV.

"We now believe it's time to completely dismiss the wet market as the source," said the report. "We also believe the preponderance of the evidence proves the virus did leak from the WIV and that it did so sometime before September 12, 2019."

The report cited what it called new and under-reported information about safety protocols at the lab, including a July 2019 request for a \$1.5 million overhaul of a hazardous waste treatment system for the facility, which was less than two years old.

In April, the top U.S. intelligence agency said it concurred with the scientific consensus that the virus was not man-made or genetically modified.

U.S. President Joe Biden in May ordered U.S. intelligence agencies to accelerate their hunt for the origins of the virus and report back in 90 days.

A source familiar with current intelligence assessments said the U.S. intelligence community has not reached any conclusion whether the virus came from animals or the WIV.

Reporting by Jonathan Landay and Mark Hosenball; Editing by Lisa Shumaker

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From: Morens, David (NIH/NIAID) [E]
Sent: Fri, 27 Aug 2021 14:22:21 +0000
To: Peter Daszak ((b)(6)); Kessler, Robert
((b)(6)); Keusch, Jerry ((b)(6))
Subject: FW: Judicial Watch: New Fauci Agency COVID Emails Detail Discussions about Wuhan Institute; Describe Gates Foundation Placement of Chinese Representatives on 'Important International Counsels' <https://bit.ly/3jqxbwR>

David

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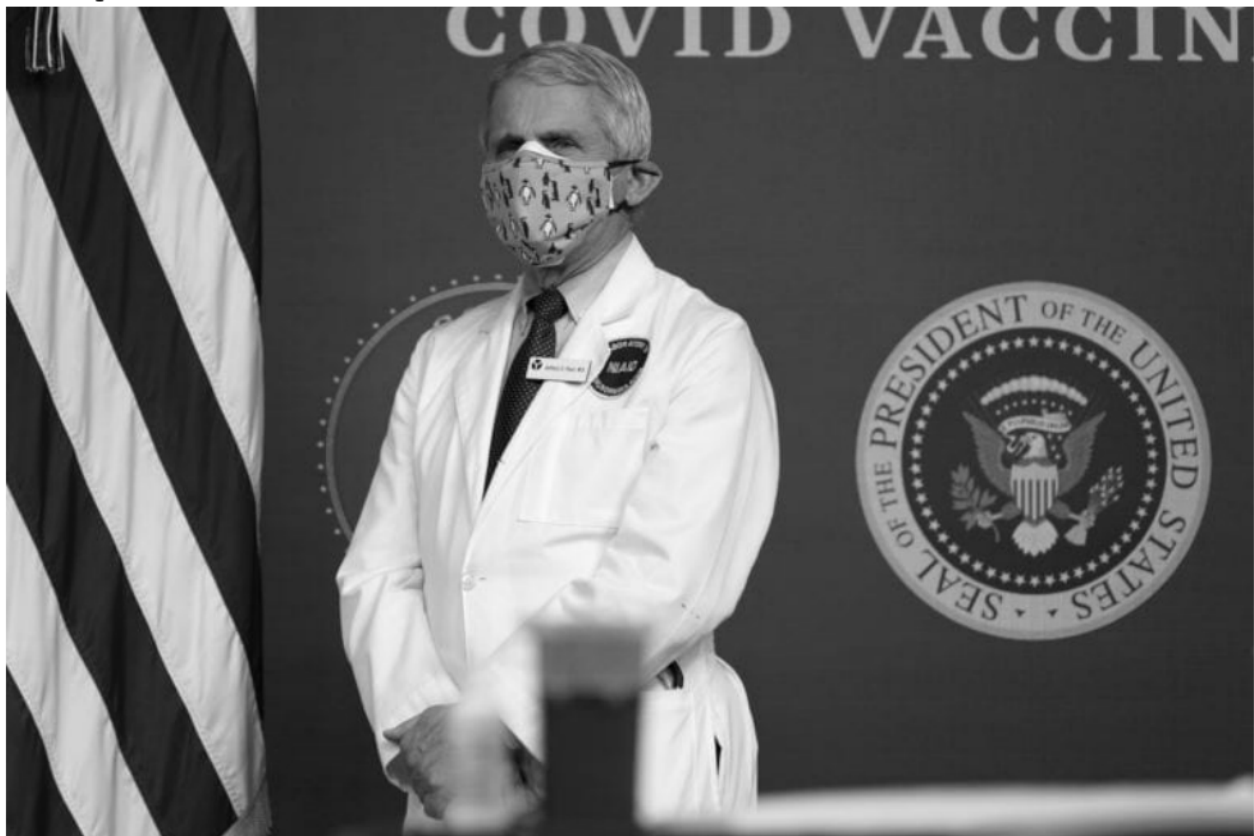
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From: Folkers, Greg (NIH/NIAID) [E] (b)(6)
Sent: Thursday, August 26, 2021 5:54 PM
To: Handley, Gray (NIH/NIAID) [E] (b)(6); NIAID COGCORE
<COGCORE@mail.nih.gov>; NIAID OCGR Leg <NIAIDOCGRLeg@mail.nih.gov>; NIAID OD AM
<NIAIDODAM@niaid.nih.gov>
Subject: Judicial Watch: New Fauci Agency COVID Emails Detail Discussions about Wuhan Institute;
Describe Gates Foundation Placement of Chinese Representatives on 'Important International Counsels'
<https://bit.ly/3jqxbwR>

August 25, 2021 | Judicial Watch

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



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

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

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

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

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

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

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

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

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

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

- In December 2019 the Wuhan Municipal Health Committee identified an outbreak of viral pneumonia cases of unknown cause.
- On December 31st the WHO China Country Office was notified of 44 patients with pneumonia of unknown etiology, 11 of which were severely ill.
- As of January 5th, 2020 there are 59 patients with a diagnosis of unknown viral pneumonia in Wuhan, 7 of which are severely ill. At least one patient is on ECMO ... The earliest case was reported December 12th, and the latest onset was December 29th. All patients are isolated and receiving treatment in Wuhan medical institutions. 163 close contacts have been identified for ongoing medical observation.

- Case-patients in the outbreak are reported to have fever, difficulty breathing, and bilateral lung infiltrates on chest radiography (CDC, <http://bit.ly/36GxY3y>).
- Hong Kong has added Wuhan Pneumonia to the list of notifiable diseases. As of January 7th, 2020 the Hong Kong Center for Health Protection has reports of 30 cases under enhanced surveillance with recent travel history to Wuhan....
- Epidemiological investigation showed that some patients operated businesses in the Wuhan South China Seafood City. As of January 1st, 2020 the market has been closed for environmental sanitation and disinfection.
- There is currently no clear evidence of human-to-human transmission, however one family cluster has been identified. No nosocomial transmission has been seen ...
- Fragments of coronavirus RNA with an 86% homology to SARS has been found in one patient...
- News reports on 1/8/2020 the virus is a novel coronavirus, sequenced in one patient and identified in others.

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

Peter Daszak (R01A | 110964-06) is funded for work to understand how coronaviruses evolve and jump to human populations, with an emphasis on bat CoVs and high-risk populations at the human-animal interface. Main foreign sites are in China (including co-investigators at the Wuhan Institute of Virology). The report notes that one of the grants, made to Fang Li, “is funded to investigate the receptor recognition and cell entry in coronaviruses using structural approaches using spike proteins in complex with receptors. This award found the first evidence of a MERS-related CoV that uses the human receptor and provides evidence of a natural recombination event between bat CoVs.” Another grant involves “a team of investigators using mouse models of SARS and MERS to investigate CoV pathogenesis and develop vaccines and therapeutics.”

A section of the report on “Vaccines” details:

“The VRC [[Vaccine Research Center](#)] and collaborators have stabilized the MERS-CoV spike protein in its prefusion conformation. The stabilized spike protein is potently immunogenic and elicits protective antibodies to the receptor binding domain, n-terminal domain and other surfaces of the spike protein. The stabilized coronavirus spike protein, and mRNA expressing the spike protein through collaboration with Moderna Therapeutics, is currently being evaluated in the humanized DPP4 mouse model at UNC. Another grant description indicates that NIH was funding research at Jefferson University using the rabies virus as a vector to deliver a potential vaccine. In an accompanying spreadsheet detailing the grants, one grant is listed as having gone to Dr. Ralph Baric of UNC-Chapel Hill to study “Mechanisms of MERV-CoV Entry, Cross Species Transmission and Pathogenesis.” That grant had been funded from 2015-2020.

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

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

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

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

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

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

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

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

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

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

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

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

In a September 5, 2017, situation report, Chen informs her colleagues that she had "attended a 'Belt and Road' High Level Meeting for Health Cooperation: towards a Health Silk Road." She also reported: Last week USAID, CDC, ESTH [Environment, Science, Technology, and Health] and I met with Gates Foundation, initially planned to talk about global Malaria eradication efforts to see if there is any area we can work together. But we ended talking in general Chinese policies and the foundation's current strategies in China — capacity building to help China raise its national standards and leverage China's resource to help others. One of the examples for raising the national standards is to help China FDA for its reform. Gates foundation has managed to work out a mechanism with China FDA to provide fund[ing] to China FDA for placing experienced Chinese-Americans who had worked at US FDA for many years to work in China FDA as senior consultants....

On the approach for leveraging China's resource to help others, Gates Foundation is working with Chinese government on donations to its neighboring countries and African countries such as anti-malaria medicines, bed nest, diagnostics etc. More specifically, it helps Chinese companies to gain pre-qualification on medications so that Chinese company manufactured drugs can be sold outside China, helps the Chinese to establish bilateral collaboration with specific countries in Africa, teaches the Chinese how to do resource mobilization, and helps raise China's voice of governance by placing representatives from China on important international counsels as high level commitment from China. Chen goes on to describe numerous other ways the Gates Foundation was helping the Chinese government by, for example, helping "Chinese companies gain pre-qualification on medications so that Chinese company manufactured drugs can be sold outside China." Chen continues: "Just met with a group from the Global Virome Project (GVP) which is funded partially by USAID. The head of the project, Peter Daszak of EcoHealth Alliance, is an NIAID funded PI. His collaborator at the Wuhan Institute of Virology in China has done excellent work on corona viruses in Chinese bat populations."

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

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

Later in the exchange, Handley tells Chen, "Please send us by e-mail your full report on the visit and then we can decide what to do with the information." After Chen emails Handley the report, he writes:

"There is enough good information in your report that it needs to be shared in some form or another."

On July 18, 2016, Chen sends an "activity update" to top NIAID officials, summarizing her activities for the prior three weeks. In a discussion of the Chinese needing assistance with conducting clinical trials of new medicines, Chen notes: "GSK's [Glaxo Smith Kline's] Zhi Hong (the head of the GSK anti-infective program and led the GSK center for infectious diseases and public health in Beijing) met with Dr. Fauci on Monday, the 11th, asking for NIAID support for this clinical trial network in China. I know Dennis

[presumably Dennis Dixon, Chief of NIAID Bacteriology and Mycology] and Carl [possibly Carl Dieffenbach, Director of NIAID AIDS Research] attended the meeting with Fauci. I don't know the outcome of the meeting." Further along, Chen writes: "I met with EcoHealth Alliance, a NY based non-profit organization on health. They have a R01 grant from DMID [Division of Microbiology and Infectious Diseases] on identifying SARS-like coronaviruses in China. They partner with Dr. Shi Zhengli at Wuhan Institute of Virology. I visited Dr. Shi over a year ago. She took bat samples in caves in certain regions of China, isolated and identified viruses and found some viruses are similar to SARS by sequencing. Now [redacted]. We are talking about close animal-human close contact in densely populated city." Chen also mentions an upcoming meeting of "Chinese NIH Alumni" and talks about NIH Director Francis Collins discussing with the head of Peking University Medical School "about the establishment of a Chinese NIH Alumni as there are so many Chinese researchers trained and worked at NIH in the past."

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

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

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

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

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

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

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

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

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

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

###

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From: Morens, David (NIH/NIAID) [E]
Sent: Thu, 9 Sep 2021 21:26:10 +0000
To: Peter Daszak ((b)(6)); Keusch, Jerry ((b)(6))
Subject: FW: 2021 reference from my EndNote library
Attachments: 2021-Horrified Anti-Vaxxer Discovers Every Ame.pdf

You heard it first here!


David

David M. Morens, M.D.

CAPT, United States Public Health Service
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From: Ksiazek, Thomas G. (b)(6)
Sent: Thursday, September 9, 2021 5:19 PM
To: Ksiazek, Thomas (Galveston National Laboratory-UT) (b)(6)
Subject: 2021 reference from my EndNote library

Bob Tesh sent a link to this article over earlier. Some of you may have already received it, I apologize for any duplication.

Onion piece, good one, also see the last sentence about ivermectin...

Tom Ksiazek

Anonymous. (2021, 20210909). **Horrified Anti-Vaxxer Discovers Every American Who Got Smallpox Vaccine In 19th Century Now Dead.** The Onion Retrieved 0909, 2021,

<https://www.theonion.com/horrified-anti-vaxxer-discovers-every-american-who-got-1847644353>

NEWS IN BRIEF

Horrified Anti-Vaxxer Discovers Every American Who Got Smallpox Vaccine In 19th Century Now Dead

Today 12:55PM | Alerts



f LYNCHBURG, VA—Astounded by the damning information, local anti-vaxxer Pete **t** Dixon was reportedly horrified Thursday after discovering that every single **l** American who got a smallpox vaccine in the 19th century was now deceased. “We’re **e** expected to follow along blindly with the CDC, but if people would simply look to the **m** history, they’d see that the thousands of people who were inoculated against smallpox in the 1800s have since dropped dead,” said Dixon, telling reporters that it was disgusting that the mainstream media had refused to share any stories about Americans who had taken the government-mandated vaccines, only to eventually perish from complications including respiratory failure, cancer, heart attack, stroke, or cholera. “They act like these shots are completely safe and tested, but I guarantee that future historians are going to look back on this time period centuries from now and discover that everyone who took the Covid vaccine is dead, too.” Dixon added that despite the media’s constant downplaying of alternative medicine, not a single person in the 19th century had died from ingesting ivermectin.

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From: Morens, David (NIH/NIAID) [E]
Sent: Wed, 18 Aug 2021 15:31:51 +0000
To: Peter Daszak ((b)(6)); Kessler, Robert
((b)(6)); Keusch, Jerry ((b)(6))
Subject: FW: NYT: 'In the Same Breath' Review: Wuhan 2019, or When Normalcy Ended


David

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

Sent: Tuesday, August 17, 2021 5:42 PM

Subject: NYT: 'In the Same Breath' Review: Wuhan 2019, or When Normalcy Ended

Critic's Pick

'In the Same Breath' Review: Wuhan 2019, or When Normalcy Ended

In her latest documentary, the director of "One Child Nation" revisits the pandemic as it unfolded in China as well as in the United States.

• • •



A scene from the documentary "In the Same Breath." Credit... HBO Documentary Films

By [Manohla Dargis](#)

Aug. 17, 2021, 4:35 p.m. ET

When you purchase a ticket for an independently reviewed film through our site, we earn an affiliate commission.

When you hear about filmmakers in conflict zones, you may flash on countries like Syria or Afghanistan. The movies produced in theaters of war often follow a similar arc: The documentarian parachutes in to take stock of a catastrophe. The focus tends to be on rubble, blood and suffering — the spectacle. In her short, stellar career, the Chinese filmmaker Nanfu Wang has repeatedly returned to a less obvious conflict zone in which the war for proverbial hearts and minds mostly takes place through state propaganda.

Her latest, "In the Same Breath," is a clear, razor-sharp look at the pandemic. And, as she did with her documentary "[One Child Nation](#)" (made with Jialing Zhang), Wang vividly fuses the political with the personal. In mid-January 2020, she flew to China with her toddler to visit her family for the New Year, a trip the two had made before. (Born in China, Wang has lived in the United States for years.) Over

images of fireworks exploding in the night sky, she ruefully says that “this was the last moment I can remember when life still felt normal.” And then she fills the screen with a rush of images: a blur of hospitals, X-rays, news reports and other visions from our Covid-19 world.

Back then, few — and certainly not Wang — knew that all normalcy was quickly disappearing when she briefly left her son with her mother, flying back to the States. The same day she flew out, China began shutting down Wuhan, the center of the outbreak. By isolating the city, China was trying to contain the virus and the pneumonialike respiratory disease it caused. At the same time, people elsewhere were traveling for the Lunar New Year’s celebration (*chunyun*), which is thought to be the biggest mass migration in the world, involving billions of trips. You know the rest of this story, or may think you do: There was no stopping the virus, though, as Wang suggests, it surely could have been attenuated.

Agilely marshaling a wealth of found and original material — as well as 10 camera people across China, some of whom remain anonymous — Wang brings you back to the first stages of the pandemic, before the Wuhan shutdown, before the virus had been officially named. She pulls out cellphone videos, collects news reports and finds some extremely eerie surveillance footage from inside a clinic in Wuhan. It’s unsettling, at times haunting, to watch people just going about their business, sometimes jammed together in celebration or just living their everyday, poignantly normal life, while others cough, stagger into emergency rooms and, in some distressing images, lie helpless in the streets.

Some of this will be familiar given the enormity of the disaster and its coverage. And there are moments here that recall the recent documentary “76 Days,” an immersive account of the Wuhan shutdown from inside the city. Yet Wang brings new insights to the crisis, and she manages to both surprise and alarm you. She also quickens your pulse, and not just through the brisk editing, notably during the short period when she’s separated from her child. But even after her husband safely brings their son home, a sense of profound urgency — and mystery — suffuses the movie as she toggles between the past and near-present, and revisits what was known and what was hidden.

To that end, as she has in her earlier work, Wang shrewdly and methodically homes in on China’s propaganda machine, showing how misinformation shapes ordinary life, how it defines a people’s consciousness of themselves and of the country. She is unrelentingly hard on its leadership. Nothing if not a crack dialectician, she repeatedly underscores the disconnect between what was happening on the ground in China, in hospitals and elsewhere, and how the government reacted to a situation that was spiraling out of its control. In speeches, conferences and smiling news reports, officials and their mouthpieces insisted that everything was fine. It was a message that, as Wang reminds you with crushing lucidity, American officials were sending to their people, too.

One of the attractions of Wang’s work is how she inserts herself into her movies in a way that never slides into solipsistic narcissism. Rather, she uses her own history and identity — as a daughter and as a mother, as a Chinese national and as an American transplant — to open up other histories and identities, telling stories that are invariably greater than any one person.

If “In the Same Breath” — the title becomes more resonant with each new scene and shock — were simply about China and its handling (mishandling) of the pandemic, it would be exemplary. But the story that she tells is larger and deeper than any one country because this is a story that envelops all of us, and it is devastating.

In the Same Breath

Not rated. Running time: 1 hour 35 minutes. [Watch on HBO platforms.](#)

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From: Morens, David (NIH/NIAID) [E]
Sent: Fri, 16 Jul 2021 22:10:06 +0000
To: Peter Daszak; Gerald Keusch
Subject: just reported

Senior Biden officials including Jake Sullivan have just reported to the media that they have concluded the “lab leak” theory is highly credible and must be pursued. d


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


From: Morens, David (NIH/NIAID) [E]
Sent: Mon, 4 Oct 2021 15:30:34 +0000
To: Peter Daszak ((b)(6)); Kessler, Robert
((b)(6)); Keusch, Jerry ((b)(6))
Subject: FW: Guardian, 2/2020: Coronavirus closures reveal vast scale of China's secretive wildlife farm industry <https://bit.ly/3A3ITCj>


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

Sent: Sunday, October 3, 2021 11:00 AM

Subject: Guardian, 2/2020: Coronavirus closures reveal vast scale of China's secretive wildlife farm industry <https://bit.ly/3A3ITCj>

Animals farmedWildlife

Coronavirus closures reveal vast scale of China's secretive wildlife farm industry



Freshly-slaughtered meat from wildlife and farm animals is preferred over meat that has been slaughtered before being shipped. Photograph: Visual China Group/Getty

Peacocks, porcupines and pangolins among species bred on 20,000 farms closed in wake of virus
Mon 24 Feb 2020 22.01 EST

Last modified on Wed 1 Jul 2020 13.22 EDT

Nearly 20,000 wildlife farms raising species including peacocks, civet cats, porcupines, ostriches, wild geese and boar have been shut down across China in the wake of the coronavirus, in a move that has exposed the hitherto unknown size of the industry.

Until a few weeks ago wildlife farming was still being promoted by government agencies as an easy way for rural Chinese people to get rich.

But the Covid-19 outbreak, which has now led to 2,666 deaths and over 77,700 known infections, is thought to have originated in wildlife sold at a market in Wuhan in early December, prompting a massive rethink by authorities on how to manage the trade.

China issued a temporary ban on wildlife trade to curb the spread of the virus at the end of January and began a widespread crackdown on breeding facilities in early February.



[Make ban on Chinese wildlife markets permanent, says environment expert](#)

[Read more](#)

The country's top legislative officials are now rushing to amend the country's wildlife protection law and possibly restructure regulations on the use of wildlife for food and traditional Chinese medicine.

The current version of the law is seen as problematic by wildlife conservation groups because it focuses on utilisation of wildlife rather than its protection.

"The coronavirus epidemic is swiftly pushing China to reevaluate its relationship with wildlife," Steve Blake, chief representative of WildAid in Beijing, told the Guardian. "There is a high level of risk from this scale of breeding operations both to human health and to the impacts on populations of these animals in the wild."

The National People's Congress released new measures on Monday restricting wildlife trade, banning consumption of bushmeat and sales of wildlife for meat consumption at wet markets between now and the time the [Wildlife](#) Protection Law can be amended and adopted. Untouched however, are breeding operations for traditional Chinese medicine, fur and leather, lucrative markets known to drive illegal poaching of animals including tigers and pangolins.

For the past few years China's leadership has pushed the idea that "wildlife domestication" should be a key part of rural development, eco-tourism and poverty alleviation. A 2017 report by the Chinese Academy of Engineering on the development of the wildlife farming industry valued the wildlife-farming industry those operations at 520bn yuan, or £57bn.



Civet cats – thought to be potential carriers of Sars – are among the animals farmed for meat in China. Photograph: China Photos/Getty

Advertisement

Just weeks before the outbreak, China’s State Forestry and Grassland Administration (SFGA) was still actively encouraging citizens to get into farming wildlife such as civet cats – a species pinpointed as a carrier of Sars, a disease similar to Covid-19. The SFGA regulates both farming and trade in terrestrial wildlife, and quotas of wildlife products – such as pangolin scales – allowed to be used by the Chinese medicine industry.

“Why are civet cats still encouraged to [be eaten] after the Sars outbreak in 2003? It’s because the hunters, operators, practitioners need that. How can they achieve that? They urged the government to support them under the pretext of economic development,” Jinfeng Zhou, secretary-general of the China Biodiversity Conservation and Green Development Foundation (CBCGDF), told the Guardian. On state TV the popular series *Secrets of Getting Rich*, which has aired since 2001, often touts these kinds of breeding operations – bamboo rats, snakes, toads, porcupines and squirrels have all had starring roles.

But little was known about the scale of the wildlife farm industry before the coronavirus outbreak, with licensing mainly regulated by provincial and local-level forestry bureaus that do not divulge full information about the breeding operations under their watch. A report from state-run Xinhua news agency on 17 February revealed that from 2005–2013 the forestry administration only issued 3,725 breeding and operation licenses at the national level.

But since the outbreak at least 19,000 farms have been shut down around the country, including about 4,600 in Jilin province, a major centre for traditional Chinese medicine. About 3,900 wildlife-farming

operations were shuttered in Hunan province, 2,900 in Sichuan, 2,300 in Yunnan, 2,000 in Liaoning, and 1,000 in Shaanxi.



Breeding of animals such as rats has been seen as central to alleviating poverty in rural areas.

Photograph: Zhang Ailin/Alamy

There is little detail available about the animals farmed across China, but local press reports mention civet cats, bamboo rats, ostriches, wild boar, sika deer, foxes, ostriches, blue peacocks, turkeys, quails, guinea fowl, wild geese, mallard ducks, red-billed geese, pigeons, and ring-necked pheasants.

Neither do reports offer much detail about the shutdowns and what is happening to the animals, although Blake said he does not think animals are being culled, due to issues over compensation. Chen Hong, a peacock farmer in Liuyang, Hunan, said she is concerned about her losses and whether she will get compensation after her operations were suspended on 24 January.

“We now aren’t allowed to sell the animals, transport them, or let anyone near them, and we have to sanitise the facility once every day,” Chen said. “Usually this time of year would see our farm bustling with clients and visitors. We haven’t received notice on what to do yet, and the peacocks are still here, and we probably won’t know what to do with [them] until after the outbreak is contained.

“We’re very worried about the farm’s future,” she added. “The shutdown has resulted in a loss of 400,000–500,000 yuan (£44,000–55,000) in sales, and if they decide to put an outright ban on raising peacocks, we’ll lose even more, at least a million yuan (£110,000).”



Peacock breeders use plastic bags to wrap up the birds in transit to stop their feathers falling off.

Photograph: Visual China Group/Getty

Advertisement

On a visit to Shaoguan, Guangdong province, last year, the Guardian and staff from CBCGDF saw a caged facility previously used for attempted breeding of the notoriously hard-to-breed pangolin.

While there were no longer pangolin at the site, several locals near the facility confirmed the species had been raised there, along with monkeys and other wildlife.



[Appetite for 'warm meat' drives risk of disease in Hong Kong and China](#)

[Read more](#)

Besides being used for Chinese medicine, much of the meat from the wildlife trade is sold through online platforms or to “wet markets” like the one where the Covid-19 outbreak is thought to have started in Wuhan.

“All animals or their body parts for human consumption are supposed to go through food and health checks, but I don’t think the sellers ever bothered,” said Deborah Cao, a professor at Griffith University in Australia and an expert on animal protection in China. “Most of them [have been] sold without such health checks.”

There have been calls for a deep regulatory overhaul to remove the conflicting duties of the forestry administration, and for a shift in government mindset away from promoting the utilisation of wildlife and towards its protection.



Zhangjiakou city has more than 1,500 firms processing furs from animals including foxes and raccoons. Photograph: Greg Baker/Getty

“The ‘referee-player’ combination needs to be addressed and is the toughest [challenge],” Li Shuo, a senior campaigner at Greenpeace East Asia told the Guardian. “This goes back to the institutional identity [of the SFGA] which was established to oversee timber production. Protection was an afterthought.”

uProposals include fully banning trade in wildlife that is protected or endangered within and outside of China, plus bans on raising and selling meat from known carriers of diseases that can impact humans such as civets, bats and rodents.

There are concerns that in trying to prevent outbreaks authorities may go too far in the culling of wild animals that can carry disease.

“Some law professors have suggested ‘ecological killing’ of disease-transmitting wild animals, such as pangolins, hedgehogs, bats, snakes, and some insects,” Zhou said. “We believe lawmakers need to learn [more about] biodiversity before advising on the revisions to the law, or they’ll bring disaster.”

Additional research and reporting assistance provided by Jonathan Zhong.


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From: Morens, David (NIH/NIAID) [E]
Sent: Wed, 6 Oct 2021 16:22:36 +0000
To: Peter Daszak ((b)(6)); Keusch, Jerry ((b)(6));
Kessler, Robert ((b)(6))
Subject: FW: National Review: Leaked Grant Proposal Confirms Chinese and American Scientists Planned to Create Novel Coronavirus


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

Sent: Wednesday, October 6, 2021 11:57 AM

To: NIAID COGCORE <COGCORE@mail.nih.gov>; NIAID OCGR Leg <NIAIDOCGRLeg@mail.nih.gov>; NIAID OD AM <NIAIDODAM@niaid.nih.gov>

Subject: National Review: Leaked Grant Proposal Confirms Chinese and American Scientists Planned to Create Novel Coronavirus

Leaked Grant Proposal Confirms Chinese and American Scientists Planned to Create Novel Coronavirus

By CAROLINE DOWNEY

• October 6, 2021 9:54 AM



Security personnel stand outside Wuhan Institute of Virology in Wuhan, China, February 3, 2021. *(Thomas Peter/Reuters)*

A World Health Organization (WHO) collaborator, who reviewed a coronavirus research grant application unearthed last month, confirmed that the language of the documents suggests American and Chinese scientists planned to collaborate on the creation of a new coronavirus not found in nature.

The grant proposal, obtained by the analysis group DRASTIC last month, was submitted to the U.S. Defense Advanced Research Projects Agency (DARPA) in

2018 by the EcoHealth Alliance, an American research non-profit that planned to collaborate with Chinese scientists at the Wuhan Institute of Virology to create a new virus using the funding.

“We will compile sequence/RNAseq data from a panel of closely related strains and compare full length genomes, scanning for unique SNPs representing sequencing errors,” the application states. “Consensus candidate genomes will be synthesised commercially using established techniques and genome-length RNA and electroporation to recover recombinant viruses.”

The WHO source explained the procedure and how the brand new virus could still closely resemble the natural viruses it was derived from.

“They would then synthesise the viral genome from the computer sequence, thus creating a virus genome that did not exist in nature but looks natural as it is the average of natural viruses,” the individual said. “Then they put that RNA in a cell and recover the virus from it. This creates a virus that has never existed in nature, with a new ‘backbone’ that didn’t exist in nature but is very, very similar as it’s the average of natural backbones.”

While the grant was never approved, it provides further evidence that American and Chinese scientists were exploring gain-of-function research, in which scientists manipulate existing viruses to make them more transmissible and/or dangerous. [Other EcoHealth Alliance grant proposals](#) obtained by the *Intercept* also suggests the group and its Chinese partners were heavily involved in gain-of-function research.

Dr. Anthony Fauci, who leads the NIH’s Institute of of Allergies and Infectious Diseases, has repeatedly denied in congressional testimony that any U.S. funding went to gain-of-function research at the Wuhan Institute of Virology.

In an interview with the *Telegraph*, the anonymous WHO source suggested that [artificial lab engineering](#) could explain why a close match for Sars-CoV-2 has not yet been identified in nature despite a massive Chinese and international effort to do just that.

“This means that they would take various sequences from similar coronaviruses and create a new sequence that is essentially the average of them. It would be a new virus sequence, not a 100 per cent match to anything,” the WHO contact said.

The closest cousin to Sars-CoV-2 that’s been found in nature so far is a strain called Banal-52, which shares 96.8 per cent of the genome. However, for a virus to be the direct ancestor of another, the genome should be around a 99.98 percent match, according to the publication.

It was revealed earlier this year that the Wuhan Institute of Virology deleted its main database of samples and viral sequences months before the pandemic erupted. The Chinese government has sequenced the genomes of tens of thousands of animals living in and around Wuhan but has yet to identify the Sars-Cov-2 virus in nature, casting doubt on the natural transmission theory.

“If Sars-CoV-2 comes from an artificial consensus sequence composed of genomes with more than 95 per cent similarity to each other... I would predict that we will never find a really good match in nature and just a bunch of close matches across parts of the sequence, which so far is what we are seeing,” the WHO source said.


“The problem is that those opposed to a lab leak scenario will always just say that we need to sample more, and absence of evidence isn’t evidence of absence. Scientists overall are afraid of discussing the issue of the origins due to the political situation. This leaves a small and vocal minority of biased scientists free to spread misinformation,” he added.

From: Morens, David (NIH/NIAID) [E]
Sent: Wed, 11 Aug 2021 21:38:48 +0000
To: Peter Daszak ((b)(6)); Kessler, Robert
((b)(6)); Keusch, Jerry ((b)(6))
Subject: FW: CNN: Intel officials draft classified report as they near finish of 90-day Covid probe <https://cnn.it/2Ub2xO7>


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

Sent: Wednesday, August 11, 2021 5:37 PM

Subject: CNN: Intel officials draft classified report as they near finish of 90-day Covid probe
<https://cnn.it/2Ub2xO7>

Intel officials draft classified report as they near finish of 90-day Covid probe

By [Kylie Atwood](#), [Natasha Bertrand](#), [Zachary Cohen](#) and [Katie Bo Williams](#), CNN
Updated 4:03 PM ET, Wed August 11, 2021

Washington (CNN) Intelligence officials are nearing the end of a 90-day investigation into the origins of Covid-19 that was ordered by President Joe Biden, and have drafted a classified report that is now in the preliminary review process, according to three sources familiar with the probe.

Sources familiar with the initial report say that after three months of poring over data and raw intelligence, the intelligence community is still divided over two theories -- one suggesting the virus originated from a lab in Wuhan, China, and the other suggesting it jumped naturally to humans from animals, the sources said. The report as it stands now contains "nothing too earth shattering," one source explained.

In May, Biden told US intelligence agencies to "redouble" their efforts to investigate how the virus originated, including the possibility that it emerged from a lab accident. Biden ordered the investigation after receiving an earlier report on the origins and asking for follow-up information, he said in a statement. The 90-day clock that Biden set for this investigation will be up in late August.

It's possible that the draft report could undergo significant revisions during the remaining review process. Biden also tasked the intelligence community with declassifying as much of the report as possible, a process now underway as it undergoes initial reviews.

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

The intelligence community's inability to present one theory with high confidence after three months of intense work underscores just how hard it is to probe the origins of the Covid-19 pandemic. "We will not weigh in on the substance of the 90-day review while it is still underway," an ODNI spokesman said in a statement to CNN.

Last week, CNN reported that intelligence agencies had gotten their hands on a trove of genetic data drawn from virus samples at the lab in Wuhan that some officials believe could have been the source of the outbreak. It's unclear whether officials have finished analyzing that data.

Intelligence officials have also taken a fresh look at signals intelligence, like intercepted communications and satellite imagery, that could provide clues.

But ultimately, China's refusal to share information from the early days of the outbreak and the country's lack of transparency has been a major hurdle, and officials had been broadly pessimistic about finding a smoking gun during the 90-day push.

The report -- which was done without any Chinese participation -- is now being reviewed by the intelligence community and outside experts for feedback before it is finalized later this month, the three sources said. Once the classified version is finalized, an unclassified version will also be developed so that the Biden administration can share something with the public, one source explained.

Officials told CNN that the Biden administration has considered whether to launch another investigation if this one proves inconclusive, but it is unclear whether a decision has been made to reopen the probe after the 90-day report is released.

Last month, a bipartisan group of lawmakers made clear they want Biden to continue investigating the origins issue until the intelligence community reaches a high confidence assessment, even if that takes longer than 90 days.

But there are some concerns that the political debate around Covid origins and China's refusal to share pertinent information means that the US may never reach a definitive conclusion on that front, two sources said.

"The failure to get our inspectors on the ground in those early months will always hamper any investigation into the origin of Covid-19," Biden said when he announced that he had launched the investigation, noting that he had previously called for the CDC to get access to China to learn about the virus in order to help fight it more effectively.

Collecting intelligence about the breadth of Chinese actions that may have inhibited the World Health Organization or other origins investigations was one of the two primary objectives of the Biden administration's 90-day review earlier this summer, according to a tasking memo sent to relevant agencies that was obtained by CNN.

Chinese government rejects WHO plan for second phase of Covid-19 origins study

But unlike the question of whether the coronavirus first emerged naturally through human contact with animals in the wild or in markets, or via a lab accident, intelligence officials believe there is enough evidence to make a compelling case that the Chinese government's initial handling of the outbreak and efforts to suppress relevant information in the months since, has significantly constrained all efforts to examine the pandemic's true origins, according to a source familiar with the findings.

Despite a near consensus among those officials about the impact of China's actions, it remains unclear how far the Biden administration will go in calling out Beijing publicly once its ongoing 90-day review is over or how those findings will factor into the version of the report that is publicly released, the source said.

"What they release will be interesting ... but how far is Biden willing to go? If he tries these coercive measures on origins, how will that impact the other issues?" a former US official familiar with intelligence related to the origins investigation told CNN.

Biden's launch of the investigation came after a US intelligence report found several researchers at China's Wuhan Institute of Virology became ill with an unidentified infection or disease in November

2019 and had to be hospitalized -- a new detail that fueled fresh public pressure on Biden to delve deeper into the origin of the virus.

It also came after CNN reported that Biden's team shut down a closely held State Department effort launched late in the Trump administration to prove that Covid-19 originated in a Chinese lab over concerns about the quality of its work.

White House officials have said that getting to the bottom of the origin of the pandemic will help prevent another one, and after unsuccessful World Health Organization (WHO) efforts to investigate the matter, the Biden administration orchestrated their own effort.

In July, the White House said it was "deeply disappointed" when China rejected the WHO's plan for a second phase of an investigation into the origin of the coronavirus. And after the WHO's first investigation the White House was critical of their findings due to limited access to "complete, original data and samples."

- P


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From: Morens, David (NIH/NIAID) [E]
Sent: Wed, 22 Sep 2021 17:46:46 +0000
To: Peter Daszak ((b)(6)); Kessler, Robert
((b)(6)); Keusch, Jerry ((b)(6))
Subject: FW: Newsweek: DARPA Denies Funding Wuhan Institute of Virology Amid
Alleged Document Leak


David

David M. Morens, M.D.

CAPT, United States Public Health Service
Senior Advisor to the Director
Office of the Director
National Institute of Allergy and Infectious Diseases
National Institutes of Health
Building 31, Room 7A-03
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From: Folkers, Greg (NIH/NIAID) [E] (b)(6)

Sent: Wednesday, September 22, 2021 1:24 PM

Subject: Newsweek: DARPA Denies Funding Wuhan Institute of Virology Amid Alleged Document Leak

DARPA Denies Funding Wuhan Institute of Virology Amid Alleged Document Leak

By [Ed Browne](#) On 9/22/21 at 11:46 AM EDT

DARPA, the U.S. advanced research projects agency, has denied funding research activity at the Wuhan Institute of Virology (WIV) after a group released documents allegedly detailing a coronavirus research proposal.

Newsweek cannot confirm the veracity of the DRASTIC group or the existence of the Project DEFUSE documents described. The group says the documents were provided anonymously.

DRASTIC is a group of activists who say they are working towards solving the "riddle" of the origins of the SARS-CoV-2 virus that is behind the COVID pandemic. They say they were given documents by an anonymous source which detail something called "Project DEFUSE."

According to what appear to be funding proposal excerpts published by DRASTIC, Project DEFUSE aimed to reduce the threat of bat-borne coronaviruses through research and was headed by Peter Daszak, president of the U.S.-based research organization EcoHealth Alliance (EHA). It would have run between 2018 and 2022.

DRASTIC states the research proposal would have involved "advanced and dangerous" research into bat coronaviruses in cooperation with the WIV and other facilities, and said the research would qualify as [Gain of Function \(GoF\)](#)—a process that can be used to make viruses more dangerous so that humans can investigate them and improve understanding.

However, DRASTIC said the documents showed that DARPA rejected the DEFUSE proposal in part because of GoF concerns. DRASTIC did not publicly release the actual document it said it had seen. In a statement to *Newsweek*, DARPA denied funding any activity associated with EHA or the WIV. A spokesman said: "In accordance with U.S. Federal Acquisition Regulations, we are not at liberty to divulge who may have or may not have not submitted a proposal in response to any of the agency's solicitations. Further, information contained within bids is considered proprietary and can only be released by the bidder.

"That being said, DARPA has never funded directly, nor indirectly as a subcontractor, any activity or researcher associated with the EcoHealth Alliance or Wuhan Institute of Virology."

Newsweek has contacted Peter Daszak and EHA for comment. *Newsweek* has also contacted UNC-Chapel Hill, Duke-National University in Singapore, the USGS National Wildlife Health Center (NWHC) and Palo Alto Research Center (PARC), which DRASTIC says are also mentioned in the documents, for comment. *Newsweek* was unable to contact the WIV.

GoF research into coronaviruses has been a hot topic recently, since many are concerned that SARS-CoV-2 could have been accidentally [leaked from a lab](#), sparking the pandemic.

The National Institutes of Health (NIH), for instance, has already denied approving grants that would have supported GoF research on coronaviruses.

Investigation into the origin of SARS-CoV-2 is ongoing. In August, President [Joe Biden](#) received a report from the intelligence community into the matter [that came back inconclusive](#). He had ordered the report back in May in the hope of getting closer to a conclusion.

Earlier this year, after the World Health Organization (WHO) completed its initial investigation into the origins of COVID by visiting Wuhan, several nations jointly expressed concerns that the study was "significantly delayed and lacked access to complete, original data and samples."

The study had concluded that the lab leak theory was "extremely unlikely" at the time.



The Wuhan Institute of Virology (WIV), a virus research center in Wuhan, China, seen in February 2021 as a World Health Organization (WHO) investigation team arrive. The facility has become a hot topic amid unconfirmed theories that COVID may have leaked from a lab. Hector Retamal/AFP / Getty

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From: Morens, David (NIH/NIAID) [E]
Sent: Wed, 11 Aug 2021 20:09:41 +0000
To: Peter Daszak ((b)(6)); Keusch, Jerry ((b)(6));
Kessler, Robert ((b)(6))
Subject: FW: New Yorker: Fauci Says It Is Safe to Watch YouTube Now That Rand Paul
Has Been Suspended


On a lighter note!


David

David M. Morens, M.D.

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From: Oplinger, Anne (NIH/NIAID) [E](b)(6)
Sent: Wednesday, August 11, 2021 3:54 PM
To: Folkers, Greg (NIH/NIAID) [E](b)(6); NIAID COGCORE <COGCORE@mail.nih.gov>; NIAID OCGR Leg <NIAIDOCGRLeg@mail.nih.gov>; NIAID OD AM <NIAIDODAM@niaid.nih.gov>
Subject: RE: New Yorker: Fauci Says It Is Safe to Watch YouTube Now That Rand Paul Has Been Suspended

HAHAHA!

First couple secs of this one funny—didn't watch all—picked at random

<https://www.youtube.com/watch?v=2425wHMISK0>

Anne A. Oplinger

(b)(6)

Office of Communications and Government Relations
National Institute of Allergy and Infectious Diseases, NIH
MEDIA request phone 301-402-1663



From: Folkers, Greg (NIH/NIAID) [E](b)(6)
Sent: Wednesday, August 11, 2021 3:15 PM
To: NIAID COGCORE <COGCORE@mail.nih.gov>; NIAID OCGR Leg <NIAIDOCGRLeg@mail.nih.gov>; NIAID OD AM <NIAIDODAM@niaid.nih.gov>
Subject: New Yorker: Fauci Says It Is Safe to Watch YouTube Now That Rand Paul Has Been Suspended

Fauci Says It Is Safe to Watch YouTube Now That Rand Paul Has Been Suspended



By Andy Borowitz



Photograph by Kevin Dietsch / UPI / Alamy

WASHINGTON ([The Borowitz Report](#))—In a new health advisory, the nation’s leading epidemiologist, Dr. Anthony Fauci, said that it is “perfectly safe” for Americans to watch YouTube, following news that Senator Rand Paul had been suspended from the platform.

“In the past, I’ve warned about the health consequences of listening to Rand Paul,” he said. “People experience headaches and nausea. Sometimes, they feel like their brain cells are actually leaking straight out of their heads. That’s why I’ve consistently urged people to limit their exposure to this guy.”

Fauci said that, given Paul’s suspension from the site, previous health advisories regarding YouTube “no longer apply.”

“I think that this would be an excellent time for every American to enjoy YouTube,” he said. “Watch some funny cat videos, or maybe some

kooky skateboard stunts that went awry. Rand Paul's suspended for only seven days, so watch as much YouTube as you can while it's still safe."

More Satire from the Borowitz Report

- Republicans protest lack of rioters on the January 6th commission.
- Biden considers a new plan to convince people to get the vaccine.
- A G.O.P. punishment for Liz Cheney and Adam Kinzinger.
- Trump received a medical note to avoid serving in his own coup.
- Putin misses a former employee.
- Get the Borowitz Report in your in-box. Sign up for the newsletter.



Andy Borowitz is a Times best-selling author and a comedian who has written for The New Yorker since 1998. He writes The Borowitz Report, a satirical column on the news.

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From: Morens, David (NIH/NIAID) [E]
Sent: Fri, 13 Aug 2021 15:22:48 +0000
To: Peter Daszak ((b)(6)); Kessler, Robert
((b)(6)); Keusch, Jerry ((b)(6))
Subject: FW: WaPo: In new documentary, WHO scientist says Chinese officials pressured investigation to drop lab-leak hypothesis


In the paper this am


David

David M. Morens, M.D.

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From: Embry, Alan (NIH/NIAID) [E] (b)(6)

Sent: Thursday, August 12, 2021 10:43 PM

To: NIAID OD AM <NIAIDODAM@niaid.nih.gov>

Subject: WaPo: In new documentary, WHO scientist says Chinese officials pressured investigation to drop lab-leak hypothesis

In new documentary, WHO scientist says Chinese officials pressured investigation to drop lab-leak hypothesis

<https://www.washingtonpost.com/world/2021/08/12/who-origins-embarek/>

The World Health Organization expert who led a controversial joint probe into the origins of the coronavirus pandemic says in a documentary airing Thursday night on Danish television that Chinese colleagues influenced the presentation of their findings.

Speaking to Danish documentarians, Peter Ben Embarek said Chinese researchers on the team had pushed back against linking the origins of the pandemic to a research laboratory in Wuhan in a report about the investigation. “In the beginning, they didn’t want anything about the lab [in the report], because it was impossible, so there was no need to waste time on that,” Ben Embarek said during the interview. “We insisted on including it, because it was part of the whole issue about where the virus originated.”

In its report released earlier this year, the WHO-China team said it was “very unlikely” that the virus, officially named SARS-CoV-2, could have accidentally leaked from the Wuhan Institute of Virology or another facility in the Chinese city where infections were first found. The joint team of researchers said it would not recommend further investigation into the issue.

A discussion of whether to include the lab-leak theory at all lasted until 48 hours before the conclusion of the mission, Ben Embarek told the Danish reporters. In the end, Ben Embarek’s Chinese counterpart eventually agreed to discuss the lab-leak theory in the report “on the condition we didn’t recommend any specific studies to further that hypothesis.” Asked in the documentary whether the report’s “extremely unlikely” wording about the lab-leak theory was a Chinese requirement, Ben Embarek said “it was the category we chose to put it in at the end, yes.” But he added that this meant it was not impossible, just not likely. Ben Embarek said one similar scenario, in which a lab employee inadvertently could have brought the virus to Wuhan after collecting samples in the field, could

be considered both a lab-leak theory and a hypothesis of direct infection from a bat, which was described as “likely” in the report.

“A lab employee infected in the field while collecting samples in a bat cave — such a scenario belongs both as a lab-leak hypothesis and as our first hypothesis of direct infection from bat to human. We’ve seen that hypothesis as a likely hypothesis,” Ben Embarek said.

In further comments during the interview that were not included in the documentary but were incorporated in an account by the Danish channel TV2 on its website, Ben Embarek suggested that there could have been “human error” but that the Chinese political system does not allow authorities to acknowledge that.

“It probably means there’s a human error behind such an event, and they’re not very happy to admit that,” Ben Embarek was quoted as saying. “The whole system focuses a lot on being infallible, and everything must be perfect,” he added. “Somebody could also wish to hide something. Who knows?”

Asked for comment, Ben Embarek initially said the interview had been mistranslated in English-language media coverage. “It is a wrong translation from a Danish article,” he wrote, declining to comment further and referring The Washington Post to the WHO. He did not immediately respond to follow-up questions.

WHO spokesman Tarik Jasarevic also said that the comment was mistranslated and that the interview took place “months ago.”

“There are no new elements nor [a] change of the position [that] all hypothesis are on the table and WHO works with member states on the next step,” Jasarevic said, referring to comments by senior officials with the global health organization about the probe.

The documentary, titled “The Virus Mystery,” is scheduled to air on TV2 on Thursday evening. Ben Embarek had cooperated with the documentary filmmakers, even going so far as to film his trip to China for them on his phone to provide an inside look at a closed-off trip.

Ben Embarek led a team of international scientists on a mission to China in January to work with local officials to investigate the origins of a pandemic that

has so far led to more than 200 million confirmed cases and at least 4.3 million deaths worldwide.

From the start, the trip was mired in controversy. Beijing delayed approval for the WHO trip, pushing back the researchers' arrival, while some of the international experts on the team were criticized for prior links to Chinese research.

Even once it arrived, the WHO team, subject to strict quarantine procedures, had only two weeks in the field to conduct research.

After the team's report was released in late March, it grew only more disputed. The team looked at four different scenarios for how the virus first spread to humans, labeling the idea of zoonotic spread from animals to humans as "most likely."

Other, less likely scenarios included that the virus could have been imported to China on frozen food — a theory pushed repeatedly by Chinese officials but seen as unlikely by many international experts. The "lab-leak" theory, the subject of intense speculation in the United States, was dubbed the least likely scenario, and the WHO team said it should no longer be investigated. Even skeptics of the theory found the dismissal a surprise.

At a news conference marking the release of the report, WHO Director General Tedros Adhanom Ghebreyesus said the scenario still needed closer study.

"Although the team has concluded that a laboratory leak is the least likely hypothesis, this requires further investigation, potentially with additional missions involving specialist experts, which I am ready to deploy," Tedros said.

Ben Embarek and other researchers on the team have hinted at immense pressure during the trip from all sides, with as many as 60 Chinese colleagues working with not only scientists but also public health figures.

"The politics was always in the room with us on the other side of the table," he told *Science Magazine* during an interview published in February. In a statement released on Thursday, the WHO spoke of the need for "next steps" in the investigation into the coronavirus's origins.

It also said that China and other, unnamed U.N. member states had written to the organization to question the basis for further study into theories of origin linked to the labs in Wuhan, with these critics suggesting that "the origins study has been politicized, or that WHO has acted due to political pressure."

"In order to address the 'lab hypothesis,' it is important to have access to all data and consider scientific best practice and look at the mechanisms WHO already has

in place. WHO is only focused on science, providing solutions and building solidarity,” the statement read.

The WHO-led study is only one point of ongoing investigation. Later this month, the U.S. intelligence community is expected to complete a 90-day review of the evidence about the origins of the coronavirus.

From: David Morens
Sent: Thu, 26 Aug 2021 17:42:29 -0400
To: Jason Gale
Cc: Morens, David (NIH/NIAID) [E]
Subject: Re: Hi David,

Yes i have time but would need to get to a computer to read it carefully. A quick read i just did

As is the case with me i can always speak on background or off the record, but on the te ord requires DHHS clearance. This should be easy since the subject is not controversial.

What's your time frame? d

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

On Aug 26, 2021, at 17:34, Jason Gale (BLOOMBERG/ NEWSROOM:)
<j.gale@bloomberg.net> wrote:

Hi David,
Do you have a minute to chat informally about this paper,
perchance? [http://weekly.chinacdc.cn/en/article/doi/10.46234/ccd
cw2021.172](http://weekly.chinacdc.cn/en/article/doi/10.46234/ccd
cw2021.172)
Regards,
Jason