

**From:** Morens, David (NIH/NIAID) [E]  
**Sent:** Sun, 29 Dec 2019 23:32:30 +0000  
**To:** Ellen Carlin  
**Bcc:** Morens, David (NIH/NIAID) [E]  
**Subject:** Fwd: Lancet Infect Dis: Preparedness for emerging epidemic threats: a Lancet Infectious Diseases Commission <http://bit.ly/39oQH5N>

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

Begin forwarded message:

**From:** "Folkers, Greg (NIH/NIAID) [E]" (b)(6)  
**Date:** December 29, 2019 at 15:00:59 MST  
**Subject:** Lancet Infect Dis: Preparedness for emerging epidemic threats: a Lancet Infectious Diseases Commission <http://bit.ly/39oQH5N>

Volume 20, Issue 1, January 2020, Pages 17-19



## Comment

# Preparedness for emerging epidemic threats: a *Lancet Infectious Diseases* Commission

Author links open overlay panel [Vernon J Lee<sup>ab</sup>](#)

[Ximena Aguilera<sup>c</sup>](#) [David Heymann<sup>d</sup>](#) [Annelies Wilder-Smith<sup>d</sup>](#) for The Lancet Infectious Diseases Commission

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At any time, an emerging, lethal, and highly transmissible pathogen might pose a risk of being spread globally because of the interconnectedness of the global population.<sup>1, 2</sup> Emerging epidemic threats are occurring with increasing scale, duration, and effect, often disrupting travel and trade, and damaging both national and regional economies.<sup>3, 4</sup> Even geographically limited outbreaks such as the Ebola virus disease in Africa might have a global effect.

Preparing for epidemic threats is not a static or binary (prepared or unprepared) exercise, but a dynamic state reflecting the constantly changing world. Countries prepare in different ways based on their interpretation of disease risks and international agreements such as the International Health Regulations (IHR). The IHR were introduced in 1969 to prevent spread of specific serious diseases between countries and set out preparedness measures at international borders to stop disease spread. The 2005 revisions to the IHR reflect changes across multiple dimensions, requiring countries to develop preparedness capacities to detect and respond to outbreaks where and when they occur, supported by international partners to respond when outbreaks cannot be contained locally.<sup>5</sup> However, disruptive factors have emerged at a greater pace over the past decade, creating a new ecology that requires novel strategies for preparedness. These factors include dealing with the increasing human population density and connectivity, harnessing novel data streams and new technological advances to manage epidemics, mitigating false information on social networks, to creating informal technical networks that can work together when political forces fail to do so.

Do the recent outbreaks of Ebola virus disease, Middle East respiratory syndrome coronavirus, and yellow fever reflect this changing context of disruptions requiring dynamic responses? These outbreaks show that countries are at various stages of preparedness, and many have underdeveloped preparedness plans and response capabilities with weak or non-existent strategies to mitigate disruptive factors.<sup>6, 7</sup> Many countries face severe difficulties in providing universal health coverage, for example, and might overlook timely investments for threats that demand greater health-care facility or workforce requirements.<sup>8, 9</sup> Other challenges include shifts in within-country and between-country cooperation, the evolving need for transdisciplinary, cross-sectoral approaches and social participation,<sup>2, 3, 8, 9</sup> and effective leadership, coordination, and financing of local national and international partners.<sup>10</sup>

Against this backdrop, the *Lancet Infectious Diseases* Commission on Preparedness for Emerging Epidemic Threats was formed in mid-2019 to examine the importance of this new ecology and its disruptive factors that have resulted in an underprepared world, whether current planning assumptions still hold, and what mitigation measures need to be introduced.

A sample of the new ecology, its disruptive factors, and how they manifest are shown in the [table](#). Preparedness plans must take these factors into account to succeed and those that do not will not have the resilience and capability to fully respond. These factors are political and institutional factors that include influential stakeholders and decision-making forces; social factors that link individuals and communities, through exchange of goods and information, and building relationships that ensure



societal cohesiveness; environmental factors that influence pathogens and hosts, contribute to biodiversity and how diseases emerge and spread, these factors affect interaction between humans, vertebrate animals, and arthropod vectors, and influence human development and health systems; and pathogenic factors that define the biological basis of epidemic emergence and antimicrobial resistance, host–pathogen interactions, and available interventions to address these epidemics.

Table. Examples of disruptive factors and their manifestations that require mitigation for effective preparedness

	<b>Disruptive factors</b>	<b>Examples of manifestations</b>
Political and institutional	National governments; international agencies; non-governmental organisations and charities; corporate entities; academic institutions	Weakness in behavioural change guidance from national and international organisations; scarcity of sustainable leadership and financing in failed states leading to neglected or uncoordinated health systems; increasing duration and frequency of insecurity or conflict zones hindering efforts to recognise and respond to health threats; failure of countries to report disease outbreaks because of fear of economic consequences
Social	Travel patterns, migration, and interconnectivity; trade; technology and digital revolution, including those that affect human interaction; expansion and control of information; patterns of communication including social media; expectations and definition of expertise; social conflict and privacy	Failure of host countries to protect the health of refugees and migrants; epidemic of devastating rumours and fake news on social media due to increased digital connectivity; emergence of social influencers exerting influence on politicians and institutions; increased resistance and hesitancy within communities to health interventions because of opposition by local experts
Environment	Geography affecting biological diversity; planned and unplanned urbanisation; climate change; interaction between humans, animals, and vectors; human development; state of the economy; state of health systems	Climate change resulting in increased flooding with failed sanitation and safe water; altered distribution of zoonotic disease reservoirs and vectors; emerging zoonosis with increased agricultural production and human encroachment into animal environments; changing national priorities resulting in sharply reduced investment in health systems
Pathogenesis	Changing disease biomes; relationship between hosts and pathogens; pathogen evolution and changes; technologies such as synthetic biology, and the risks of manufacturing pathogens and their accidental or deliberate release; characteristics of a population such as underlying disease condition	Increased opportunities for mutation or reassortment of infectious agents; increasingly reduced effectiveness of conventional vaccines and therapeutics for prevention and treatment of diseases; failure of conventional control measures to break the chain of transmission of infectious agents

The *Lancet Infectious Diseases* Commission will discuss disruptive factors and how preparedness planning must consider this new ecology by exploring current preparedness platforms and their vulnerability to disruptive factors; by addressing key disruptions, identifying possible solutions, and providing recommendations for countries to strengthen preparedness; by developing a multidisciplinary

approach including a strong role for social sciences and innovative technology; by challenging leaders and stakeholders to create sustainable preparedness platforms through collaborations and investment in established and novel recommendations; and by creating a community of practice to share new ideas and monitor outcomes.

To tackle the wide-ranging issues, the Commission has brought together experts from academic, public health, policy making, international, non-governmental, and corporate institutions. They bring local and global knowledge and experience, including policy-making and field response, human and animal health (including One Health) approaches, and novel developments in communications, information technology, analytics, public health, diagnostics, and therapeutics. The Commission aims to deliver the report by 2021 and will include key recommendations for countries and international stakeholders, and monitoring indicators to evaluate the effectiveness of preparedness initiatives over time.

The Mok Hing Yiu Charitable Foundation is the sole sponsor for the *Lancet Infectious Diseases* Commission meetings and travel for some commissioners. The foundation is not involved in the technical discussions, data analysis, and drafting of the report. This Comment was written on the behalf of the *Lancet Infectious Diseases* Commission on Preparedness for Emerging Epidemic Threats; see [appendix \(pp 1–2\)](#) for the Commissions author list.

## Supplementary Material

[Download : Download Acrobat PDF file \(112KB\)](#)

Supplementary appendix.

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[Download PDF](#)[View Record in Scopus](#)[Google Scholar](#)

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**From:** Peter Daszak  
**Sent:** Sun, 5 Sep 2021 12:03:27 -0400  
**To:** Morens, David (NIH/NIAID) [E]; Robert Kessler; Keusch, Jerry  
**Subject:** RE: Times, UK: How US cash funded Wuhan lab dealing in deadly viruses

Pure unadulterated BS – the cables from Bill Switzer were lauding our research and the whole trip was set up to increase intl. collaboration. Disingenuous innuendo-filled reporting as usual. Book written by a hard right reporter who's cashing in on this conspiracy.

It's also BS to claim that international researchers weren't welcome. When Zhengli Shi spoke at the Nipah meeting in Singapore in early Dec. 2019, she openly advertised for intl. scientists to apply to WIV to work there.

Cheers,

Peter

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

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**Subject:** Times, UK: How US cash funded Wuhan lab dealing in deadly viruses

CORONAVIRUS | BOOK EXTRACT

# How US cash funded Wuhan lab dealing in deadly viruses

Controversial research to make diseases more potent was backed by Dr Anthony Fauci, chief medical adviser to the White House, reveals a new book on the cover-ups and conspiracies of the pandemic



The scientist Shi Zhengli was well known for sampling thousands of bats in her role as director of the emerging infectious diseases centre at the Wuhan Institute of Virology

CHINATOPIX VIA AP

Sharri Markson

Saturday September 04 2021, 12.01am BST, The Times

It's late March 2018 and the US career diplomat Rick Switzer has just flown home to Beijing after a trip to Wuhan. Along with his colleague Jamie Fouss, the US consul-general in Wuhan, he'd led a delegation of American environmental, science, technology and health consular staff to inspect the Wuhan Institute of Virology, where he'd met Shi Zhengli, the "batwoman".

It was two years before a pandemic would arise from that very city — perhaps even that very laboratory — and he was deeply concerned about what he saw during his visit. The consular official at the US embassy in Beijing tapped out a "sensitive but unclassified" cable to send back to the State Department. He needed to let Washington know just what was going on inside China's new level-4 biocontainment facility dealing with the world's deadliest and most contagious pathogens. The cable warned of poor safety practices at the laboratory.

Switzer pressed send on the cable two weeks later, on April 19, 2018, with the subject line: “China Virus Institute Welcomes More US Co-operation on Global Health Security”. It was an unusual choice of email subject, because the contents of his cable outlined how the opposite was true. The laboratory, built on the condition of international collaboration, was severely limiting the number of international researchers who could work inside its walls.

The Wuhan Institute of Virology level-4 lab had originally been built in conjunction with the Jean Mérieux BSL-4 Laboratory in Lyons, France. It was to be China’s first high-containment laboratory under the direction of the Chinese Academy of Sciences, which is under People’s Liberation Army control. Construction of the laboratory began in 2004 and took 11 years to complete, finally finishing on January 31, 2015. The project cost \$44 million. It is a vast building, with four floors stretching over 3,000 sq m (32,000 sq ft). It was accredited in February 2017 by the China National Accreditation Service for Conformity Assessment, and began working on live viruses by 2018.

There were “intense clashes” between the French and Chinese parties during the construction phase, according to a Chinese Academy of Sciences video. It was far from a smooth process. Even before the deal was signed, there was strong objection in France to co-operating on such a laboratory in Wuhan, but the scientists advocating the collaboration won.

Once the laboratory was up and running, the French were soon kicked out. While the initial funding, training and construction was in conjunction with the French, according to Switzer and Fouss’s cable, “it is entirely China-funded and has been completely China-run since a ‘handover’ ceremony in 2016”. And despite being built in the name of international scientific collaboration, few international researchers were welcome to work inside the facility. “Institute officials said there would be ‘limited availability’ for international and domestic scientists who had gone through the necessary approval process to do research at the lab,” the cable stated.

So a laboratory working with the most lethal pathogens known to humankind had effectively cut off collaboration with the international community.



Security keep watch outside the Wuhan institute during a visit by the World Health Organisation in February. The institute was accredited in 2017 and began working on live viruses by 2018

THOMAS PETER/REUTERS

What made this particularly alarming was the work the laboratory was conducting. Disturbingly, Switzer and Fouss discovered the laboratory was setting up its very own database identifying all deadly viruses with pandemic potential. It would be its own version of a concept called the Global Virome Project (GVP), the cable stated. “The GVP aims to launch this year as an international collaborative effort to identify within ten years virtually all of the planet’s viruses that have pandemic or epidemic potential and the ability to jump to humans,” the cable read.

The cable quoted a Wuhan Institute of Virology official saying: “We hope China will be one of the leading countries to initiate the Global Virome Project.” But in the meantime, the institute official told Switzer and Fouss that they were already running a similar project of their own.

This revelation — of such a database being developed by a laboratory where the US had no oversight — should have been highly alarming. Except it's unclear whether anybody with any level of seniority ever read this cable after it was sent to the State Department and intelligence apparatus in Washington. The cable made clear the extent of the US involvement with the Wuhan Institute of Virology. "In the last year, the institute has also hosted visits from the National Institutes of Health (NIH), National Science Foundation and experts from the University of Texas Medical Branch in Galveston." It said the Galveston branch had trained the Wuhan lab technicians in lab management and maintenance while the US National Science Foundation had just concluded a workshop with the Wuhan Institute in Shenzhen involving 40 scientists from the US and China.

It also made clear — at this early stage — how America was funding the coronavirus research at the Wuhan lab. "NIH was a major funder, along with the National Science Foundation of China, of Sars research by the Wuhan Institute of Virology," the cable states. The paragraphs that follow are redacted. Shi Zhengli was well known in the close-knit scientific community that studied bat coronaviruses. She had become a scientific celebrity after discovering the closest virus to Sars in bats. As the director for the Centre for Emerging Infectious Diseases at the Wuhan Institute of Virology, she became known as the "batwoman" for her sampling of thousands of bats in remote caves.

It was nothing compared with the global fame she would attract after the pandemic outbreak. Her institute's research, with all its risks, would be exposed for the world to judge.

Shi has in total collected 19,000 samples and coronavirus was detected in 2,481 of them, according to information she provided to the World Health Organisation in February this year. She had been engaging in genetically modifying viruses since at least 2006. A paper published in the *Journal of Virology* that year shows she was trying to determine how coronaviruses gain the ability to skip from one species to another by "inserting different segments from the human SARS-CoV spike protein into the spike protein of the bat virus".



Dr Anthony Fauci defended the scientists who had undertaken the controversial gain-of-function research which aims to make viruses more infectious and deadlier or more virulent, often to humans  
STEFANI REYNOLDS/XINHUA/ALAMY

When questions arose in China about whether her laboratory was the source of the outbreak at the start of February last year — three months before President Trump raised the prospect — Shi snapped. "Those who believe and spread rumours, shut your dirty mouth," she posted on the WeChat social media app on February 6. Instead, she said, Covid-19 "is nature's punishment for uncivilised living habits of human beings. I, Shi Zhengli, use my life to guarantee that it has nothing to do with our lab." Just how dangerous was the research she was conducting, often without the watchful eyes of international partners? What were Shi and her colleagues up to, and who was funding it? Of particular focus would be her "gain-of-function" experiments. Gain-of-function research aims to make viruses more infectious and deadlier or more virulent, often to humans. The technical definition is research that "involves experimentation that is expected to increase the transmissibility and/or



virulence of pathogens". It can result in a pathogen acquiring new abilities; for example, a bat virus becoming able to infect humans or a virus that wasn't airborne having the ability to become so. This research, which has been carried out in the US and other western countries as well as China, has been justified by scientists who claim it could help predict pandemics by discovering which viruses are capable of becoming infectious to humans. They say this allows them to pre-emptively develop vaccines and therapeutics. But only two laboratories globally were doing gain-of-function research on coronaviruses prior to the pandemic.

Other research projects may not strictly fall into the gain-of-function category but are equally dangerous. They include bringing back to life very old viruses and manipulating them in a laboratory. This type of research deals with what are referred to as "potential pandemic pathogens".

To many outside the scientific community, this type of experimentation sounds absurd. How is it even legal, given the astronomical risks? Debate has raged about the grave dangers of allowing gain-of-function research to take place. There are two main concerns. Firstly, it can be misused for malevolent military purposes such as bioweapons. Secondly, it can accidentally cause a pandemic.

Global controversy around this type of research ignited in 2012, when scientists wanted to see if it would be possible for bird flu (H5N1) to evolve naturally into a virus that was capable of human-to-human transmission, and thus cause a pandemic. Their stated intention was to be able to predict which viruses could turn into a pandemic. Scientists fiercely opposed to gain-of-function research formed a body called the Cambridge Working Group in 2014. There were 200 esteemed signatories. They released a letter specifically warning that accidents while scientists were experimenting with these dangerous viruses could cause "an accidental pandemic" that could infect a quarter of the world's population. "Accident risks with newly created 'potential pandemic pathogens' raise grave new concerns," their letter said. "Laboratory creation of highly transmissible, novel strains of dangerous viruses, especially but not limited to influenza, poses substantially increased risks. An accidental infection in such a setting could trigger outbreaks that would be difficult or impossible to control. Historically, new strains of influenza, once they establish transmission in the human population, have infected a quarter or more of the world's population within two years."

This type of research carries such a grave risk of causing a pandemic that President Obama paused funding for gain-of-function experiments in 22 fields in 2014, including research involving Sars, influenza and Mers viruses. This happened after an outcry in the scientific community about the dangerous experiments some virologists were conducting. "Specifically, the funding pause will apply to gain-of-function research projects that may be reasonably anticipated to confer attributes to influenza, Mers, or Sars viruses such that the virus would have enhanced pathogenicity and/or transmissibility in mammals via the respiratory route," the White House statement, dated October 17, 2014, said. "During this pause, the US government will not fund any new projects involving these experiments and encourages those currently conducting this type of work — whether federally funded or not — to voluntarily pause their research while risks and benefits are being reassessed."



Jamie Fouss, the US consul-general in Wuhan

[CHINA.USEMBASSY-CHINA.ORG.CN](http://CHINA.USEMBASSY-CHINA.ORG.CN)

Before the ban took effect, Dr Anthony Fauci, a director at the NIH, had welcomed a voluntary pause on gain-of-function research but argued that “the benefits of such experiments and the resulting knowledge outweigh the risks. It is more likely that a pandemic would occur in nature [than as a result of a laboratory accident or leak], and the need to stay ahead of such a threat is a primary reason for performing an experiment that might appear to be risky.”

Fauci, 80, with his calm and measured manner of speech, has cultivated an image as a wise grandfatherly figure. Called “America’s doctor” in the media, he has spent 50 years in public service, joining the NIH during the Vietnam War after studying as a physician. He was appointed director of the National Institute of Allergy and Infectious Diseases in 1984. Like many medical officials around the world, he became a household name during the pandemic.

Fauci’s organisation was very familiar with the work undertaken at the Wuhan Institute of Virology, with the NIH and the National Science Foundation visiting the facility in the year prior to April 2018. In total, the NIH has funded at least 60 scientific projects at the Wuhan Institute of Virology over the past decade. USAID, the federal aid agency, funded at least 16 (ten of which were jointly funded with the NIH), the Department of Health and Human Services funded three, the Department of Defense, Department of Energy, and the China–US Collaborative Program on Emerging and Re-emerging Infectious Diseases individually each funded one project in conjunction with the Wuhan Institute. Other institutions that frequently collaborate with the institute include the New York Blood Center, the University of North Carolina and University of Texas Medical Branch at Galveston. At the same time Obama cut off funding for gain-of-function research in America, US money was still flowing to China for risky coronavirus research.

Fauci defended the scientists who had undertaken the highly controversial gain-of-function research that had prompted the global debate, saying they had “conducted their research properly and under the safest and most secure conditions”. The same research that some international scientists said should be banned, Fauci described as “important”. “Within the research community, many have expressed concern that important research progress could come to a halt just because of the fear that someone, somewhere, might attempt to replicate these experiments sloppily,” he wrote in his 2012 paper.

The mandatory “pause” or ban on gain-of-function research was inexplicably lifted under the Trump administration in 2017. No adequate explanation has been given for why this decision was made. There

was no public debate. On December 19, 2017, the NIH announced it would resume funding gain-of-function research involving Mers, Sars, coronaviruses and influenza after a new “framework” had been developed by the Department of Health and Human Services.



Scientists from the Wuhan lab worked with bats carrying Sars-like viruses

SUNDAY TIMES INSIGHT

Senior administration officials told me Fauci did not raise the issue of kickstarting gain-of-function research with any senior figures in the White House. There was one White House meeting, which Fauci requested with the Office of Science and Technology Policy, where he raised the issue of gain-of-function research. “It kind of just got rammed through,” a senior source claimed.

I asked the former national security adviser Robert O’Brien about this. “I was in meeting after meeting with Dr Fauci, and that never came up,” he says. “I don’t know if he alerted anyone. I never heard about it until I was out of office.” Mike Pompeo, who was director of the CIA from 2017 to 2018, said he didn’t know if Fauci got permission from anyone to re-start the dangerous research, particularly with regard to contributing funding via sub-grants to the Wuhan Institute of Virology. Fauci didn’t even tell his boss, Alex Azar, the health secretary, who only found out the US restriction on gain-of-function research had been lifted from media reports in 2021.

In hindsight we can clearly see that health authorities, the US government and international governments all ignored the warnings from eminent scientists, and allowed the dangerous scientific research to go ahead. The public was never brought into these debates. A pandemic is something that affects all of us — we have lost loved ones, battled serious illness, lost jobs, had our businesses and ways of life destroyed. While the origins of Covid-19 have not yet been established, it’s clear this type of research carries grave risks.

What was even more terrifying was that not only was the NIH funding gain-of-function research in the US — but it was funding research in China, where it had no oversight and no way of knowing how safe the laboratories were where these risky experiments were taking place.

*Extracted from What Really Happened in Wuhan: the Cover-Ups, the Conspiracies and the Classified Research by Sharri Markson, to be published by HarperCollins on September 30 at £20. Available to order now at [amazon.co.uk](https://www.amazon.co.uk)*

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**Sent:** Sun, 11 Jul 2021 17:05:30 +0000  
**To:** Peter Daszak ((b)(6)); Keusch, Jerry ((b)(6))  
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**Sent:** Friday, July 9, 2021 3:42 PM

**Subject:** Science Media Center: Expert reaction to a preprint reviewing the evidence on the origins of SARS-CoV-2 <https://bit.ly/3hRzCpX>

you are here: [science media centre](#)> [roundups for journalists](#) > expert reaction to a preprint reviewing the evidence on the origins of SARS-CoV-2

**July 8, 2021**

## **Expert reaction to a preprint reviewing the evidence on the origins of SARS-CoV-2**

A preprint, an unpublished non-peer reviewed study, critically reviews the current scientific evidence on the origins of SARS-CoV-2.

Please note this is a comment from one of the authors, NOT a third party comment, but sending out in case useful as there wasn't a press release: **Prof David L Robertson, MRC Investigator, Head of CVR Bioinformatics MRC-University of Glasgow Centre for Virus Research (CVR), said:**

"In a review of the evidence as a group of experts in virus evolution and molecular virology we concluded the most parsimonious explanation for the origin of SARS-CoV-2 is a zoonotic spillover event. The contact tracing of early cases in Wuhan, obtained from the WHO report earlier this year, exhibits striking similarities to the early spread of the first SARS-virus, where humans infected early in the epidemic lived near or worked in animal markets. While the intermediate animal species has not been found, there is clear evidence of susceptible animals being present in the Wuhan market throughout 2019, and related viruses have been found circulating in horseshoe bats, again very similar to the first SARS-virus. Altogether the evidence points to a zoonotic event and not a leak from a laboratory in Wuhan. The "lab leak" scenario alternates between it was made in a lab and it was an accidental release of a natural virus, neither of which there's any evidence for. It's of critical importance to understand the origin of SARS-CoV-2 so we can assess the risk of future spillover events."

**Prof James Wood, Head of Department of Veterinary Medicine, University of Cambridge, said:**

"This manuscript represents a very considered review of all virological and epidemiological evidence regarding the origins of the cause of the COVID-19 pandemic, SARS-COV-2. The authors, who are acknowledged experts in their fields, concluded that there is a substantial body of scientific evidence supporting a zoonotic origin for SARS-CoV-2.

"They considered the uncertainties that invariably persist around retrospective investigations of this nature and also noted that a laboratory accident could not be entirely ruled out, but that this was highly unlikely relative to an origin involving human and animal contact.

"While nothing can be absolutely certain regarding the origin of the pandemic, it is important that we note the conclusions of this review and start to act to introduce changes that can reduce the likelihood of further events occurring. Regulation of laboratory experimentation will not do this. Trade in and markets for live animals, especially involving the mixing of wildlife species need banning or tightly regulating and we should work to reduce biodiversity loss, an important underlying driver for zoonotic disease emergence. Biodiverse areas should be protected, recognising that humans are an important part of biodiversity; recognising land rights of indigenous peoples can make important contributions to protecting ecosystems."

**Dr Jonathan Stoye, Group Leader, Retrovirus-Host Interactions Laboratory, The Francis Crick Institute, said:**

“The debate about the origins of SARS-CoV-2 is becoming increasingly acrimonious. The failure to detect a potential natural host has stimulated suggestions by some that the COVID-19 pandemic has resulted from the escape of an engineered virus from a lab in Wuhan, China. However, there is little or no evidence for such an event and lab leak theories remain essentially speculative, at times verging on conspiratorial.

“By contrast, the current preprint provides a refreshingly clear and reasoned description of the virological events that have taken place during the emergence of the pandemic virus. It makes a strong case for the natural origin of the virus followed by on-going adaptation in humans. The continuing evolution of the virus to give new variants, highlighted by the independent acquisition of the N501V change on multiple occasions, is clearly inconsistent with the notion of a purposely manipulated virus optimized for growth on human cells. While there are still gaps in our knowledge that should be explored further, particularly regarding events that occurred before December 2019, the conclusions reached here seem entirely consistent with those in the WHO report released earlier this year.”

**‘The Origins of SARS-CoV-2: A Critical Review’ by Edward Holmes et al. is a preprint available here:**  
<https://doi.org/10.5281/zenodo.5075888>

**All our previous output on this subject can be seen at this weblink:**  
[www.sciencemediacentre.org/tag/covid-19](http://www.sciencemediacentre.org/tag/covid-19)

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**From:** Morens, David (NIH/NIAID) [E]  
**Sent:** Thu, 15 Jul 2021 14:46:00 +0000  
**To:** Peter Daszak  
**Cc:** Keusch, Jerry  
**Subject:** RE: Science Speaks: Not until June 2021 does China report Wuhan wet markets sold palm civets, racoon dogs and mink from 2017-2019: Where are the SARS-CoV-2 results?


Yes, that's true. But he's a flake not a serious threat...


*David*

**David M. Morens, M.D.**

CAPT, United States Public Health Service  
Senior Advisor to the Director  
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 301 496 4409

 (b)(6)

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**From:** Peter Daszak (b)(6)  
**Sent:** Wednesday, July 14, 2021 9:19 PM



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

**Cc:** Keusch, Jerry (b)(6)

**Subject:** RE: Science Speaks: Not until June 2021 does China report Wuhan wet markets sold palm civets, racoon dogs and mink from 2017-2019: Where are the SARS-CoV-2 results?

Yes – exactly. It’s harmless when he’s just writing interesting summaries of outbreaks, but he’s repeatedly supported the lab leak hypothesis and was an ‘early adopter’ of that when he commented about how suspicious he was of China’s outbreak investigation, leading to a piece in NY Times in early summer 2020 that didn’t really help anyone get closer to the truth, but raised his profile, I guess...

<https://www.nytimes.com/2020/07/08/health/coronavirus-origin-china-lucey.html>

Cheers,

Peter

**Peter Daszak**

*President*

EcoHealth Alliance  
520 Eighth Avenue, Suite 1200  
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USA

Tel.: (b)(6)

Website: [www.ecohealthalliance.org](http://www.ecohealthalliance.org)

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

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

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

**Sent:** Wednesday, July 14, 2021 8:42 PM

**To:** Peter Daszak (b)(6)

**Cc:** Keusch, Jerry

**Subject:** Re: Science Speaks: Not until June 2021 does China report Wuhan wet markets sold palm civets, racoon dogs and mink from 2017-2019: Where are the SARS-CoV-2 results?

I didnt want to say so, but that’s an apt description, or as we would say “gad fly”.... Without any expertise in anything, he flies off to every epidemic anywhere in the world, and then starts opining on

it. Quite an expensive out of pocket but gig, but no one here in town takes him seriously. He's kind of like a little kid, always trying to get a seat at the grownups table.... d

Sent from my iPhone

David M Morens

OD, NIAID, NIH

On Jul 14, 2021, at 19:55, Peter Daszak (b)(6) wrote:

I know him quite well. He's what we'd call in England a 'busy-body'. It's crazy to turn every single paper and event into an attack on China – just because one group was doing studies at a university with the goal of analyzing welfare and ethics at wildlife markets does not mean the China team involved in the WHO mission knew about it.

If China was trying to cover up this, why did they let this group publish a paper on it in Scientific Reviews!

Cheers,

Peter

**Peter Daszak**

*President*

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

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

**Sent:** Wednesday, July 14, 2021 5:23 PM

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

(b)(6); (b)(6)


**Subject:** FW: Science Speaks: Not until June 2021 does China report Wuhan wet markets sold palm civets, racoon dogs and mink from 2017-2019: Where are the SARS-CoV-2 results?


Presumably you guys know Dan Lucey?


*David*

**David M. Morens, M.D.**

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

**Sent:** Wednesday, July 14, 2021 5:01 PM

**Subject:** Science Speaks: Not until June 2021 does China report Wuhan wet markets sold palm civets, racoon dogs and mink from 2017-2019: Where are the SARS-CoV-2 results?

# Not until June 2021 does China report Wuhan wet markets sold palm civets, racoon dogs and mink from 2017-2019: Where are the SARS-CoV-2 results?

By [IDSA Contributor](#) on [July 14, 2021](#).

By **Daniel R. Lucey MD, MPH, FIDSA**

Last month a paper titled "[Animal sales from Wuhan wet markets immediately prior to the COVID-19 pandemic](#)" by Xiao et al., in *Nature Scientific Reports* listed 18 mammalian species sold May 2017 - November 2019 in Wuhan wet markets (Table 1). These mammalian species included masked palm civets (*Paguma larvata*) and racoon dogs (*Nyctereutes procyonoides*), species linked with SARS-CoV-1 in 2003 and known to be susceptible to SARS-CoV-2. Mink (*neovision vison*) were also sold, and the authors state these mink: . . . originated from fur farms — noting that SARS-CoV-2 has been reported in mink farms in Europe and North America." (paragraph 3 of the Discussion section).

Notably, Figure 2 shows photos of **caged live mammals in the Huanan seafood market** including a racoon dog, amur hedgehogs, Chinese bamboo rat, marmots and hog badger.

In sharp contrast, the WHO-China joint team report from their work in Wuhan Jan. 14-Feb. 10, 2021 and posted March 30, 2021 (p. 98): "Although there is photographic evidence in a published paper that live mammals were sold at the Huanan market in the past (2014) (36) (date confirmed by author in statement Annex F) and unverified media reports in 2020, **no verified reports of live mammals being sold around 2019 were found.**" (my bolding added for emphasis and contrast with Figure 2 of the paper by Xiao et al. above).

Xiao et al., also state in the next to last paragraph of the Discussion section: "Furthermore, the WHO reports that market authorities claimed all live and frozen animals sold in the Huanan market were acquired from farms officially licensed for breeding and quarantine, as such no illegal wildlife trade was identified. In reality, however, because China has no regulatory authority regulating animal trading conducted by small-scale vendors or individuals it is impossible to make this determination".

Specific information regarding racoon dogs is provided by Xiao et al:

"Racoon dog fur farming is legal in China; however, due to a drop in fur prices, racoon dogs are now frequently sold off in live animal markets, augmented by wild-caught animals." (3<sup>rd</sup> paragraph of the Discussion section).

Xiao et al. state that no pangolins or bats were found in the Wuhan markets.

Memorably, Xiao X. (X.X.) et al. explained how these data were acquired:

"Serendipitously, prior to the COVID-19 outbreak, over the period May 2017-November 2019, we were conducting unrelated routine monthly surveys of all 17 wet market shops selling live wild animals for food and pets across Wuhan City (surveys were conducted by X.X.). This was intended to identify the source of the tick-borne (no human -to-human transmission) Severe Fever with Thrombocytopenia (SFTS), following an outbreak in Hubei province in 2009-2010 . . . these shops selling live, often wild, animals included two at Baishazhou market . . . seven at Huanan seafood market . . . four at Dijiao outdoor pet market . . .and four at Qiyimen live animal market . . ." (1<sup>st</sup> paragraph of Materials and Methods section).

"As an objective observer unconnected to law enforcement X.X. was granted unique and complete access to trading practices. On each visit, vendors were asked what species they had sold over the

preceding month and in what numbers, along with the prices...and origin of these goods (wild caught or captive bred/farmed). Additionally . . . the number of individuals available for sale at the time of each visit was noted, and animals were checked for gunshot wounds . . ." (2<sup>nd</sup> paragraph of Materials and Methods section).

Even more people than the five co-authors (from China, Canada, and UK), and the multiple market vendors, were well aware of this study and its findings of live mammalian species in Wuhan wet markets, including the Huanan seafood market because:

"All protocols in the market survey were reviewed and approved by the Ethics Committee of Hubei University of Chinese Medicine (no 20161111). All vendors provided written informed consent to participate in these surveys, and all protocols were performed with relevant guidelines and regulations". (4<sup>th</sup> paragraph of the Materials and Methods).

Two of the many key questions raised by this June 2021 publication are:

- **Will the WHO Director General, Dr. Tedros, determine from China why the WHO international team in Wuhan Jan-Feb 2021 was not informed of these important data**, especially with regard to the live masked palm civets, racoon dogs, and mink being sold in Wuhan wet markets May 2017 until November 2019 "immediately prior to the COVID-19 pandemic"?
- Will Dr. Tedros determine from China what became of these 18 live mammalian species in Wuhan wet markets in December 2019-January 2020 **and what were the results of (so far undisclosed) testing of these animals for SARS-CoV-2, especially the masked palm civets, the raccoon dogs, and the mink?**



Dr. Daniel Lucey

**Daniel Lucey, M.D. MPH, FIDSA, FACP**, is a Clinical Professor of Medicine at Dartmouth Geisel School of Medicine, Infectious Disease adjunct Professor at Georgetown Medical Center, senior scholar at Georgetown Law, Anthropology Research Associate at the Smithsonian Museum of Natural History and a member of the Infectious Diseases Society of America Global Health Committee. He served as a volunteer to outbreaks overseas including hands-on Ebola patient care in Sierra Leone and Liberia (Doctors without Borders) 2014, MERS 2013, SARS 2003, as well as HIV, H5N1, Zika, yellow Fever, and pneumonic plague 2017 (with WHO/USAID/CDC). Since Jan. 6, 2020 he has contributed more than 100 posts to Science Speaks on COVID-19 and traveled to China in February 2020. He initially proposed, then fundraised and helped design the content for 2018-2022 Smithsonian Exhibition on Epidemics due to zoonotic viruses. From 1982-1988 he trained at University of California San Francisco and Harvard and was an attending physician at the NIH (NIAID) in the 1990s while in the U.S. Public Health Service.

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**From:** Peter Daszak  
**Sent:** Sun, 15 Aug 2021 13:48:49 -0400  
**To:** Morens, David (NIH/NIAID) [E]; Robert Kessler; Keusch, Gerald T  
**Subject:** RE: Sunday Wash Post editorial

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

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

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

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

Play Video

[Jonathan Calvert](#)

and

[George Arbuthnott](#)

| Insight

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

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**A**fter being heavily criticised by the World Health Organisation for its

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

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

Our investigation reveals:

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

## A catastrophe in the making

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

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



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



Tedros Adhanom Ghebreyesus with Chinese premier Li Keqiang in 2017

GETTY IMAGES

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

In fact the WHO would receive considerable criticism for failing to help stop the spread of the Sars-CoV-2 virus in the opening weeks of the Covid-19 pandemic. Not only did the organisation fail to act but it also promulgated misinformation about the virus originating from China and even discouraged other nations from taking steps

that might have contained the spread. For all his foresight, Tedros would be accused of being ineffective when the big test came.

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

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



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

## Beijing's man

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

As a result, years later, a body that was set up with the lofty goal of “attainment by all peoples of the highest possible level of health” has been co-opted into aiding the Chinese state's campaign for global economic dominance. Its leadership began to speak differently, espousing statements and pursuing policies that were markedly

convenient to China — even praising Beijing’s questionable allies such as North Korea, despite its appalling health and human rights record.

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

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

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

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

When the world’s nations gave Tedros the job of discovering how the virus first came to infect humans, his team struck an agreement in secret with China that emasculated the inquiry. It meant that the WHO’s “independent” mission — its fact-finding team travelled to Wuhan early this year to carry out an investigation — was, in the words of

one expert, little more than a “shameful charade”. There may well be no second chance.

## Legacy of Sars

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

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

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

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

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



Tough on China: former WHO director-general Gro Harlem Brundtland  
PAUL HILTON/EPA/REX/SHUTTERSTOCK

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

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

"The WHO really stepped into a vacuum, and it really exerted its authority as an emergency manager," Burci said. "I would say the unanimous perception is that the

WHO played a central role and essential role in allowing Sars to be controlled in a matter of months.”

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

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

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

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

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

One of the leading candidates was Dr Margaret Chan, a Chinese national. She was a former Hong Kong health director who had been criticised during the Sars crisis for



her supine attitude to mainland China. The Hong Kong legislative council found she had been too slow to respond to the Sars outbreak and too unquestioning of the misleading information from Beijing. Hong Kong suffered a higher Sars death rate than anywhere else in the world.

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



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

FABRICE COFFRINI/AFP/GETTY IMAGES

Just five days before the vote, a summit was held in Beijing for leaders of the African nations. China pledged to cancel large amounts of their debts and double aid



donations to the continent in a move that was openly acknowledged by state-backed analysts in the country as designed to secure backing for Chan.

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

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

## The African link

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

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

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

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

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

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

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

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

His lie went unchallenged. "Margaret Chan's WHO was accused of being too close to Alpha Condé," the senior source from the WHO said. In the end the UN took the highly unusual step of appointing David Nabarro, a British doctor, to co-ordinate the

international effort on ebola because it was so concerned about the WHO's failure to get to grips with the outbreak.

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

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

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



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



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



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



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

Graphic: The Times and The Sunday Times

## Turning on the money taps

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

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

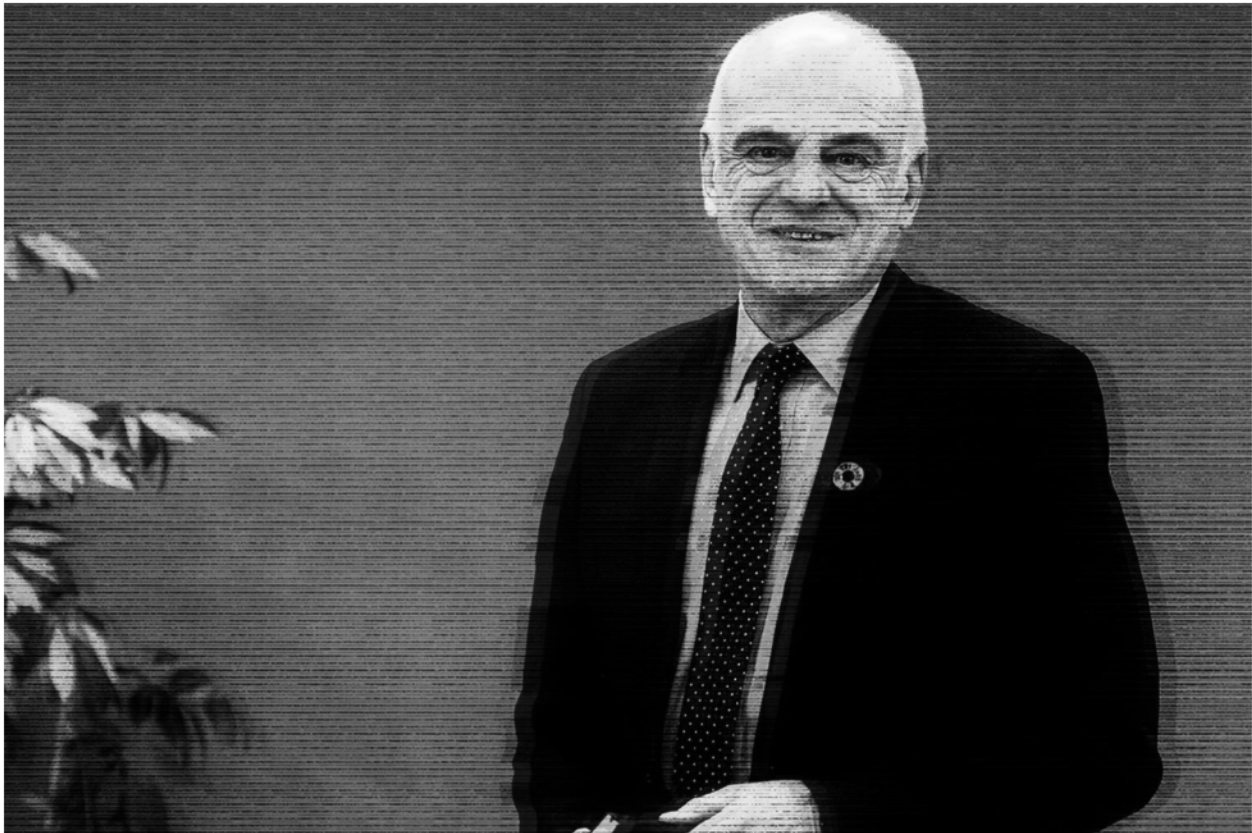
Tedros, a former epidemiologist then aged 52, had been the health and then foreign minister after joining the government in 2005. Last year David Steinman, a US economist nominated for the Nobel peace prize, called for Tedros to be personally prosecuted for genocide over his alleged involvement directing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

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

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

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

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



David Nabarro witnessed at first hand the WHO leadership's incompetence during the Ebola crisis  
FABRICE COFFRINI/AFP/GETTY IMAGES

Tedros's main opponent was Nabarro, whose first-hand experience of the WHO leadership's incompetence during the ebola crisis had convinced him of the need for reform. Nabarro was not alone in his concerns about the WHO, and he reportedly

received support from the US, the UK and Canada. This appears to have been the first time the West had woken up to China's creeping influence over the health agency.

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

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

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

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

## 'Model' China

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

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

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

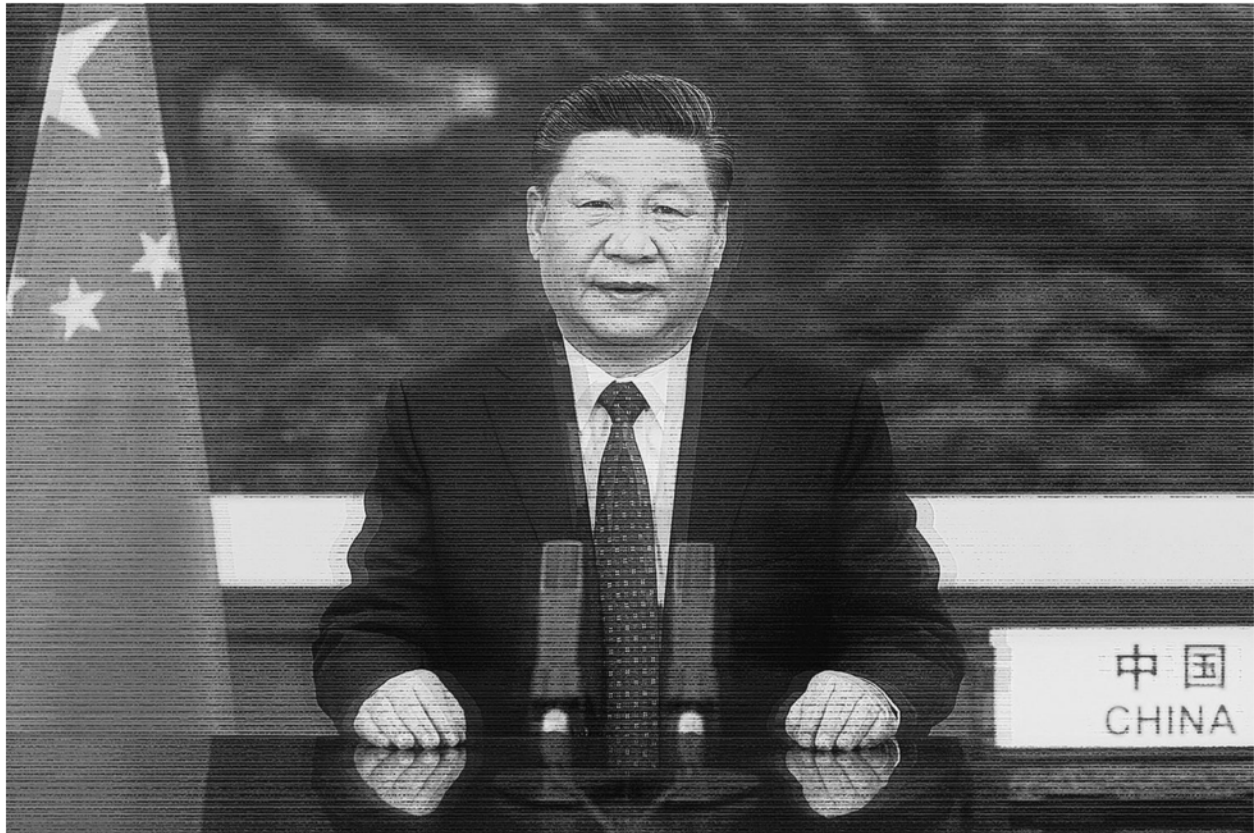
Xi has described Zimbabwe as China’s “all-weather friend”. In turn Mugabe called Xi “a God-sent person”. The Chinese government’s connection to Mugabe stretches back to the 1970s, when it helped fund his guerrilla war in Zimbabwe before he took power. More recently it ploughed cash into his regime when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

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

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

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

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



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

LI XUEREN/XINHUA/AP

Gostin described the vast shortfall as "galling". He is critical of the way China instead uses its money to pay for health projects in deals it negotiates directly with individual countries. This gives Beijing more diplomatic and economic leverage with the



countries themselves. “China’s foreign policy is extraordinarily mercantile and self-interested,” he said. “It’s all done on bilateral country negotiations, where [China] has got a ton of leverage.”

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

## The cover-up begins

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

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

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

What the statement did not say was that the illness had already been identified by the Chinese authorities as a new coronavirus — not unlike Sars — that appeared to be passing between humans. This crucial information — as well as any indication of the

alarm already secretly felt by scientific and health officials in China — was withheld from the world.

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

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

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

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

In the first two weeks of January desperate scenes were unfolding at Wuhan hospitals as patients with flu-like symptoms began to flood in. The mayhem and death were

described by Dr Peng Zhiyong, the director of the intensive care unit in Wuhan University's Zhongnan Hospital, several weeks later in an interview he gave to the Chinese media outlet Caixin Global.

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

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

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

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

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

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

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

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

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

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



Chinese authorities desperately tried to cover up the spread of the coronavirus  
NOEL CELIS/AFP/GETTY IMAGES

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

Ryan appears to have been keen to raise the lack of co-operation by China in public, pointing out that the health agency had criticised Tanzania a few months earlier for withholding details of an ebola outbreak. “We have to be consistent,” Ryan said. “The

danger now is that despite our good intent ... especially if something does happen, there will be a lot of finger-pointing at the WHO.”

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

## Deadly delay

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

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

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

But Tedros decided to wait, and nine more days passed before he even gathered the committee members for their advice. During this period he was talking directly on the

phone about the outbreak to Ma Xiaowei, the Chinese minister of health, whom he had described warmly as his “brother” in a tweet on January 11.

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

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

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

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

The number of known cases jumped from 314 to 581 during those two days and the virus had spread to 24 regions of China, killing 18 people. The true figures will have

been many times greater because of underreporting by China. And the virus had now escaped the country's borders: ten cases had been identified in four other countries.

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

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

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

The calm ripples of this cool approach were felt in Britain a day later. Matt Hancock, the health minister, chaired the first meeting of the Cobra national security committee, which spent an hour discussing the virus before concluding that the risk to the UK public was “low”. Hancock had first been alerted to the unusual pneumonia-like cases on January 3 but the government had done little in the meantime to prepare for the potential arrival of the virus. Downing Street would later defend Boris Johnson's decision to skip the Cobra meeting — the first of five the prime minister missed — by pointing out that the WHO had not considered the crisis sufficiently serious to declare a global emergency.



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

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

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

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

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

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

“Not only did it have a role; it has had a decisive role,” he said. “It was the only motivation. There was no scientific or medical or policy justification for the stance that the WHO took in January and February 2020. That was entirely premised on maintaining satisfactory ties to the Chinese government. So at every step of the way, the WHO promoted the position that was sought by the Chinese government ... the WHO actively resisted and obstructed efforts by other nations to implement effective border controls that could have limited the spread or even contained the spread of the outbreak.”

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

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

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

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

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

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

A year later a report by an independent panel set up at the request of the WHA was critical of the delay in calling the emergency. The panel, led by the former New Zealand prime minister Helen Clark, said the health agency should have assumed human-to-human transmission and issued warnings as a precaution, given what was known about respiratory infections.

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

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

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

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



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

ROMAN PILIPEY/EPA

## A flawed investigation

If the cordial relationship between Tedros and China had survived the opening months of the pandemic, the strength of their friendship would be tested once again in the

early summer of 2020. It was over the very important, yet highly sensitive, issue of how and where the virus originated.

The Sars outbreak in 2003 is thought to have originated in bats in Yunnan province, southwest China, and to have been introduced into markets in the surrounding area through an intermediary host animal. Sars-CoV-2 is believed to have had similar beginnings because of its resemblance to other bat coronaviruses.

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

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

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

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

from wild bats and has a team of scientists who often travel to those same Yunnan caves.

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

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

There were therefore questions about whether the pandemic had been caused by a leak from the Wuhan institute or one of its researchers who had been infected in the bat caves and then accidentally carried the virus back to the city. It was certainly not inconceivable: the Sars virus had leaked from the National Institute of Virology lab in Beijing in 2004. Nine people were infected by the outbreak and one died.

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

in the summer of last year. The lab has refused to answer questions on whether it was experimenting on the virus in the run-up to the pandemic.

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

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

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

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

On May 19 the assembly agreed on a form of words for the inquiry. The resolution required the director-general of the WHO to work closely with member states to "identify the zoonotic source of the virus and the route of introduction to the human population". There was no mention of the word "investigation" or the timescale.



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



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



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



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

Graphic: The Times and The Sunday Times

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

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

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



In July, Peter Ben Embarek, a WHO expert on infections that jump from animals to people, spent three weeks in China with a colleague horse-trading over the terms of reference of the “study”. Two weeks were spent in quarantine in a gloomy hotel on the outskirts of Beijing, and their requests to interview Chinese researchers on Zoom were largely rebuffed. “It was a real struggle to get this going while they were on the ground and really depressing,” said the WHO source.

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

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

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

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

That was when Garrett Grigsby, the US representative on the WHO executive board, immediately raised objections that the terms were “not negotiated in a transparent way

with all WHO member states” and appeared to be “inconsistent” with the mandate. The complaints were ignored.

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

By then the team of scientists had already been selected for the study. The health agency had deliberately chosen zoonotic experts rather than scientists who might be qualified to examine laboratory leaks. The team consisted of 34 scientists, and the agreement reached with Beijing was that it would include 17 members from China, who would mostly be employed by the Chinese state.

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

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

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

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

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



Peter Daszak had been hunting viruses with the Wuhan Institute of Virology for 15 years  
ALY SONG/REUTERS

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

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

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

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

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

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

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

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

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

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

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

## Playing politics

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

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

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

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

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

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

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

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

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



WHO investigators at the Huanan seafood market in January this year

GETTY IMAGES

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

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

The decision was perhaps unsurprising, given this was a team that had been specifically picked to concentrate solely on the natural animal causes of the pandemic.



In addition, the joint mission's Chinese contingent were under pressure from their government to dismiss any suggestion of culpability.

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

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

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

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

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

Last week, Emabarek gave an extraordinary interview for a Danish television documentary in which he disclosed that the joint mission had been forced to rule out a lab leak because of pressure from Beijing. He said the final report had been vetted by the Chinese government employees and the team were only allowed to mention the theory if they agreed that they would not pursue it further.

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

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

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

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

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

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



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



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



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



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

Graphic: The Times and The Sunday Times

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

“This outbreak was serious enough to potentially damage China’s image, its legitimacy, its interests, its ambitions and the image it was trying to project

internationally,” said Fidler, the former lawyer for the health agency. “So that political dynamic led China to control and decide the way in which these investigations were going to happen. And that’s made nobody outside China happy.”

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

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

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

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

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

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

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

Cheers,

Peter

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

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

**Sent:** Sunday, August 15, 2021 1:30 PM

**To:** Peter Daszak (b)(6); Robert Kessler (b)(6);  
Keusch, Gerald T (b)(6)


**Subject:** RE: Sunday Wash Post editorial

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


*David*

**David M. Morens, M.D.**

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**From:** Peter Daszak (b)(6)  
**Sent:** Sunday, August 15, 2021 1:23 PM  
**To:** Morens, David (NIH/NIAID) [E] (b)(6); Robert Kessler (b)(6); Keusch, Gerald T (b)(6)  
**Subject:** RE: Sunday Wash Post editorial

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

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

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

Cheers,

Peter

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

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

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

Sent: Sunday, August 15, 2021 10:32 AM

To: Peter Daszak (b)(6); Robert Kessler

(b)(6)

Subject: Sunday Wash Post editorial

Touting Embarek's supposed recantating. d

Sent from my iPhone

David M Morens

OD, NIAID, NIH

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**From:** Peter Daszak  
**Sent:** Thu, 8 Jul 2021 13:18:28 -0400  
**To:** Morens, David (NIH/NIAID) [E]; Keusch, Jerry  
**Subject:** RE: NAS workshop: Potential Benefits of Gain-of-Function Research  
<https://bit.ly/3jY9zjM>

Great to see this – I haven't had chance to read up on the pro-GoF arguments, and this is a good start...

Cheers,

Peter

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**From:** Morens, David (NIH/NIAID) [E] (b)(6)  
**Sent:** Thursday, July 8, 2021 11:04 AM  
**To:** Peter Daszak (b)(6); (b)(6); Keusch, Jerry  
(b)(6); (b)(6)  
**Subject:** FW: NAS workshop: Potential Benefits of Gain-of-Function Research <https://bit.ly/3jY9zjM>


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

**Sent:** Thursday, July 8, 2021 10:12 AM

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

**Subject:** NAS workshop: Potential Benefits of Gain-of-Function Research <https://bit.ly/3jY9zjM>

## Potential Benefits of Gain-of-Function Research

The benefits that have resulted from the billions of dollars invested in biomedical research over the past several decades are seldom disputed. Biomedical research has made enormous contributions to the

understanding of disease and the development of cures through the creation of countless innovations for improving and protecting human health, including new animal models and more effective vaccines and drugs. However, as pointed out by Dr. Ronald Atlas, from the University of Louisville and one of the symposium planning committee members, the benefits of basic biomedical research for medical practice and public health may be long term and their value not immediately evident. The results of particular types of research cannot always be predicted, and benefits are often serendipitous. Because it is not possible to predict what breakthroughs may occur as a result of fundamental research, it is impossible to quantify the benefits of fundamental research for risk/benefit analyses. Long-term research benefits are achievable, but it is not possible to specify what these are when the research is initiated.

Research using Gain-of-Function (GoF) techniques is no different with respect to what it can achieve in the long term, at least according to many of the symposium participants. Atlas noted that, although there was no attempt to achieve a consensus, no disagreement was voiced to the repeated claims of various presenters that in the short term GoF research is helpful for adapting viruses to growth in culture and for developing essential animal models for emerging pathogens, such as Middle East Respiratory Syndrome coronavirus (MERS-CoV), and escape mutations to understand drug resistance and viral evasion of the immune system. In the long-term it may also allow the generation of information that is not obtainable through other methods, but whether all the long-term benefits envisioned for GoF research will actually be realized is still unclear. Vaccine producers in particular disagree on whether GoF methods are essential for vaccine development, so the contributions of GoF research to vaccine development need careful evaluation. Increasing reliance on gene sequences to predict phenotypes may increase GoF research's importance over time. As was clear from the presentations in Session 4 of the symposium, there is wide recognition that it is not yet possible to predict phenotype from genotype, but Dr. Philip Dormitzer, from Novartis Vaccines and a member of the symposium planning committee, noted that as more genotype-phenotype linkages are established, it may enable keeping certain viral characteristics out of vaccine strains.

Two symposium sessions were devoted to presentations on the potential benefits of GoF research, one focusing on the role of GoF in surveillance, detection, and prediction and the other on its role in treatment and response.

[Go to:](#)

## **SURVEILLANCE, DETECTION, AND PREDICTION**

The first presentation in Session 4 was given by Dr. Stacey Schultz-Cherry, St. Jude Children's Research Hospital, who discussed the information garnered from GoF studies about what she believes are its public health implications. Her home institution is one of five National Institute of Allergy and Infectious Diseases (NIAID) Centers of Excellence for Influenza Research and Surveillance in the United States and focuses on the animal-human interface. St. Jude is also a World Health Organization (WHO) collaborating center for studies on the ecology of influenza and is part of a global influenza surveillance and response system that includes six WHO collaborating centers and 144 national influenza centers throughout the world. St. Jude collaborates with colleagues in the animal health sector and their main role is to decide on the influenza strains that are incorporated into the seasonal flu vaccines. They also decide whether vaccines or candidate vaccine viruses are needed for emerging zoonotic threats. The national influenza centers conduct viral strain surveillance throughout the year, looking at the genetic information from human as well as emerging zoonotic viruses. Every February and September, representatives from the WHO centers and central regulatory laboratories as well as animal health experts go through the surveillance data to decide on which viruses to choose as vaccine strains. This information is given to the vaccine manufacturers and regulatory agencies, and 6-9 months later the vaccines become available. She described many of the complexities of the process. She noted, in

particular, that determining the function of amino acid changes in the viruses circulating in the field is one of the key tasks. As an example, she discussed an ongoing outbreak of H5 viruses in Cambodia. Through GoF research, it has been determined that the presence of certain genetic markers in the outbreak strain suggested that this particular virus could be more readily transmitted, at least in ferrets. This information has provided the persuasive factor to move forward with the development of a vaccine.

Schultz-Cherry noted that GoF research-derived information is also used for risk assessment. The U.S. Centers for Disease Control and Prevention has developed a risk assessment tool, the Influenza Risk Assessment Tool, to rank the risk associated with particular viruses. She stated that the result of using the Tool is not a prediction of the next pandemic, but rather an objective means of prioritizing viruses for future risk management. The Tool looks at the properties of a virus. What kind of receptors does it bind to? Is it more mammalian or avian? Does it transmit in animal models, or does it have molecular signatures that would suggest transmissibility? What is its genomic variation? She stated that all of this information, especially the molecular determinants of transmissibility, has been generated through GoF studies at some point, perhaps even as far back as the 1970s. She stated that the ability to prioritize is important because of limited resources; vaccines cannot be made for every new emerging virus. Schultz-Cherry's final points dealt with the limitations of these studies. Phenotype still cannot be predicted from genotype. We may know a lot from studies of particular amino acid changes in one strain of virus that may not apply to another strain. She noted that opponents of GoF research have said that this is a reason to not continue this work. She would argue, however, that inability to predict phenotype is precisely why GoF studies must continue so that eventually this inability can be overcome. During the discussion following the presentations, Schultz-Cherry was asked what is the trajectory of the information being used for vaccine candidate selection? She explained that the risk assessment tool is continually updated to add new information about molecular determinants of virulence and transmissibility. She believes that the more information we have, the better we will be able to predict the risk of a pandemic and then use that prediction to prioritize vaccine strain selections and make the vaccines available.

Dr. Christophe Fraser of Imperial College, London next spoke about potential pandemics. He began by stating that he would scrutinize the benefits of GoF experiments using a narrow definition of GoF as dealing with the transmissibility of the highest risk potential pandemic pathogens (PPPs). He is the Deputy Director of the Center for Outbreak Analysis and Modeling, which is also a WHO Collaborating Centre for Infectious Disease Modelling, located in London. He and his colleagues at the Centre have worked on the Severe Acute Respiratory Syndrome (SARS) outbreak, the initial response to the 2009 influenza pandemic, and have synthesized a variety of surveillance, neurological, and epidemiological information. In 2014, their work turned to both MERS, for which they were trying to quantify its transmissibility to humans, and Ebola as part of the WHO response team. He noted that, on a global scale, the interventions in the event of an outbreak are quite simple—well-organized classical public health tools. The key aspect is timeliness, and the classical tools are diagnostics, social distancing, and risk communication. Probably the area most lacking at the moment on a global scale is rapid diagnostics to allowed triaging of people, which has been made very clear with Ebola. Data systems, multidisciplinary validation, and sharing of data and samples are all required. There is also a huge role for basic science, but once an epidemic has started, the value of information from this limited realm of GoF work on transmissibility is unclear. The role of such work is clearly going to be in predicting pandemics. He stated, however, that H5N1, H7N9, MERS, and Ebola had all clearly been identified as threats prior to any GoF-PPP experiments, although this is less the case for the 2009 H1N1 outbreak and SARS. Nevertheless, the failure to predict outbreaks of the first four pathogens he listed was due to surveillance gaps, not a lack of understanding. Of the viruses that emerged in 2009, there were no

closely related viruses found by surveillance in any swine populations for 12 years prior to the emergence of H1N1. MERS also emerged from a complete surveillance gap.

The next utility that has been claimed for GoF research-derived data is for predicting emergence. The data from the two experiments on H5N1 transmissibility were plugged into a model by Colin Russell and Derek Smith ([Russell et al., 2012](#)), who concluded that it is not possible to calculate the level of pandemic risk precisely because of uncertainties in some aspects of the biology. Fraser stated that he very much endorses that statement; it is not possible to calculate the level of risk from the mutational landscape. The aim in [Russell et al. \(2012\)](#) was to conduct basic science to understand the factors that increase or decrease risk, not to assess the actual risk. Russell's work built on earlier work that attempted to predict pandemics. The earlier work from Jamie Lloyd Smith tried to establish a general rule, which is that infection begets transmission and transmission begets epidemics. Things that can cause transmission are much more likely to result in epidemics than things that are not already transmissible.

The WHO uses an empirical, rather than a theoretical, approach, meaning that alarm bells should be based on human cases and clusters and the key is surveillance and sharing of data. However, as Fraser had previously noted, there are limitations, especially given that for many years there was reluctance to acknowledge clusters of infections because of the fear of escalating the WHO alert levels and the resulting consequences. In terms of surveillance and response, it is of course very useful to know what viruses are out there, but it is promptness that is critical. To contain an epidemic at its source, there is a window of days in which to intervene. Once the epidemic gets going, the scale of the problem will double every week. The most suitable response would be based on the timely reporting of cases. Fraser believes that pre-pandemic vaccine strain selection is the crux of the argument. Timely development of vaccines could be transformative. Vaccine seed stocks can speed this up, but there are other rate-limiting steps, especially international agreements on the regulation and conduct of human trials. He also believes that the objectives should be to:

- prioritize strains with evidence of infection and transmission;
- cover antigen space, and monitor antigenic drift;
- plug gaps in surveillance;
- make more/faster seed stocks ([Dormitzer et al., 2013](#))?

Fraser concluded with the following:

- The direct benefits for enhanced surveillance and model-based prediction of GoF experiments with PPP should not be overstated.
- The indirect benefits of basic science are likely huge, but the rationale for working with dangerous pathogens requires benefits that outweigh risks and opportunity costs.
- The benefits of GoF with PPP for pre-pandemic vaccine production should be probed in depth.
- The risks are real and present ([Lipsitch and Inglesby, 2014](#)).

A participant asked Fraser about what he would require to be confident about using data from GoF or other experiments in his modeling? He responded that the tools required for this lengthy, although worthwhile, journey must be available. The issue centers on the risk taken at the beginning of the journey. Earlier in the morning, Fineberg mentioned that, by their nature, pandemics provide many years to think about the tools but only infrequent and limited time to actually test them. Weather forecasting has improved dramatically because weather forecasters can test their models daily and receive many complaints when they are wrong. The situation with pandemics is not like that. Dr. Colin Russell of Cambridge University Infectious Diseases responded to the two previous presentations as the last speaker of Session 4. He noted that both of the previous speakers touched on the ability to predict risks for pandemic viruses and on the ability to produce vaccines in a timely

manner, and to ensure that there are enough vaccines to go around and provide a chance to mitigate the early spread of disease. However, the more we learn about nature, the more we understand that there are a vast number of undescribed viruses out there, many known only through sequence data. He stated that genotype to phenotype prediction is one of the holy grails of influenza biology research. However, much more research is required to reach this goal. He referred to a National Institutes of Health workshop for which he was lead organizer in the fall of 2013 that brought together experts in virology, epidemiology, and other fields. It included participants from both sides of the GoF debate, and a key focus of the meeting was to rectify the limitations in the ability to make inferences about the phenotype of influenza viruses from genetic sequence data alone. A full report of this workshop was published in October (Russell et al., 2014). A key question in the discussions was whether the effects of mutations are dependent on the viruses in which they occur. A variety of studies suggest that the effects of particular mutations are strongly likely to depend on the genetic context in which they appear. First, in 2006 Jane Stevens, Ian Wilson, and others published a paper in the journal *Science* (Stevens et al., 2006) about GoF research, investigating the potential for a virus to switch receptor binding from avian-like to human-like. This work was among the first to demonstrate that single amino acid substitutions could cause such a switch. But the authors concluded that knowledge of genetic changes in circulating virus isolates by themselves obviously cannot be used to predict the impact of receptor binding specificity, let alone affect the results of future mutations (Stevens et al., 2006). It is worth bearing in mind, Russell stated, that there is a great degree of genetic diversity in the H5 virus. Other studies have found that the effects of mutations in other H5 viruses depend on the clade of H5 viruses in which the substitutions were produced. These residues alone cannot be used as reference points with respect to specificity in H5N1 strains, but when combined with other data, the presence or absence of these mutations can be informative. None of this should be in any way construed to undermine the value of the studies, but highlight the impressive need for further work. In short, Russell believes that, given the incomplete state of knowledge, there is a risk of overestimating what is known based on sequence data alone. Focusing too much attention on the presence or absence of particular mutations may cause other mutations or even other traits yet to be identified to be overlooked.

Gavin Huntley-Fenner asked the panel members what sort of public health system would be needed to justify the status quo and whether the risks and benefits of GoF research are balanced from this public health perspective. Fraser answered that transmissible viruses makes GoF research a very special case. In terms of general basic science, we never have to justify that to the same degree, luckily, because otherwise we would find it difficult to move forward. Basic science is a much broader portfolio where the risks are very small. The real crux of the GoF issue is separating out that very small number of experiments. We need a much wider frame for all experiments, where occupational health risks are not an order of magnitude higher than public health risks.

Laurie Garrett of the Council on Foreign Relations commented to Schultz-Cherry that her statement that the risk assessment model would be adjusted differently if H5 was in Canada speaks to the core of the whole problem. Risk is about rich people, which is about 5 percent of the global population, if that. She stated that we have never once delivered vaccine to poor people around the world for any epidemic/pandemic situation in the history of the planet, have never delivered clinical tools, and have never delivered diagnostic tools. Garrett had just come out of quarantine for Ebola, and there is nothing that can possibly be called a rapid diagnostic available for Ebola. So when the Council on Foreign Relations reviewed the whole question of GoF use and issued its memorandum to the White House (available at [www.CFR.org](http://www.CFR.org)), it concluded that the most fundamental problem is that the International Health Regulations have never been fully implemented. Garrett stated that none of the wealthy nations has assisted poor nations to raise them to capacity and that “none of the benefits will ever be available to the majority of planet Earth and none of them are getting the toolkit to minimize or mitigate risk. We are having a very American conversation that excludes the rest of the planet.”

Schultz-Cherry responded that her remark about having H5 in Canada was designed to make people think about risk versus benefit and to reflect that doing more work can democratize the surveillance process. With more work, it could become cheap and easy to assess the threat of viruses. If this could be done, we could radically change the way we do surveillance worldwide and we would not have the same sort of geographic distributional issues that are of concern now.

Dr. Gregory Koblenz, George Mason University, asked Schultz-Cherry about the proven accuracy of the risk assessment tool used for selecting flu strains for yearly vaccines. She, in turn, called on Dr. Ruben Donis of the CDC to comment more about the risk assessment tool. Donis noted that the risk assessment tool is a product of the global community of scientists working on both human and animal health. It is a product of the realization of the gaps in surveillance that were noted in Fraser's presentation. It was developed to ensure that we have a comprehensive way of evaluating all the possible viruses that are circulating in animals that could reassort, recombine, and change the phenotype and eventually emerge as pandemic viruses. The tool attempts to develop a comprehensive review of all of the potential threats.

Via the web, Dr. Daniel Perez, University of Maryland, asked whether the potential of strains that resulted in past pandemics to affect humans would have been moderated if we had had the opportunity to sequence them. Fraser stated that understanding how a virus expands its host range from swine to humans requires a lot of information. The validation of the genotype to phenotype prediction tools really should address that question. Russell added that he did not think that having sequence information at the time of earlier pandemics would have forewarned of the emergence of those viruses, which again speaks to the incomplete nature of knowledge and the critical need for further work.

Another participant pointed out that there is probably a very large number of variables involved in understanding viral pathogenicity. Given the number of variables, is there much chance of doing anything useful? Russell and Fraser both agreed that this is a very complicated problem, which is why more experimental work is needed to help reduce the dimensionality. But what we currently know cannot help us very much in understanding what will occur in the next 5 years. However, science is an incremental process. The increases in understanding that have been achieved from the work that has been done so far have been helpful. In terms of translating directly into public health improvements, that is a pretty substantial leap to make. But saying we will not get there will not undermine science. Nevertheless, tools that can deal with perhaps thousands of genetic traits and phenotypes are needed. It is not about the mutations but rather about the function of the mutations. We could reach the state where we sufficiently understand the traits that a virus needs to adapt to humans and identify ways to test for those that are either independent of sequence or a metalevel of sequences.

Another participant made the point that had the 2009 pandemic strain been seen in animals instead of humans, it might have been falsely viewed as having low virulence and transmissibility and would have been discounted. Fraser agreed that the fact that our knowledge is incomplete right now creates a risk of discounting viruses that lack a certain number of substitutions when in fact we should be concerned about the risk.

Dr. Ron Fouchier, Erasmus MC, commented that he believes a lot is being asked of papers that were only published in 2012 and for which the follow-up work has been shut down twice for extended periods. This is work in which the phenotypes, not just the genotypes, are being studied. He agreed with Fraser that although he cannot yet predict phenotypes from genotypes, the assays produced by his work are being used to look at phenotypes in surveillance, which means a better job is already being done. He made a plea for more basic science to follow up on his work, which is still in the early stage. Fraser responded that the basic science is not under question. The question is: Should we be starting with experiments that have orders of magnitude higher risk than other work in the area?

Go to:

## TREATMENT AND RESPONSE

Session 5, moderated by Baruch Fischhoff, consisted of a panel discussion with four speakers. Each panelist was given about 5 minutes and then the session was opened up for discussion.

The first speaker was Philip Dormitzer, who described how GoF research and the regulation around research affect the real-world case of trying to apply virology to a public health situation. For the purpose of his talk, Dormitzer described the chronology for the production and delivery of the 2009 H1N1 influenza pandemic vaccine, an “historical reminder,” for which the response was the “fastest ever, but still came after the disease peaked” (Borse et al., 2013). In fact, an estimate published in *Emerging Infectious Diseases* (EID) showed that for every week of acceleration of vaccine supply, an additional 300,000 to 430,000 U.S. cases could have been prevented. Dormitzer explained that Novartis, in collaboration with the J. Craig Venter Institute (JCVI) and Synthetic Genomics Vaccines (SGVI), are now working together to establish a process for rapid generation of synthetic influenza viruses that includes GoF studies based on sequence motif data to guide the genetic assembly of the vaccine. For instance, the Novartis research team routinely screens for phenotypic traits of interest and can specifically remove or mutate strains with either polybasic cleavage sites in the hemagglutinins (HA) (found in highly pathogenic avian influenza viruses [HPAIV]) or neuraminidase (NA) gene markers of resistance. For that specific example, Dormitzer explained that the process from the identification of the relevant HA and NA sequences for the new influenza strain to the genetic identity confirmation of the vaccine virus lasted about 1 week. However, the next phase leading to the first large-scale clinical trial took months because of various well-intentioned regulations and policies to protect the food supply in the United States. Notably, because Novartis could not obtain a U.S. Department of Agriculture permit, this phase involved international research collaboration with Germany before taking the vaccine back to the United States, which unintentionally slowed down the human vaccine development. Under U.S. government regulations on select agents, vaccine development against HPAIV is counter-productive because “you can’t really put an entire manufacturing facility under select agent conditions and still have a factory that can produce seasonal vaccines in an economically competitive way” and in a timely manner. Also, as Dormitzer pointed out, he “couldn’t apply any of this [GoF research] technology.” Therefore, if adaptation of vaccine virus to increase yield or more modern synthetic biology were captured by GoF regulations, then additional unintended impediments to timely vaccine supply could be created.

Next, Ralph Baric presented his view on the impact of GoF restrictions to the emerging coronavirus vaccine and therapeutic research. Baric started his talk by reiterating that no vaccine has been approved for MERS-CoV or SARS-CoV in the midst of an ongoing MERS-CoV outbreak. Baric explained how new restrictions reduce public health preparedness to respond to future SARS-like CoV outbreaks. He explained that the original vaccine target for the SARS-CoV outbreak 2002-2004 strain was 99 percent identical between human and civet (Ge et al., 2013). However, metagenomic sequencing showed that bat SARS-like CoV (SL-CoV) with 65 percent to 95 percent sequence homology, can constitute a large pool of strains with pandemic potential against which countermeasures need to be developed. To evaluate whether the existing vaccine and drugs work on these strains, Baric’s team and others used two types of approaches. The first was based on the production of CoV pseudotypes coated with virus spike-like proteins that can potentially engage the human angiotensin converting enzyme II (ACE2), which is the SARS-CoV cellular receptor molecule. This method constitutes a safe and ethical research alternative approach. Similarly, chimeric recombinant viruses that encode spike-like proteins as part of the virus particle can also be used. While studies using pseudotypes and structure-based prediction confirmed the existence of a bat SL-CoV that can infect human cells, only studies using GoF chimeric virus identified an additional bat SL-CoV as a potential threat. Baric noted that both bat SL-CoV were less virulent in a mouse model. Importantly for public health implications, data further showed that existing vaccine and human monoclonal antibody therapy failed to protect against these two newly identified



bat SL-CoVs, leading Baric to point out that “we are vulnerable” to SL-CoV bat strains that currently exist in nature. The second part of Baric's talk described how robust animal models are essential for vaccine/drug design, safety testing, and performance outcomes. He explained that SARS-CoV replicates poorly in mice (Frieman et al., 2012) and although his team and Subbarao's lab have developed mouse-adapted strains, the in vivo correlates of infection vary widely depending on the model used. For example, he described some collaborative work done on inbred and outbred mice demonstrating that in some cases the vaccine could have caused increased mortality in some individuals and emphasized the need for better animal models for SARS-CoV vaccine research. In the case of MERS-CoV, the epidemic is ongoing and no robust animal model exists because routine GOF studies, including passage in small animal models, have failed. Baric called for an immediate lifting of the restrictions on MERS-CoV research on animal model development. This was echoed by other participants during the final discussion. For example, Peter Hale of the Foundation for Vaccine Research stated that he thought the inclusion of the coronaviruses in the “pause” was “muddying the waters” and that he did not detect any enthusiasm among SARS and MERS investigators to increase their transmissibility. This point was also made strongly during the discussion following the session.

The next speaker was Dr. Jerry Weir from the Food and Drug Administration's Center for Biologics Evaluation and Research, whose team participates in the selection of strains for the yearly influenza vaccines and regulates viral vaccines to ensure that they are safe and efficacious for human use. Weir offered some comments about how the regulatory process views some of the experiments and techniques addressed by the symposium speakers. He stated that there are actually not very many, if any, regulatory issues associated with the type of virus manipulations that were under discussion (i.e., improved types of seed development, reverse genetics, manipulation of virus genomes to improve vaccine virus stability or performance). Manufacturers already licensed can submit a supplement to the license that is evaluated for using a fairly standard process. In lieu of giving examples of how GoF research can influence a process, Weir mentioned a few challenges that still remain in vaccine development for the influenza virus. In general, for the seasonal strain selection and the preparation of pandemic vaccine strains, the major challenge is the existence of very large gaps in our knowledge of how genotype sequences relate to phenotypic changes. Weir stated that strain prediction and selection remain a “guessing game ... for which improvements are desperately needed.” In addition, for other factors such as transmissibility or virulence, a lot is not known and improvements are also needed there. To complicate the matter, the incorporation of four, instead of three influenza strains in the seasonal vaccine is a challenge every year for the different players in the global community that pick the vaccine strains as well as the manufacturers who need to deliver the vaccines in a timely manner. For them the yields of vaccine viruses need to be improved with the challenge of limiting factors such as poorly growing strains among the four chosen. In his view, Weir believes that, as broadly defined, “GoF studies have had an enormous influence on how we develop vaccines over the years ... and can help improve the process with the challenges that we still face.”

The final speaker was Mark Denison, who explained his view of GoF studies in MERS-CoV and SARS-CoV countermeasure development and how oversight or regulation might be limiting. Denison reminded the audience about the basic research and ongoing challenges that remain in the development of therapeutics to SARS and MERS-CoVs, emphasizing, like other speakers, the need for in vivo and in vitro models to identify common mechanisms and determinants of resistance. He then moved to a case study involving GoF research and asked the audience whether they would consider giving or taking “a live vaccine with a virus that has an engineered increased mutation rate,” for which only a few people raised their hands. The question was an introduction to a series of studies showing that CoVs, contrary to other viruses, express a proofreading exonuclease (ExoN) normally only found in bacteria and eukaryotes. When this ExoN was inactivated, the CoV mutation rate was increased by 20-fold. Normally, mutations allow tremendous variation in viral populations and presumably increase adaptation, fitness, virulence,

and therefore public health risks. However, GoF studies demonstrated that SARS-CoV with the inactivated ExoN were less fit, attenuated in a mouse model of lethal SARS-CoV, could not compete with the wild-type virus, and could therefore be used as a target for therapeutics development. This work was also adapted to other RNA viruses with encouraging results. Denison used this case study to reflect on the implications of new regulations and guidelines if he wanted to create a mutated strain of a virus and test it in an animal model. In conclusion, Denison stated that he believes that because assumptions are usually wrong, GoF research that includes “passage for adaptation and resistance in in vitro and animal models are essential components of therapeutics development” and that to his knowledge no bioinformatics or predictive safer alternative approaches are effective to develop new countermeasures. Following the panel member's presentations, there was discussion with the audience. Fraser asked Dormitzer how he would propose to reconcile, practically, the need to conduct very dangerous research without casting the net too wide. Dormitzer responded that what is first needed is a very clear and limited definition of the sorts of research that require particular attention. As Relman discussed, experiments that combine increased transmissibility, virulence, and lack available countermeasures are very concerning. But we have to make sure that the definitions are not too broad so that they do not capture a lot of other work. Second, there needs to be a distinction between the highly diverse work performed for basic research and the much more restricted, but more urgent, work needed for vaccine development. A classic example is H5N1 vaccine development. There have been at least 26 H5N1 strains that have been attenuated all in the same way. But for the 27th one, the often months-long routine must be gone through again. We need clearly established, well-defined pathways to get vaccines quickly and not encumber the process with regulations.

Relman also stated that he does not think that there is a major question about the value of MERS and SARS research, even that research that currently falls under the rubric of GoF. Restrictions do, in fact, hamper the quest to develop countermeasures, etc. What he thinks is a more interesting question is whether there is a very discreet and specific set of experiments with MERS and SARS that you might not want to see undertaken. For example, would it be appropriate to deliberately start with a highly virulent human isolate of MERS and then attempt to add to that much enhanced human-to-human transmissibility by the respiratory route? Baric responded that he did not know of anyone doing transmissibility studies with the human coronaviruses. Unlike flu, there are currently no small animal models suitable for MERS or SARS transmissibility assays. This is mostly due to receptor incompatibility between the human and any small animal models. Optimization assays to enhance virus transmissibility between ferrets, for instance, would probably decrease the ability of that modified virus to bind to the human ACE2 receptor. Relman reformulated the question to include the possibility of using transgenic ferrets with the human receptor, but Baric explained that the human receptor itself is not sufficient and that other proteins are essential for viral transmissibility and, therefore, the results in transgenic models would not be predictable.

Denison added that nobody would have as a goal or would support trying to increase virulence and transmissibility of MERS or SARS. That is why he recommends the use of a case-based approach that looks at how we really do science. Denison shared his approach when sending a proposal through study sessions or review process at a funding institution. For him, instead of trying to define “boundaries of absolute,” the real question should always be, “What is the best approach to answer that question?” Then, depending on the stage of the review process, the response should be iterative to be adequately addressed.

Inglesby asked Dormitzer whether the annual process of production of flu vaccine relies on research using highly transmissible and highly virulent strains. Dormitzer responded that this is not the case and that the goal is quite opposite—to take a strain found in nature and transform it into something that can be manufactured efficiently by increasing its growth rate in cell culture or eggs. Inglesby then asked whether virulence and transmissibility are traits that can be distinguished from increased growth

capability. Dormitzer stated that there is precedent that shows that adapting viruses to grow better in cell culture does not, in general, increase their virulence or transmissibility, whereas passaging from animal to animal often does. He stated that we also need to distinguish between two things: the need for very rapid production of new antigenic variants, which should start on the day it is found that there is a new variant causing disease, and the development of the vaccine backbone, which could be used in multiple variants and which you do not want to take forever. It is not the same issue when facing an emergency.

Dr. Simon Wain-Hobson, Institut Pasteur, echoed Denison's presentation by citing work done on polio by John Holland 15 years ago that showed that when chemical mutagenesis is combined with a rapidly evolving RNA virus such as polio, the fitness of the virus goes down. Several members of the panel agreed. However, Denison raised the issue of perception in the current environment and under the current policy circumstances. Such proposals might not necessarily be vetted even though most of the time we can not know the answers until the experiments are conducted.

Another questioner from the webcast asked Dormitzer whether, in his opinion, GoF research is essential for future development of intervention strategies against various pathogens. Dormitzer responded that he thinks it depends on whether you are talking about the short- or long-term. He stated that GoF research is not going to help pick next year's flu vaccine, but if one is making viruses for use in manufacturing and a certain genetic motif that correlated with high transmissibility is known, then one could make sure that the motif is not included in the vaccine strain. GoF research has utility for such purposes. The other thing is that vaccine manufacturers are increasingly figuring out how to take genetic data and use it to predict what they want to make. That would be a genuine utility if it could be done. The question is whether we can do that kind of science in a way that does not create more problems than it solves. There is potential for GoF research to improve vaccine production, but it is not today except for limited instances; it has long-term potential for this purpose as long as the work can be done without inordinate risk. Denison asked whether any "bad" GoF experiments were performed to discover the polybasic cleavage site associated with high virulence. Dormitzer listed what is believed to have led to this discovery, including studies on correlations between the presence of these sites and clinical observation of virulence in birds; discovery of plausible mechanisms looking at cleavage proteins expressed in different cells; and loss-of-function and GoF studies to make sure that the gene identified is the correct one. Denison's point was that a series of experiment led to that conclusion.

It was clear, however, that there is a substantial disagreement over the value of GoF research for vaccine development. Lamb, in a later session (Session 8), stated that he thought we should modify the mantra that GoF research is useful for vaccine and antiviral drug development. He thinks that this point is overused and oversold. Hale also commented during the final discussion that he agreed with Lamb, we do need to modify the mantra that this research will help develop vaccines and antivirals. He said that he and his Foundation fully endorse that sentiment. It is an argument that is made over and over again without evidence to substantiate it. He believes that in terms of development of better vaccines, GoF research has little or no benefit, and if there is any benefit, then it is tiny and way down the road. In the meantime, he said, it is not worth the risk and there are other priorities.

Dormitzer responded to the latter comment and acknowledged that the community of people who make vaccines is divided just as much of the symposium audience was divided. He stated that the basis for that division is informative. Flu vaccines today are still made by very, very old techniques. One looks at what is spreading, sees if it has changed, and then picks the strain. There is not a lot of basic science in this; rather it is 1960s science. In 2009 we were not able to get the H1N1 vaccine out until after the outbreak had peaked, and many people have commented that the current flu vaccines, although somewhat effective, are not good enough. A lot of people who work on vaccines think we need to do things better. One way to do things better is to take advantage of the available information, particularly sequence-based information, so we can do things faster and make vaccines better. Information from

GoF research can contribute to identifying risks earlier so countermeasures can be taken earlier. Dormitzer said he does not think it is the case that GoF research is essential to the current vaccine system as it is generally practiced today, but it is not useless. It is clearly part of the trend to understand and predict what can be done better and to help respond quickly. That does not mean it is open season to do what you want and forget the risks. A balance is needed. But he was firm in his statement that the vaccine producers are not universally of the opinion that there is no use for GoF research.

Koblentz asked whether the coronavirus researchers had a sense and could comment on why MERS and SARS were included in the “pause” on GoF along with influenza. Denison believes that, despite the circumstances, the inclusion of SARS- and MERS-CoV in the “pause” demonstrates that this is not about one virus but more about the issue of how we address critical questions in science and what constitutes appropriate review and safety among the different research institutions. He believes that whatever the question asked, whether about replication or virulence and transmissibility, the science should be the same and should follow an iterative process that incorporates risks, milestones, and points to change along the way.

As a follow-up from Relman's question on transmissibility in MERS and SARS animal models, Koblentz asked Baric to clarify which set of experiments he would use to study transmissibility. Baric explained that many variables are needed to make a model to enhance transmissibility, but if he had the perfect model to do these experiments he would not do them. Later during the discussion, prompted by Inglesby, Baric added that because the CoV interaction barriers are species specific, the only real absolute model that could be used would be human, so he certainly would not do the experiment. Fraser asked Denison to clarify what he meant when he said that no one would want to increase the pathogenesis or transmissibility of MERS and, therefore, that the regulation should not apply to MERS and SARS research, especially because this is what the debate is about. Denison explained that he thinks that increasing transmissibility of human coronaviruses is not a goal. He then described the importance of research on wild-type or genetically modified animal models or cell cultures to understand determinants of pathogenesis or virulence factors. No one has the goal to increase these characteristics, but researchers need to be able to study the virus or they would need to rely on epidemiology and surveillance, which are not adequate to answer the question. Denison also stated that to his knowledge there is no other approach to develop countermeasures and vaccines.

Richard Roberts, New England Biolabs, asked whether experiments on dangerous traits that exist in highly pathogenic and virulent strains could also be done on strains that have already been incapacitated in some way. Denison agreed that on a case-by-case basis, if it is possible, then a safer approach is always preferred, but that it depends on the genetic background of the strain of interest. As an example, Denison explained that sometimes a certain type of loss- or gain-of-function experiment is undertaken on BSL-2 strains that are 90 percent identical to more virulent strains, but that the small genetic background differences and therefore structure can greatly influence the outcome of the experiment. When one has strains that are not genetically identical or from the same clade, it may not be possible to make the right determination without doing the experiments.

A participant from the Department of State noted that although there may be ways to do the research in a safer manner, Denison had just argued that in a competitive environment the research question should be answered in the best and most direct way to get funding. The participant wondered whether, in this competitive context, a researcher would prefer the safest, but perhaps more indirect, option assuming it would get at the question. Denison commented that sometimes there are safer options such as when he used a mouse model for hepatitis virus to identify determinant proteins such as those for proofreading. This approach is of public health importance because it proves that certain mechanisms might be a useful target across multiple strains, including those we have not yet tested, such as the basic cleavage site. Returning to his earlier comment about the funding, Denison explained that professors not only try to educate students to do the best science in the best way, but also ask them about finding

alternatives that will eventually answer the question in a less direct way. Dormitzer added that although one may get NIH funding through a grant that incorporates safety considerations, institutional safety boards and questionnaires about dual use research of concern are procedures already in place to make sure it is not only the most direct way to a scientific answer taken, but also that safety is considered. Each of the panel members was then given an opportunity for closing remarks. Dormitzer's closing remarks were that he believes that there is long-term potential in GoF research. He believes that we must be very careful with any sort of restrictions or regulations to make sure we do not inadvertently capture a lot of work that is not only good for basic science, but also a core part of the public health response. He stated that as a practitioner of vaccine development, he has realized that there really are road blocks that were never intended by the people who drafted the restrictions.

Baric agreed with those comments and affirmed the importance of reverse genetics and GoF research in understanding viral pathogenesis as well as vaccine and therapeutic design. NIH should be very careful about delineating the boundaries of the restrictions to be placed on the research community because there could be dire consequences if these restrictions are too broad. Weir affirmed one of his earlier points: if we had great vaccines for all of these agents, we might be having a different discussion, but the fact is that we do not.

Denison closed by proposing an iterative process whereby scientists do a review along the way. For critical pathogens of high human consequence there should be a mechanism that allows for a case-based, iterative approach that identifies problems along the way. Investigators need to have their research supported and be allowed to integrate best practices when doing GoF research.

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**From:** Peter Daszak  
**Sent:** Tue, 27 Jul 2021 14:18:30 -0400  
**To:** Morens, David (NIH/NIAID) [E]; Keusch, Jerry  
**Subject:** RE: Physician-Scientist Steven Quay: Forensic examination of Wuhan Institute of Virology COVID-19 patient specimens from December 2019 reveals extensive laboratory contamination, including evidence of genetic manipulation of the Nipah Viru

No – keep them coming – I miss some of these and I like to be aware.

It's also a chance for me to fill you in on any background if I've heard anything – can be useful given both of your positions...

Cheers,

Peter

**Peter Daszak**  
*President*

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

Tel.: (b)(6)

Website: [www.ecohealthalliance.org](http://www.ecohealthalliance.org)

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

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

---

**From:** Morens, David (NIH/NIAID) [E] (b)(6)  
**Sent:** Tuesday, July 27, 2021 2:16 PM  
**To:** Peter Daszak (b)(6); Keusch, Jerry (b)(6)  
**Subject:** RE: Physician-Scientist Steven Quay: Forensic examination of Wuhan Institute of Virology COVID-19 patient specimens from December 2019 reveals extensive laboratory contamination, including evidence of genetic manipulation of the Nipah Viru


I probably shouldn't even send you this sort of crap, but just want to give you a heads up from a friendly source, before someone blind-sides you. If you have a cat, you can use this paper to line the kitty litter box.....


*David*

**David M. Morens, M.D.**

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

 301 496 4409

 (b)(6)

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**From:** Peter Daszak (b)(6)

**Sent:** Tuesday, July 27, 2021 1:42 PM

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

**Subject:** RE: Physician-Scientist Steven Quay: Forensic examination of Wuhan Institute of Virology COVID-19 patient specimens from December 2019 reveals extensive laboratory contamination, including evidence of genetic manipulation of the Nipah Viru

This is part of a continuing saga of BS that's something to do with how when you use a certain type of sequencing machine, you get partial bleeds from other samples including previously used. It's extremely

common and not at all interesting. It's also not a 'menagerie of viruses' – these are cDNA read outs from a sequencer (or something).

I checked this out previous with Eddie Holmes, Kristian Andersen and a bunch of other well-known virology genetics folks. These people are really scraping the bottom of the barrel!

Worst of all, it's a preprint, which means it might actually get published somewhere and sully the scientific system. It happened with another paper a few weeks ago that was published in American Chemical Society transactions or something. Zhengli, Linfa, Angela Rasmussen, Bob Garry and me wrote in demanding it be retracted – we'll see how that goes...

Cheers,

Peter

**Peter Daszak**  
*President*

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

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

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**From:** Morens, David (NIH/NIAID) [E] (b)(6)  
**Sent:** Monday, July 26, 2021 5:39 PM  
**To:** Peter Daszak (b)(6) (b)(6); Keusch, Jerry (b)(6) (b)(6)  
**Subject:** FW: Physician-Scientist Steven Quay: Forensic examination of Wuhan Institute of Virology COVID-19 patient specimens from December 2019 reveals extensive laboratory contamination, including evidence of genetic manipulation of the Nipah Viru




David

**David M. Morens, M.D.**

CAPT, United States Public Health Service  
Senior Advisor to the Director  
Office of the Director  
National Institute of Allergy and Infectious Diseases  
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**From:** Folkers, Greg (NIH/NIAID) [E] (b)(6)

**Sent:** Monday, July 26, 2021 5:37 PM

**Subject:** Physician-Scientist Steven Quay: Forensic examination of Wuhan Institute of Virology COVID-19 patient specimens from December 2019 reveals extensive laboratory contamination, including evidence of genetic manipulation of the Nipah Virus

# Physician-Scientist Steven Quay: Forensic examination of Wuhan Institute of Virology COVID-19 patient specimens from December 2019 reveals extensive laboratory contamination, including evidence of genetic manipulation of the Nipah Virus, a BSL-4 pathogen more lethal than Ebola

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News provided by

[Dr. Steven Quay](#)

Jul 26, 2021, 09:00 ET

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SEATTLE, July 26, 2021 /PRNewswire/ -- Physician-Scientist Steven Quay and a group of international scientists have published a pre-print, available [here](#), entitled, "CONTAMINATION OR VACCINE RESEARCH? RNA Sequencing data of early COVID-19 patient samples show abnormal presence of vectorized H7N9 hemagglutinin segment." In the paper, a forensic examination of the sequencing data from five COVID-19 bronchial lavage patient specimens reveals that the laboratory at the Wuhan Institute of Virology (WIV) was contaminated with a wide range of viruses, including Nipah virus genes in a cloning vector. Nipah is a BSL-4 pathogen with a lethality of 50% to 92%. A video summary of the paper can be found [here](#).

The highlights of the paper are:

- Five patient specimens were sequenced by the WIV in December 2019 and were part of an early report on SARS-CoV-2 published by Dr. Zhengli Shi and colleagues (Nature 579, 270–273 (2020). This paper has been viewed over one million times, making it one of the most highly read papers on the pandemic virus.
- The most abundant contaminant is an undisclosed H7N9 influenza vaccine, which in one specimen is over six-times as abundant as SARS-CoV-2.
- The Nipah virus gene sequences were found in infectious cloning vectors of the type used for genetic manipulation.
- Nineteen other contaminants, including Japanese Encephalitis virus, HIV, human T-cell leukemia virus, and hepatitis delta virus were found.

"It was surprising to find a menagerie of deadly viruses, strange pathogens, and even honeysuckle, plant genes in patient specimens sequenced at the WIV in December 2019, especially since this patient sequencing data has been publicly available to the entire scientific community inside of the US NIH GenBank database since February 2020," stated Dr. Steven Quay, MD, PhD. "The apparent widespread contamination of the laboratory at the very time the pandemic was just beginning is of course

worrisome. But more important is getting answers to these questions: Why do these patient specimens contain an unreported influenza vaccine? What was the purpose of creating an undisclosed, apparently infectious clone of the deadly Nipah virus? Is this Nipah research part of another gain-of-function research project at the Wuhan Institute of Virology?"

#### **About the Nipah Virus**

Nipah virus, scientific name *Nipah henipavirus*, is a bat-borne virus that causes an infection in humans and other animals, with a high mortality rate. Numerous disease outbreaks caused by Nipah virus have occurred in South and Southeast Asia. Symptoms from infection vary from none to fever, cough, headache, shortness of breath, and confusion. This may worsen into a coma over a day or two, and 50% to 92% of those infected die. Complications can include inflammation of the brain and seizures following recovery. At this time there is no specific treatment for Nipah virus infection nor is there a vaccine..

#### **About Steven Quay, M.D., Ph.D.**

Dr. Steven Quay has over 360 published contributions to medicine and has been cited over 10,500 times, placing him in the top 1% of scientists worldwide. He holds 87 US patents and has invented seven FDA-approved pharmaceuticals which have been prescribed to over 80 million people. He is the author of the best-selling book on surviving the pandemic, Stay Safe: A Physician's Guide to Survive Coronavirus. He is the CEO of Atossa Therapeutics Inc. (Nasdaq: ATOS), a clinical-stage biopharmaceutical company developing novel therapeutics for oncology and infectious diseases. He received his M.D. and Ph.D. from The University of Michigan, was a postdoctoral fellow in the Chemistry Department at MIT with Nobel Laureate H. Gobind Khorana, a resident at the Harvard-MGH Hospital, and spent almost a decade on the faculty of Stanford University School of Medicine. A TEDx talk he delivered on breast cancer prevention has been viewed over 220,000 times. His scientific manuscript entitled, "A Bayesian analysis concludes beyond a reasonable doubt that SARS-CoV-2 is not a natural zoonosis but instead is laboratory derived," has been viewed over 175,000-times. For more information, visit [www.DrQuay.com](http://www.DrQuay.com)

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SOURCE Dr. Steven Quay

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**From:** Peter Daszak  
**Sent:** Tue, 27 Jul 2021 14:23:29 -0400  
**To:** Morens, David (NIH/NIAID) [E]; Keusch, Jerry  
**Subject:** RE: Fox: Biden to visit intelligence community as investigation into COVID-19 origin continues

Another one I hadn't seen – key comment from CIA Director:

Burns, though, admitted it is "possible" that the intelligence community "may never be able to come to a definitive judgment" on the origins of COVID-19, but stressed that it is "not going to be for lack of hard work or effort on this issue to try to uncover as much as we can about what happened."

In other words – Biden successfully kicked the can down the road to the end of summer. Hopefully it'll reduce some of the ardor of the right wing nutjobs who keep pushing this. The fact that publications have now come out showing multiple new viruses in bats related to SARS-CoV-2, evidence of live wild CoV reservoir mammals in the markets, a review by eminent virologists, etc. etc. should help, but people aren't actually interested in the truth at this point I expect.

Cheers,

Peter

**Peter Daszak**  
*President*

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

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**From:** Morens, David (NIH/NIAID) [E] (b)(6)  
**Sent:** Tuesday, July 27, 2021 12:05 PM  
**To:** Peter Daszak (b)(6); (b)(6); Keusch, Jerry

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

**Subject:** FW: Fox: Biden to visit intelligence community as investigation into COVID-19 origin continues

*David*

**David M. Morens, M.D.**

CAPT, United States Public Health Service  
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**From:** Folkers, Greg (NIH/NIAID) [E] (b)(6)

**Sent:** Tuesday, July 27, 2021 11:43 AM

**Subject:** Fox: Biden to visit intelligence community as investigation into COVID-19 origin continues

White House

**Published** 1 hour ago

# Biden to visit intelligence community as investigation into COVID-19 origin continues

## Intel community has less than 30 days before Biden's deadline on COVID-19 investigation



By [Brooke Singman](#) | Fox News

### **China refuses to allow independent probe as COVID origins pressure mount**

Fox News correspondent Rich Edson has the latest on China's accountability on 'Special Report' [President Biden](#) is set to visit the Office of the Director of National Intelligence Tuesday afternoon amid the intelligence community's ongoing investigation into the origins of [COVID-19](#).

The intelligence community is "aggressively" investigating the origins of COVID-19, after the president in May revealed that the U.S. intelligence community had "coalesced around two likely scenarios" for the origins of COVID-19, "including whether it emerged from human contact with an infected animal or from a laboratory accident," and asked for "additional follow-up."

### **INTEL COMMUNITY 'AGGRESSIVELY' INVESTIGATING ORIGINS OF COVID-19**

The president asked the intelligence community to "redouble their efforts to collect and analyze information that could bring us closer to a definitive conclusion, and to report back to me in 90 days," Biden said.

It has been 62 days since Biden's announcement.

Last week during an interview with [NPR](#), CIA Director Bill Burns said the intel community at this point "cannot offer a definitive conclusion about whether this originated in a lab accident or whether it originated in a natural transmission from infected animals to human beings."

"We are working very hard on this," Burns [said](#). "It's not an academic problem. I mean, this affects not only the hundreds of thousands and millions of people around the world who have been affected by

this, but it's also absolutely essential as we think ahead, not just to the United States, but in other parts of the world – about how do you prevent another pandemic crisis of this magnitude."

Burns said it is "extremely important to get to the bottom of this."

**CHINA REFUSAL TO SUPPORT WHO COVID ORIGINS PROBE ACCELERATED BIDEN ANNOUNCEMENT ON US INVESTIGATION: OFFICIAL**

"And the two realities are that the Chinese government has not been transparent, has not fully cooperated in the WHO's investigation initially — and it's more recently suggested it's going to refuse to cooperate in a follow up as well," Burns said. "And that is deeply unfortunate."



Video

He added: "We will continue to do everything we can to collect on this, work with the rest of the intelligence community and provide the best answers we can on this."

Burns, though, admitted it is "possible" that the intelligence community "may never be able to come to a definitive judgment" on the origins of COVID-19, but stressed that it is "not going to be for lack of hard work or effort on this issue to try to uncover as much as we can about what happened."

**BIDEN: INTEL COMMUNITY TORN BETWEEN 'TWO LIKELY SCENARIOS' ON COVID-19 OUTBREAK SOURCE**

Meanwhile, the president is set to address the intelligence community workforce and its leadership during his visit to thank them for their work in what the White House described as a "challenging time" for the community during the Trump administration.

"He's someone who believes in the role of the intelligence community of civil servants," White House press secretary Jen Psaki said Monday in previewing the president's visit. "He believes they are the backbone of our government, and certainly he'll make that clear."

Psaki was asked whether Biden would have a different or contrasting message compared to his predecessor, former President Trump, who was skeptical of the intelligence community throughout his administration due to the investigation into whether his campaign colluded with the Russians to influence the 2016 presidential election, and the subsequent investigation into the origins of that probe and whether it began improperly.



Psaki on Monday replied, saying reporters can "make the inherent contrast" but said she did not believe that would be a "central part of his message" during Biden's visit to ODNI.

Brooke Singman is a Politics Reporter for Fox News. Follow her on Twitter at [@BrookeSingman](#).

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**From:** (b)(6)  
**Sent:** Mon, 23 Aug 2021 07:36:19 -0400  
**To:** Jason Gale  
**Cc:** (b)(6); (b)(6)  
(b)(6); Garry, Robert F; (b)(6)  
**Bcc:** Morens, David (NIH/NIAID) [E]  
**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,.. d

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

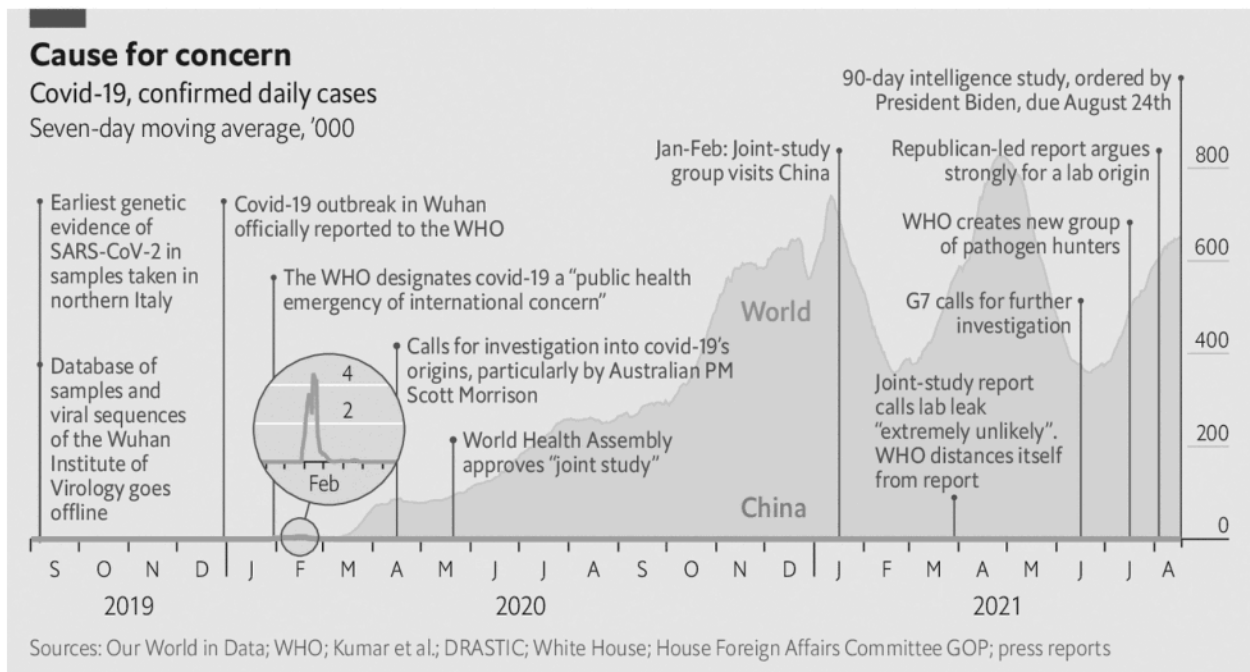
who's decision-making body, passed a motion calling for a study into the origins of the pandemic. But in order to be acceptable to China—which had reacted furiously to Mr Morrison's original suggestion—the work was set up as a joint research project between two teams of scientists, one Chinese, one international. 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.



#### The Economist

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: (b)(6) 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.com/international/2021/08/19/the-world-needs-a-proper-investigation-into-how-covid-19-started?frsc=dg%7Ce>

**From:** EcoHealth Alliance  
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**Subject:** Join EcoHealth Alliance at the Cosmos Club

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**From:** Peter Daszak  
**Sent:** Wed, 11 Aug 2021 15:36:50 -0400  
**To:** Morens, David (NIH/NIAID) [E]; Keusch, Jerry; Robert Kessler  
**Subject:** RE: WaPo: Chinese state media has seized on a Swiss scientist critical of a covid origins probe. The one problem: He might not exist.

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

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

Cheers,

Peter

**Peter Daszak**  
*President*

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

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**From:** Morens, David (NIH/NIAID) [E] (b)(6)  
**Sent:** Wednesday, August 11, 2021 2:28 PM  
**To:** Peter Daszak ((b)(6)); (b)(6); Keusch, Jerry ((b)(6)); Kessler, Robert ((b)(6))  
(b)(6)  
**Subject:** FW: WaPo: Chinese state media has seized on a Swiss scientist critical of a covid origins probe. The one problem: He might not exist.


David

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

**Sent:** Tuesday, August 10, 2021 4:07 PM

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

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

By [Adam Taylor](#)

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

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

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

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

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

The dispute over the supposed Swiss biologist and his prominence in Chinese state media came amid continuing disputes about the origin of the coronavirus and a renewed push for the WHO to investigate further. More than a year and a half since the virus was first detected

in Wuhan, China, before going on to kill millions around the world, the exact path it took remains unclear.

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

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

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

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

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

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

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

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



By Adam Taylor

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

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**Sent:** Mon, 9 Aug 2021 11:45:07 -0400  
**To:** Morens, David (NIH/NIAID) [E]; Keusch, Jerry  
**Subject:** RE: Xinhua: French biosecurity expert dismisses Wuhan "lab leak" theory

Good to see that – if only because it adds to the ‘drip, drip’ of credible articles refuting the lab leak theory..

Cheers,

Peter

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**Sent:** Monday, August 9, 2021 11:13 AM  
**To:** Peter Daszak (b)(6); (b)(6); Keusch, Jerry  
(b)(6); (b)(6)  
**Subject:** FW: Xinhua: French biosecurity expert dismisses Wuhan "lab leak" theory


*David*

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

**Sent:** Friday, August 6, 2021 7:10 AM

**Subject:** Xinhua: French biosecurity expert dismisses Wuhan "lab leak" theory

## French biosecurity expert dismisses Wuhan "lab leak" theory

1

2021-08-04 18:50:01Xinhua Editor : Zhang Dongfang [ECNS App Download](#)

**Special: Battle Against Novel Coronavirus**

"The theory that the virus escaped from the Wuhan lab is not credible," a French biosecurity expert who had monitored the construction of the Biosafety level 4 (BSL-4) laboratory of the Wuhan Institute of Virology has said recently in reference to COVID-19.

The lab "was built under the close cooperation between China and France," and "there is no doubt about its compliance with the highest international biosafety standards," Gabriel Gras said.



"I am not speculating, I prefer to rely on facts," said Gras in an interview on Sunday amid growing speculation about a possible laboratory accident that could have triggered the COVID-19 pandemic. During his stay in China, Gras participated in implementing the 2004 Sino-French Cooperation Agreement in Prevention and Control of Emerging Infectious Diseases, and supervised the construction and accreditation of the Wuhan Institute of Virology's BSL-4 laboratory in 2017.

The construction and operation of the Wuhan lab conform to very strict standards, he said. "It was my job to check all of this, and there was no doubt about the level of safety of the facility."

Gras also noted that coronaviruses, including the SARS-CoV-2 virus, "doesn't need to be dealt with in a BSL-4 lab" considering the high cost of operating a BSL-4 lab.

Biosafety levels, which are a set of biocontainment precautions required to isolate dangerous biological agents in an enclosed laboratory facility, range from the lowest BSL-1 to the highest BSL-4. A BSL-4 laboratory works with the most dangerous agents that can generate fatal diseases in humans such as Ebola hemorrhagic fever.

"It is very expensive to operate a BSL-4 lab, in money but also in time, since the experiments take longer to set up due to safety constraints such as wearing a high-pressure diving suit," Gras explained, saying that it's "just common sense" that they don't work in BSL-4 labs with BSL-3 pathogens any more than they do in BSL-3 labs with BSL-2 pathogens.

Coronaviruses are mostly classed at BSL-2, sometimes at BSL-3, such as SARS-CoV of 2002, MERS-CoV of 2012, and finally SARS-CoV-2 of 2019, but never at 4, Gras said.

The classifications of pathogens and guidelines on the conditions of their culture are public and available online, and have been established by the World Health Organization and relevant national authorities.

"Using a BSL-4 to work with a coronavirus is like using a 20-ton crane to move a 30-kg refrigerator. It would be completely illogical," said the French expert, adding that "the theory of leak of the SARS-CoV-2 virus from the Wuhan BSL-4 lab is against common sense."

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**From:** EcoHealth Alliance  
**Sent:** Wed, 24 Nov 2021 14:59:56 +0000  
**To:** Morens, David (NIH/NIAID) [E]  
**Subject:** Thank you!

## This year has just flown by!



We recently met this brown long-eared bat (*Plecotus auritus*) during some work in Armenia. Our scientists are getting back out into the field to help protect animals like this one and the environments they depend on from the emergence of disease.

EcoHealth Alliance scientists have resumed field work in many countries around the world and that is thanks to your support. We know the last couple years have been hard and we hope that you and yours are well. COVID-19 has strengthened our resolve and our dedication to our mission: to develop solutions that prevent pandemics and promote conservation.

Pandemics do not have to be a reality of life on Earth and it is with you in mind that we seek better knowledge of where they come from and how we can stop them.



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**To:** Peter Daszak ((b)(6)); Keusch, Jerry ((b)(6));  
Taubenberger, Jeffery (NIH/NIAID) [E] ((b)(6)); Jason Gale (BLOOMBERG/  
NEWSROOM:); Eddie Holmes ((b)(6)); Kessler, Robert  
((b)(6)); Wang Linfa  
**Subject:** FW: House report on Origins  
**Attachments:** ORIGINS-OF-COVID-19-REPORT (1).pdf


*David*

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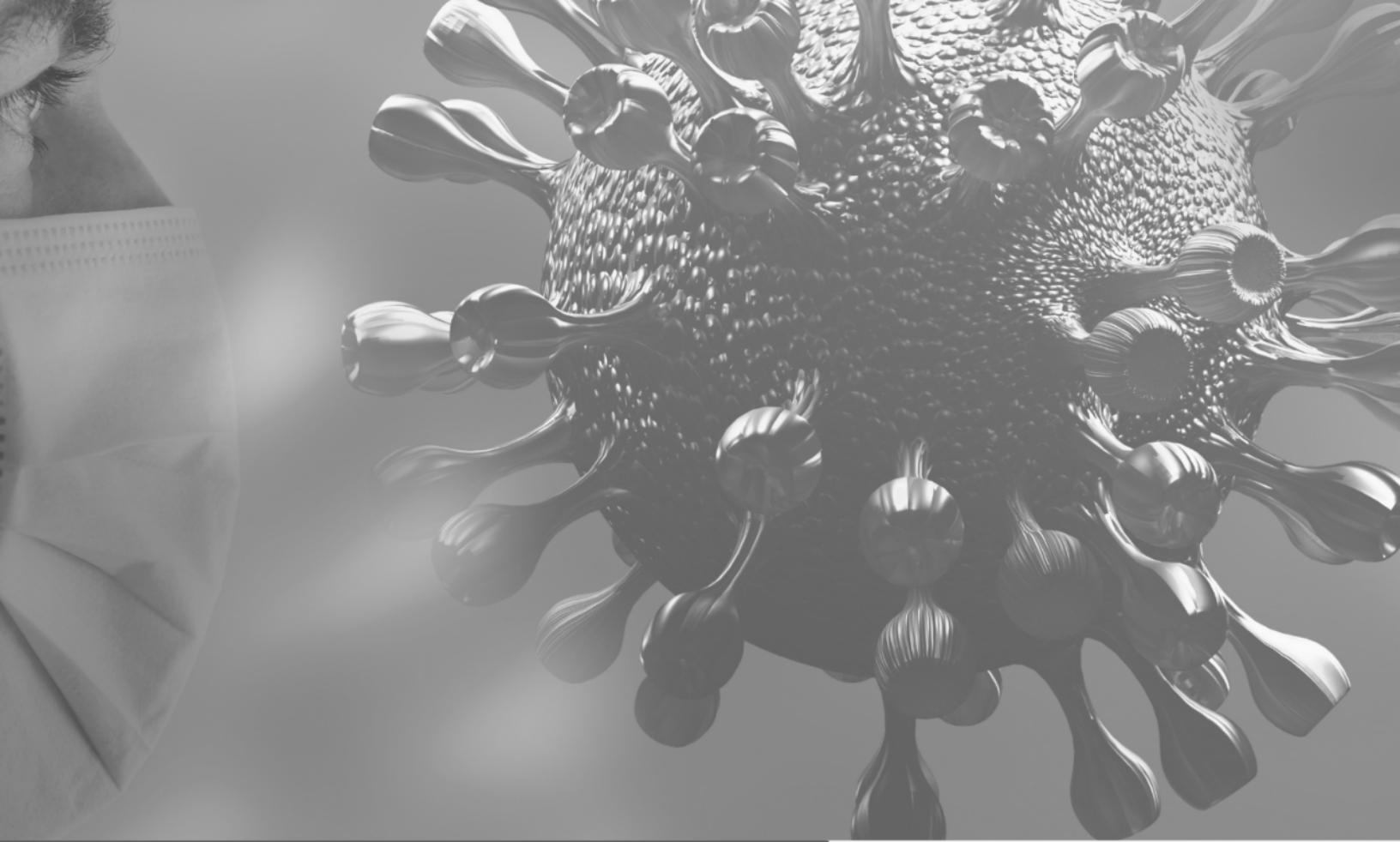
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**From:** Embry, Alan (NIH/NIAID) [E] (b)(6)  
**Sent:** Monday, August 2, 2021 11:19 AM  
**To:** NIAID OD AM <NIAIDODAM@niaid.nih.gov>  
**Subject:** House report on Origins



AUGUST 2021

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# THE ORIGINS OF COVID-19:

AN INVESTIGATION OF THE  
WUHAN INSTITUTE OF  
VIROLOGY

NIH-57707-001164

HOUSE FOREIGN AFFAIRS COMMITTEE  
REPORT MINORITY STAFF

---

LEAD REPUBLICAN MICHAEL T. MCCAUL

---

ONE HUNDRED SEVENTEENTH CONGRESS



# TABLE OF CONTENTS

## INTRODUCTION TO ADDENDUM TO THE FINAL REPORT

### EXECUTIVE SUMMARY

### GLOSSARY OF TERMS

### KEY PEOPLE

## ADDENDUM TO THE FINAL REPORT

<b>I. The City of Wuhan: Epicenter of a Pandemic.....</b>	<b>13</b>
<b>II. Evidence of a Lab Leak.....</b>	<b>14</b>
<b>III. Evidence of Genetic Modification.....</b>	<b>29</b>
<b>IV. Evidence of a Lab Leak Cover-Up .....</b>	<b>41</b>
<b>V. Hypothesis: A Lab Leak That Caused a Pandemic.....</b>	<b>58</b>
<b>VI. Recommendations.....</b>	<b>60</b>
<b>VII. Conclusion.....</b>	<b>62</b>
<b>VIII. Appendix.....</b>	<b>63</b>
Timeline of the WIV Lab Leak and the Start of the COVID-19 Pandemic.....	63
China Center for Disease and Control Memo on Supplementary Regulations.....	67
JPCM Confidential Notice on the Standardization of the Management of Publication of Novel Coronavirus Pneumonia Scientific Research.....	72
February 6, 2020, Email at 12:43am from Peter Daszak to Ralph Baric, Linfa Wang, and Others Inviting Them to Sign the Statement.....	78
February 6, 2020, Email at 3:16pm from Peter Daszak to Ralph Baric Relaying Wang’s Request Not to Sign the Statement.....	82
February 8, 2020, Email at 8:52pm from Peter Daszak to Rita Colwell Alleging WIV Researchers Requested the Statement.....	83

# INTRODUCTION

Five hundred and four days ago, on March 16, 2020, Committee Minority Staff began its investigation into the origins of SARS-CoV-2 and the COVID-19 global pandemic at the direction of Ranking Member Michael T. McCaul. The House Foreign Affairs Committee Minority Staff Final Report on The Origins of the COVID-19 Global Pandemic, Including the Roles of the Chinese Communist Party and the World Health Organization was published in late September 2020. At the time of its release, there were an estimated 30.8 million cases of COVID-19 around the world, and a death toll of approximately 958,000. Today, the cumulative count stands at more than 196.4 million cases and 4,194,061 dead.

The House Foreign Affairs Committee Minority Staff has continued to investigate the origins of COVID-19, examining new information as it became available, including through expert testimony. We have done so because approximately 48 million of our population are under the age of 12 and without access to a vaccination, while others remain unvaccinated due to underlying medical conditions, leaving a large portion of American citizens at risk of infection. We prepared this addendum as reports increase regarding various strains around the globe, and as PRC authorities continue to withhold critical information about the early months of the pandemic. We have strongly urged our Majority colleagues to take this investigation seriously and conduct a full bipartisan investigation into the origins of COVID-19, and will continue to do so. President Biden has said he wants to discover how the pandemic began, and it is our duty to the American people to use all the tools in our arsenal in pursuit of that goal. As always, we stand ready to address this and other foreign policy challenges together and in a bipartisan manner. We must not let up on pressing General Secretary Xi and CCP authorities for answers.

Here we share the result of these efforts in an addendum to our September 2020 Final Report. In particular, this update focuses on whether the virus may have leaked from a medical research laboratory in Wuhan, Hubei Province, PRC, and the efforts to conceal such a leak. The evidence used to inform this report is based upon open source information and includes published academic work, official PRC publications (both public and confidential), interviews, emails, and social media postings.

Since the publication of the September 21, 2020 Final Report new questions have been raised pertaining to the origins of COVID-19. The PRC's continued lack of transparency resulted in President Joseph R. Biden, Jr.'s May 26, 2021, order to the United States Intelligence Community to prepare a report in 90 days on the origins of COVID-19, "including whether it emerged from human contact with an infected animal or from a laboratory accident."<sup>1</sup>

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<sup>1</sup>"Statement by President Joe Biden on the Investigation into the Origins of COVID-19." The White House, 26 May 2021, [www.whitehouse.gov/briefing-room/statements-releases/2021/05/26/statement-by-president-joe-biden-on-the-investigation-into-the-origins-of-covid-19/](https://www.whitehouse.gov/briefing-room/statements-releases/2021/05/26/statement-by-president-joe-biden-on-the-investigation-into-the-origins-of-covid-19/).



# INTRODUCTION



Based on the material collected and analyzed by the Committee Minority Staff, the preponderance of evidence suggests SARS-CoV-2 was accidentally released from a Wuhan Institute of Virology laboratory sometime prior to September 12, 2019. The virus, or the viral sequence that was genetically manipulated, was likely collected in a cave in Yunnan province, PRC, between 2012 and 2015. Researchers at the WIV, officials within the CCP, and potentially American citizens directly engaged in efforts to obfuscate information related to the origins of the virus and to suppress public debate of a possible lab leak. It is incumbent on these parties to respond to the issues raised herein and provide clarity and any exonerating evidence as soon as possible. Until that time, it must be assumed General Secretary Xi and the Chinese Communist Party, prioritizes preserving the Party over the lives of its own people and those around the global suffering the effects of the COVID-19 pandemic.

# EXECUTIVE SUMMARY

More than one year after the World Health Organization declared a pandemic, the world is still reeling from the emergence of the SARS-CoV-2 virus and the disease it causes, COVID-19. More than four million people have lost their lives worldwide, including more than 612,000 Americans, while economies around the world have been devastated by the fallout. This report investigates the origin of this virus and looks at how it became a deadly pandemic.

## **The Wuhan Institute of Virology**

Last September, the House Foreign Affairs Committee Minority Staff, under the direction of Ranking Member Michael T. McCaul, released a report on the origins of the COVID-19 pandemic. That report highlighted the possibility SARS-CoV-2 could have leaked from the Wuhan Institute of Virology (WIV). However, as we continued our investigation and uncovered more information, we now believe it's time to completely dismiss the wet market as the source of the outbreak. 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.

This is based upon multiple pieces of evidence laid out in the report, including:

- The sudden removal of the WIV's virus and sample database in the middle of the night on September 12, 2019 and without explanation;
- Safety concerns expressed by top PRC scientists in 2019 and unusually scheduled maintenance at the WIV;
- Athletes at the Military World Games held in Wuhan in October 2019 who became sick with symptoms similar to COVID-19 both while in Wuhan and also shortly after returning to their home countries;
- Satellite imagery of Wuhan in September and October 2019 that showed a significant uptick in the number of people at local hospitals surrounding the WIV's headquarters, coupled with an unusually high number of patients with symptoms similar to COVID-19;
- The installation of a People's Liberation Army's bioweapons expert as the head of the WIV's Biosafety Level 4 lab (BSL-4), possibly as early as late 2019; and
- Actions by the Chinese Communist Party and scientists working at or affiliated with the WIV to hide or coverup the type of research being conducted at there.

# EXECUTIVE SUMMARY

## Genetic Modification

This report also lays out ample evidence that researchers at the WIV, in conjunction with U.S. scientists and funded by both the PRC government and the U.S. government, were conducting gain-of-function research on coronaviruses at the WIV, at times under BSL-2 conditions. Much of this research was focused on modifying the spike protein of coronaviruses that could not infect humans so they could bind to human immune systems. The stated purpose of this work was to identify viruses with pandemic potential and to create a broad-spectrum coronavirus vaccine. In many instances, the scientists were successful in creating “chimeric viruses” – or viruses created from the pieces of other viruses – that could infect human immune systems. With dangerous research like this conducted at safety levels similar to a dentist’s office, a natural or genetically modified virus could have easily escaped the lab and infected the community.

Committee Minority Staff has also identified scientists who are directly tied to the WIV, and who worked on gain-of-function research in the years prior to the start of the current pandemic, who had the ability to genetically modify coronaviruses without leaving any trace evidence. An American scientist, Dr. Ralph Baric, assisted in creating a method to leave no trace of genetic modification as early as 2005. And as early as 2016, scientists working at the WIV were able to do the same. This makes it clear that claims by the scientific community that SARS-CoV-2 could not be man-made because it has no genetic modification markers are disingenuous.

We conclude there is ample proof that the virus could have been genetically manipulated, and that it is vitally important we fully investigate this hypothesis to determine if that happened here.

## The Cover-Up

In the original report, we laid out many of the ways the Chinese Communist Party (CCP) and the World Health Organization (WHO) went to great lengths to cover up the initial epidemic, and how their cover-up likely turned what could have been a local outbreak into a global pandemic. The CCP detained doctors in order to silence them, and disappeared journalists who attempted to expose the truth. They destroyed lab samples, and hid the fact there was clear evidence of human-to-human transmission. And they still refuse to allow a real investigation into the origins. At the same time, the WHO, under Director General Tedros, failed to warn the world of the impending pandemic. Instead, he parroted CCP talking points, acting as a puppet of General Secretary Xi.

In this addendum, we have uncovered further evidence of how top scientists at the WIV and Dr. Peter Dazsak, an American scientist, furthered that cover-up. Their actions include bullying other scientists who questioned whether the virus could have leaked from a lab; misleading the world about how a virus can be modified without leaving a trace; and, in many, instances directly lying about the nature of the research they were conducting, as well as the low-level safety protocols they were using for that research.

These actions not only delayed an initial investigation into the possibility of a lab leak costing valuable time, but provide further proof the virus likely leaked from the WIV. These actions also call into question the way in which U.S. government grants are used in overseas labs and call for more oversight of those grants.

# EXECUTIVE SUMMARY

## Next Steps

After this extensive investigation, we believe it is time to call Peter Daszak to testify before Congress. There are still many outstanding questions about the type of research he funded at the WIV that only he can answer. In addition, we believe there is legislation Congress can pass that would not only hold those responsible accountable but also help to prevent a future pandemic, including but not limited to:

- Institute a ban on conducting and funding any work that includes gain-of-function research until an international and legally binding standard is set, and only where that standard is verifiably being followed.
- Sanction the Chinese Academy of Sciences and affiliated entities.
- List the Wuhan Institute of Virology and its leadership on the Specially Designated Nationals and Blocked Persons List and apply additional, appropriate secondary sanctions.
- Authorize new sanctions for academic, governmental, and military bioresearch facilities that fail to ensure the appropriate levels of safety and information sharing.

# GLOSSARY OF TERMS

Gain-of-Function Research	“Research that improves the ability of a pathogen to cause disease.” – U.S. Department of Health and Human Services
Spike Protein	A protein structure on the surface of an enveloped virus responsible for anchoring the virus to the host cell’s surface and enabling the injection of the virus’ genetic material into the host cell.
RBD	Receptor-Binding Domain. The specific short fragment in a spike protein of a virus that binds the virus to a specific receptor on the host cell.
Primary Author	The first listed author of an academic paper, usually the person who contributes the most to a paper.
Corresponding Author	The point of contact for editors and outside readers who have questions about an academic paper.
USAID Predict	An epidemiological research grant program funded by the United States Agency for International Development. PREDICT provided funding for biological sampling aimed at virus identification and collection. The program provided grant funding to EcoHealth Alliance.
SARS	Severe Acute Respiratory Syndrome. A viral respiratory disease caused by SARS-CoV, a betacoronavirus. First identified as the cause of a 2002-2003 epidemic.
MERS	Middle East Respiratory Syndrome. A viral respiratory disease caused by MERS-CoV, a betacoronavirus. First identified as the cause of a 2012 outbreak.
SARS-CoV-2	The betacoronavirus that causes COVID-19.
Coronavirus	An RNA virus that causes disease in mammals and birds. Range in severity from the common cold to SARS-CoV-2.
Betacoronavirus	One of the four subclassifications of coronaviruses. Found in bats and rodents, this is the genus includes SARS, MERS, and SARS-CoV-2.
Biosafety Level 1 (BSL1)	Designed for work on microbes not known to cause disease in healthy adults and present minimal potential hazard to laboratorians and the environment. Work can be performed on an open bench or table.

# GLOSSARY OF TERMS

<p>Biosafety Level 2 (BSL2)</p>	<p>For work with microbes that pose moderate hazards to laboratorians and the environment. The microbes are typically indigenous and associated with diseases of varying severity. Personal protective equipment includes lab coats and gloves. Work can be performed in the open or in a biological safety cabinet. Commonly compared to the level of safety observed in a dentist’s office.</p>
<p>Bio Safety Level 3 (BSL3)</p>	<p>For work with microbes that are either indigenous or exotic, and that can cause serious or potentially lethal disease through respiratory transmission. Respiratory transmission is the inhalation route of exposure. Researchers should be under medical surveillance and potentially immunized for the microbes they work with. Respirators may be required, in addition to standard personal protective equipment. Work must be performed within a biological safety cabinet. Exhaust air cannot be recirculated, and the laboratory must have sustained directional airflow by drawing air into the laboratory from clean areas towards potentially contaminated areas.</p>
<p>Biosafety Level 4 (BSL4)</p>	<p>This is the highest level of biological safety. The microbes in a BSL-4 lab are dangerous and exotic, posing a high risk of aerosol-transmitted infections. Infections caused by these microbes are frequently fatal and without treatment or vaccines. Researchers must change clothing prior to entering the lab, shower upon exiting, and decontaminate all materials before exiting. All work with microbes must be performed in a Class III biological safety cabinet or while wearing a full body, air-supplied, positive pressure suit. The lab must be in a separate building or in a restricted zone, and must have a dedicated supply and exhaust air, as well as vacuum lines and decontamination systems.</p>
<p>Wuhan Institute of Virology (WIV)</p>	<p>A research institute in Wuhan, PRC focused on focused on virology, that consists of at least two facilities – the Wuhan National Biosafety Laboratory and the Wuhan Institute of Virology Headquarters.”</p>

# GLOSSARY OF TERMS

Wuhan National Biosafety Laboratory	The WIV's new campus, located in the Zhengdian Scientific Park in Jiangxia District, Wuhan. The location of the WIV's Biosafety Level 4 laboratory space.
WIV Headquarters	The older WIV facility, located in Wuchang District, Wuhan near the Wuhan Branch of the Chinese Academies of Science.
Chinese Academy of Sciences	The national academy for natural sciences in the PRC. Reports to the State Council of the People's Republic of China.
WIV1	The first novel coronavirus isolated by WIV researchers. Isolated from bat fecal samples in 2013. A SARS like coronavirus.
WIV16	The second coronavirus isolated by WIV researchers. Isolated from a single bat fecal sample in 2016. A SARS like coronavirus.
Rs4874	The third coronavirus isolated by WIV researchers. Isolated from a single bat fecal sample in 2017. A SARS like coronavirus.
ID4491/RaTG13	A SARS like coronavirus collected in 2013 in a mining cave. 96.1% similar to SARS-CoV-2.
ACE2	Angiotensin-converting enzyme-2, found on the surface of certain cells in a variety of animals, including humans, mice, and civets. The entry point for coronaviruses.
hACE2	The human version of ACE2. Primarily found on the surface of cells and tissues throughout the human body, including the nose, mouth, and lungs. In the lungs, hACE2 is highly abundant on type 2 pneumocytes, an important cell type present in chambers within the lung called alveoli, where oxygen is absorbed, and waste carbon dioxide is released. The primary entry point for SARS-CoV-2 into human cells.
Chimeric Virus	An artificial, man-made virus. Created by joining two or more viral fragments.
Natural Virus	A virus found in nature; "wild type."

# GLOSSARY OF TERMS

Reverse Genetics System	A method in molecular genetics that is used to help understand the function(s) of a gene by analyzing the phenotypic effects caused by genetically engineering specific nucleic acid sequences within the gene. Can be used to create chimeric viruses indistinguishable from natural viruses.
Furin Cleavage Site	An enzyme in the spike protein of SARS-CoV-2 that increases how infectious the virus is in humans. SARS-CoV-2 is the only betacoronavirus to have this structure.
Phylogenetic Analysis	The study of the evolutionary development of a species or a group of organisms or a particular characteristic of an organism. Used to identify the relationship between different viruses in the same family.
CGG Double Codon	“CGG-CGG.” This group of six nucleotides (a group of three nucleotides is also known as a codon) is half of the 12 nucleotides that create the furin cleavage site. The CGG double codon is relatively rare in coronaviruses, and SARS-CoV-2 is the only coronavirus in its family to have one.



# KEY PEOPLE

Dr. Wang Yanyi	Director General of the Wuhan Institute of Virology.
Dr. Yuan Zhiming	Director of the WNBL BSL-4 lab. General Secretary of the Chinese Communist Party Committee within the Wuhan Branch of the Chinese Academy of Sciences, to which the WIV belongs.
Dr. Shi Zheng-li	Senior scientist at the Wuhan Institute of Virology (WIV). Serves as Director, Research Center for Emerging Infectious Diseases; Director, Chinese Academy of Sciences Key Laboratory of Special Pathogens; Director, Biosafety Working Committee; and Deputy Director of the Wuhan National Biosafety Laboratory's Biosafety-Level 4 lab.
Dr. Ben Hu	WIV researcher and former doctoral student of Shi Zheng-li. Deeply involved in the WIV's coronavirus research.
Dr. Linfa Wang	PRC national, Director and Professor of the Program in Emerging Infectious Diseases at the Duke-NUS Graduate Medical School in Singapore. Chair of the Scientific Advisory Board for the Center for Emerging Diseases at the WIV.
Dr. Peter Daszak	CEO of EcoHealth Alliance. Longtime collaborator of Shi and others at the WIV. Provided subgrants to the WIV to help fund coronavirus research.
Dr. Ralph Baric	Researcher at the University of North Carolina at Chapel Hill who has collaborated with Shi and other WIV researchers on coronavirus research.

# ADDENDUM TO THE REPORT

## I. THE CITY OF WUHAN: EPICENTER OF A PANDEMIC

Wuhan is the epicenter of the coronavirus pandemic. Located in central PRC where the Yangtze River, the PRC's longest river, and the Han River meet, Wuhan is the capital city of Hubei Province and boasts a population of about 11.1 million in about 3,280 square miles.<sup>2</sup> It is home to the PRC's tallest skyscrapers, multiple colleges and universities, including the prominent Wuhan University, major historical and cultural sites, and an influential research laboratory, the Wuhan Institute of Virology (WIV). To put the scale of Wuhan in perspective, the city covers an area five times the size of Houston and has a larger population than New York City and Chicago combined.

Wuhan is home to the Hankou railway station, central PRC's biggest European-style Railway station, and two other major train stations. Hankou Station connects directly to the Tianhe International Airport, the busiest airport in central PRC and the geographic center of the PRC's airport network. From the Tianhe airport, travelers can fly direct to New York City, San Francisco, Paris, Milan, Rome, Hamburg, Bangkok, Tokyo, Seoul, and Dubai, among many other destinations around the world.

The PRC calls Wuhan one of its nine "National Central Cities," an official state label that means it leads the way, along with the capital Beijing, Shanghai, and other major cities, in developing culture, politics, and the economy.<sup>3</sup> An August 2016 report by the Netherlands Enterprise Agency, a government agency that operates under the auspices of the Ministry of Economic Affairs and Climate Policy, identified Wuhan as a major hub not just within the PRC, but also globally within the Chinese "One Belt One Road" initiative due to its accessibility.<sup>4</sup> The city is also home to significant railway commerce. A 2018 report from Xinhua news expected an estimated 500 freight trains from Wuhan to Europe for the export of goods.<sup>5</sup>

France, the U.S., the Republic of Korea, and the UK maintain Consulates in the city, which was selected to host the 7th International Military Sports Council (CISM) Military World Games. During the games, more than 9,000 military personnel from over 100 countries stayed in Wuhan in accommodations at an athletes' village built specifically for the games.

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2 "WHO-convened Global Study of Origins of SARS-CoV-2: China Part." Joint WHO-China Study. 30 March 2021, <https://www.who.int/health-topics/coronavirus/origins-of-the-virus>

3 Xu, Zongwei. "China Unveils National Central City Strategy." *China Watch*, 29 Mar. 2018, [www.chinawatch.cn/a/201803/29/WS5ad061d6a310cc9200067c6c.html](http://www.chinawatch.cn/a/201803/29/WS5ad061d6a310cc9200067c6c.html).

4 Van de Bovenkamp, Judith and Yuan Fei. "Economic Overview of Hubei Province." *Netherlands Business Support Office Wuhan*, Aug. 2016, <https://www.rvo.nl/sites/default/files/2016/08/Economic-overview-Hubei-province-China.pdf>

5 "Central China-Europe Rail Freight to Surge in 2018." *Xinhua*, 1 Feb. 2018. [http://www.china.org.cn/china/Off\\_the\\_Wire/2018-02/01/content\\_50372222.htm](http://www.china.org.cn/china/Off_the_Wire/2018-02/01/content_50372222.htm)

## II. EVIDENCE OF A LAB LEAK

As discussed in the previously issued report, the WIV continues to be a focal point of debate concerning the origins of SARS-CoV-2 and the COVID-19 pandemic. In recent months, new information about the WIV has come to light, enabling us to better understand the institute, the type of research conducted by scientists working there, and its ties to the CCP and their military, the People's Liberation Army (PLA). We now believe the preponderance of evidence shows the virus accidentally leaked from one of the WIV's facilities.

### The Wuhan Institute of Virology

The WIV was founded in 1956 as the Wuhan Microbiology Laboratory and has operated under the administration of the Chinese Academy of Sciences since 1978.<sup>6</sup> The institute currently occupies at least two campuses – the much-discussed Wuhan National Biosafety Laboratory (WNBL) in Zhengdian Scientific Park (see Figure 1), and the older facility (hereafter WIV Headquarters) located in the Xiaohongshan park in the Wuchang District of Wuhan (see Figure 2). The WNBL is a large complex with multiple buildings that house 20 Biosafety Level II (BSL-2) laboratories, two Biosafety Level III (BSL-3) laboratories, and 3000 square meters of Biosafety Level IV (BSL-4) space, “including four independent laboratories areas and two animal suites.”<sup>7</sup> Construction was completed in 2015, but due to delays the BSL-4 space did not become operational until early 2018.<sup>8</sup>



Fig. 1: Wuhan National Biosafety Laboratory (WNBL)

Missing from the majority of public debates regarding the WIV is the research conducted at the WIV Headquarters, the older location in the Wuchang District of Wuhan. Located 12 miles northeast of the WNBL, in the Wuchang District, this facility remains the administrative headquarters of the WIV. In addition to the BSL-2 labs at this location, the WIV constructed a BSL-3 laboratory at the facility in 2003.<sup>9</sup>

<sup>6</sup> “History.” *Wuhan Institute of Virology*, [http://english.whiov.cas.cn/About\\_Us2016/History2016/](http://english.whiov.cas.cn/About_Us2016/History2016/).

<sup>7</sup> World Health Organization. “WHO Consultative Meeting on High/Maximum Containment (Biosafety Level 4) Laboratories Networking.” Meeting Report, Lyon, France, 13-15 Dec. 2018, <https://apps.who.int/iris/bitstream/handle/10665/311625/WHO-WHE-CPI-2018.40-eng.pdf>

<sup>8</sup> Zhiming, Yuan. “Current status and future challenges of high-level biosafety laboratories in China.” *Journal of Biosafety and Biosecurity*, 1 Sept. 2019, 1(2): 123-127. <https://doi.org/10.1016/j.jobb.2019.09.005>

<sup>9</sup> Zheng Qianli, “Jiang Xia plays new essays and plays Yoko on the crane——The construction and research team of P4 laboratory of Wuhan Institute of Virology, Chinese Academy of Sciences.” *Chinese Journal of Science*, 1 Jan. 2018, <https://archive.is/V3GHk#selection-517.35-517.202>

It was here, in the center of Wuhan, that Dr. Shi Zheng-li and her team conducted gain-of-function research on coronaviruses in the years leading up to the COVID-19 pandemic.



Fig. 2: WIV Headquarters in Wuchang

According to the WIV's website, Shi Zheng-li serves as the Director of the WIV's Research Center for Emerging Infectious Diseases, the Deputy Director of the WNBL BSL-4 lab, the Director of the BSL-3 lab, and the Director of the Biosafety Working Committee.<sup>10</sup> Shi is also the Director of the Chinese Academy of Sciences (CAS) Key Laboratory of Special Pathogens and Biosafety,<sup>11</sup> which includes the majority of scientists who are conducting gain-of-function research on coronaviruses at the WIV.

It should be noted that the WIV has a Chinese Communist Party Committee within the institute, as well as a Commission for Discipline Inspection. The Party Committee is divided into four party branches, which are then divided into subbranches organized around the individual WIV departments, research centers, and offices. Each subbranch has its own Propaganda Committee. Committee Minority Staff were able to identify eight WIV researchers on these committees, including several who are affiliated with the Key Laboratory that Shi directs.

WIV Researcher	Lab Affiliation	Propaganda Committee <sup>12</sup>
Liu Qiaojiue	Key Laboratory of Special Pathogens and Biosafety <sup>13</sup>	Party Branch of Research Center for Emerging Infectious Diseases
Zhang Xiaowei	Key Laboratory of Special Pathogens and Biosafety and Key Laboratory of Virology <sup>14</sup>	Party Branch of the Research Center for Microbiology and Nanobiology

<sup>10</sup> "Shi Zhingli." Wuhan Institute of Virology, [http://www.whiov.cas.cn/sourcedb\\_whiov\\_cas/zw/rck/200907/t20090718\\_2100074.html](http://www.whiov.cas.cn/sourcedb_whiov_cas/zw/rck/200907/t20090718_2100074.html)

<sup>11</sup> "Prof. SHI Zhengli elected a fellow of the American Academy of Microbiology." *Wuhan Institute of Virology*, [http://english.whiov.cas.cn/ne/201903/t20190308\\_206697.html](http://english.whiov.cas.cn/ne/201903/t20190308_206697.html)

<sup>12</sup> "Party Branch." Wuhan Institute of Virology, <http://www.whiov.cas.cn/djxwh/dqzz/dzb/>

<sup>13</sup> Wang Q, et. al. "Structural Basis for RNA Replication by the SARS-CoV-2 Polymerase." *Cell*, 23 July 2020, 182(2):417-428.e13, <https://pubmed.ncbi.nlm.nih.gov/32526208/>

<sup>14</sup> Zhang, Xiaowei et al. "Tick-borne encephalitis virus induces chemokine RANTES expression via activation of IRF-3 pathway." *Journal of Neuroinflammation*, 30 Aug. 2016, 13(1):209. <https://pubmed.ncbi.nlm.nih.gov/27576490/>

Shen Xurui	Key Laboratory of Special Pathogens and Biosafety <sup>15</sup>	Graduate Party Branch of the Research Center for Emerging Infectious Diseases
Tang Shuang	State Key Laboratory of Virology <sup>16</sup>	Party Branch of the Research Center for Microbial Resources and Bioinformatics
Wu Yan	State Key Laboratory of Virology <sup>17</sup>	Party Branch of Molecular Virus and Pathology Research Center
He Lihong	State Key Laboratory of Virology <sup>18</sup>	Party Branch of the Research Center for Microbial Resources and Bioinformatics
Wang Qingxing	State Key Laboratory of Virology <sup>19</sup>	Graduate Party Branch of the Research Center for Molecular Viruses and Pathology
Yang Mengsi	State Key Laboratory of Virology <sup>20</sup>	Graduate Party Branch of the Research Center of Microbiology and Nanobiology

Table 1: WIV Researchers on CCP Propaganda Committees

The Committee for Discipline Inspection is charged with “the implementation of the party's line, policy, party discipline, relevant laws and regulations, and the institute's rules and regulations.”<sup>21</sup>

In addition to the researchers serving on propaganda committees, other key figures at the WIV also serve as CCP officials. Dr. Wang Yanyi serves as the Director of the WIV and joined the China Zhi Gong Party, a CCP controlled minority party, in 2010. In 2018, the same year she became the Director General of the WIV, she was elected the Deputy Director of the Wuhan Municipal Party Committee.

- 15 Zhou, Peng et al. “A pneumonia outbreak associated with a new coronavirus of probable bat origin.” *Nature* March 2020, 579(7798): 270-273. <https://pubmed.ncbi.nlm.nih.gov/32015507/>
- 16 Abudurexiti, Abulikemu, et al. “Taxonomy of the order Bunyavirales: update 2019.” *Archives of Virology*, July 2019, 164(7): 1949-1965. <https://pubmed.ncbi.nlm.nih.gov/31065850/>
- 17 Su, Hai-Xia et al. “Anti-SARS-CoV-2 activities in vitro of Shuanghuanglian preparations and bioactive ingredients.” *Acta Pharmacologica Sinica*, September 2020, 41(9): 1167-1177. <https://pubmed.ncbi.nlm.nih.gov/32737471/>
- 18 Shao, Wei et al. “Functional Characterization of the Group I Alphabaculovirus Specific Gene ac73.” *Virologica Sinica*, Dec. 2019, 34(6): 701-711. <https://pubmed.ncbi.nlm.nih.gov/31317397/>
- 19 Su, Haixia et al. “Identification of pyrogallol as a warhead in design of covalent inhibitors for the SARS-CoV-2 3CL protease.” *Nature Communications*, 15 June 2021, (2(1): 3623. <https://pubmed.ncbi.nlm.nih.gov/34131140/>
- 20 Zhang, Juan, et. al. “Passive cancer targeting with a viral nanoparticle depends on the stage of tumorigenesis.” *Nanoscale*, 8 July 2021, 13(26):11334-11342, <https://pubmed.ncbi.nlm.nih.gov/34165123/>
- 21 “Commission for Discipline Inspection.” *Wuhan Institute of Virology*. <http://www.whiov.cas.cn/djkw/dqzz/jw/>

Until late 2019, the BSL-4 lab was managed by Dr. Yuan Zhiming. Yuan is the General Secretary of the Chinese Communist Party Committee within the Wuhan Branch of the Chinese Academy of Sciences, to which the WIV belongs. Local CCP leaders not only run the WIV itself but also directly managed the BSL-4 lab.<sup>22</sup>

Director Wang's 2021 New Year's speech makes reference to the Party Committee of Wuhan Institute of Virology, pledging that the party committee will "effectively play the role of a battle fortress of grassroots party organizations."<sup>23</sup> The WNBL also has its own party branch, the Zhengdian Laboratory Party Branch, which was "awarded the title of 'Red Flag Party Branch' by the Hubei Provincial Party Committee and Provincial Organization Working Committee, effectively playing an advanced and exemplary role."<sup>24</sup> Notably, in discussing the COVID-19 pandemic, Director Wang's 2021 speech takes pains to address questions of lab safety – "The institute's high-level biosafety laboratory operates safely for more than 300 days throughout the year."<sup>25</sup> Her 2020 address, posted sometime after April 2020, makes no such mention.

The WNBL's BSL-4 lab was constructed as a result of an agreement between the PRC and France that was signed after the 2003 SARS pandemic.<sup>26</sup> At the time, all BSL-3 labs in the PRC were controlled by the PRC's People's Liberation Army (PLA). Then-President of France, Jacques Chirac, and his Prime Minister, Jean-Pierre Raffarin, approved the project despite concerns from both the French Ministry of Defense and French intelligence services – Raffarin himself described it as "a political agreement."<sup>27</sup> The PRC was suspected of having a biological warfare program, and the military and intelligence services were worried that the dual-use technology required to build a BSL-4 lab could be misused by the PRC government. The uneasy compromise reached within the French government was that the agreement would require joint PRC-France research to be conducted in the lab, with French researchers present.<sup>28</sup>

In 2016, the PRC requested dozens of the containment suits required to work in the lab. The French Dual-Use Commission, tasked with considering exports of sensitive equipment, rejected their request. According to French reporting, the request was "well above the needs of the Wuhan [lab]."<sup>29</sup> **This continued to fuel concerns within the French Ministry of Defense that the PRC was seeking to engage in military research or open a second BSL-4 lab for military means.** Despite the agreement that the BSL-4 lab would be a site of joint research, and an announcement at the 2017 inauguration by then Prime Minister Bernard Cazeneuve of €5 million in funding, there has only been one French scientist assigned to the lab. His tour ended in 2020.<sup>30</sup>

22 Izambard, Antoine. "L'histoire Secrète Du Laboratoire P4 De Wuhan Vendu Par La France à La Chine." *Challenges*, 30 Apr. 2020 [www.challenges.fr/entreprise/sante-et-pharmacie/revelations-l-histoire-secrete-du-laboratoire-p4-de-wuhan-vendu-par-la-france-a-la-chine\\_707425](http://www.challenges.fr/entreprise/sante-et-pharmacie/revelations-l-histoire-secrete-du-laboratoire-p4-de-wuhan-vendu-par-la-france-a-la-chine_707425).

23 "New Year's Speech by the Director in 2021." *Wuhan Institute of Virology*, [http://www.whiov.cas.cn/gkjj/szcc\\_160220/](http://www.whiov.cas.cn/gkjj/szcc_160220/)

24 "New Year's Message from the Director in 2020." *Wuhan Institute of Virology*, [https://web.archive.org/web/20200701032318/http://www.whiov.cas.cn/gkjj/szcc\\_160220/](https://web.archive.org/web/20200701032318/http://www.whiov.cas.cn/gkjj/szcc_160220/)

25 *Ibid.*

26 "About WIV." *Wuhan Institute of Virology*, [http://english.whiov.cas.cn/About\\_Us2016/Brief\\_Introduction2016/](http://english.whiov.cas.cn/About_Us2016/Brief_Introduction2016/).

27 Izambard, Antoine. "L'histoire Secrète Du Laboratoire P4 De Wuhan Vendu Par La France à La Chine." *Challenges*, 30 Apr. 2020, [www.challenges.fr/entreprise/sante-et-pharmacie/revelations-l-histoire-secrete-du-laboratoire-p4-de-wuhan-vendu-par-la-france-a-la-chine\\_707425](http://www.challenges.fr/entreprise/sante-et-pharmacie/revelations-l-histoire-secrete-du-laboratoire-p4-de-wuhan-vendu-par-la-france-a-la-chine_707425).

28 *Ibid.*

29 *Ibid.*

30 Izambard.

### Safety Concerns and Unusual Maintenance

There have been several reports of safety concerns at PRC labs starting as early as 2004, when it was discovered SARS leaked from a lab in Beijing. Several other accidental releases have happened in the years since.

As discussed in our original report released last year, in 2018 U.S. State Department officials sent cables to Washington, D.C. highlighting concerns with safety issues at the WIV. The cables reported that scientists at the WIV noted “a serious shortage of appropriately trained technicians and investigators needed to safely operate this high-containment laboratory.”<sup>31</sup> The cables also questioned the PRC’s commitment to prioritizing the important research for which the lab was designed.

(b)(6) **Thus, while the BSL-4 lab is ostensibly fully accredited, its utilization is limited by lack of access to specific organisms and by opaque government review and approval processes. As long as this situation continues, Beijing’s commitment to prioritizing infectious disease control - on the regional and international level, especially in relation to highly pathogenic viruses, remains in doubt.**

*Fig. 4: Excerpt from January 19, 2018 Cable from the U.S. Embassy in Beijing to State Department Headquarters in Washington, D.C.*

One year later, in June 2019, George Gao, the Director of the Chinese Center for Disease Control and Prevention, expressed concerns about safety protocols at the WIV. In an almost prophetic statement published in *Biosafety and Health*, Gao wrote (emphasis added):

Advances in biomedical technologies, such as genome editing and synthetic biotechnology, have the potential to provide new avenues for biological intervention in human diseases. These advances may also have a positive impact by allowing us to address risks in new approaches. **However, the proliferation of such technologies means they will also be available to the ambitious, careless, inept, and outright malcontents, who may misuse them in ways that endanger our safety.** For example, while CRISPR-related techniques provide revolutionary solutions for targeted cellular genome editing, it can also lead to unexpected off-target mutations within genomes or the possibility of gene drive initiation in humans, animals, insects, and plants. Similarly, genetic modification of pathogens, which may expand host range as well as increase transmission and virulence, may result in new risks for epidemics. For example, in 2013, several groups showed that influenza H5N1 viruses with a few nucleotide mutations and H7N9 isolates reasserted with 2009 pandemic H1N1 virus could have the ability for airborne transmission between ferrets. **Likewise, synthetic bat-origin SARS-like coronaviruses acquired an increased capability to infect human cells. Thus, modifying the genomes of animals (including humans), plants, and microbes (including pathogens) must be highly regulated.**<sup>32</sup>

Three months later, in September 2019, Yuan Zhiming, the Director of the BSL-4 lab at the WNBL and Shi’s superior, published an article in the *Journal of Biosafety and Biosecurity*.

<sup>31</sup> Rogin, Josh. “Opinion | State Department Cables Warned of Safety Issues at Wuhan Lab Studying Bat Coronaviruses.” *The Washington Post*, 14 Apr. 2020, [www.washingtonpost.com/opinions/2020/04/14/state-department-cables-warned-safety-issues-wuhan-lab-studying-bat-coronaviruses/](https://www.washingtonpost.com/opinions/2020/04/14/state-department-cables-warned-safety-issues-wuhan-lab-studying-bat-coronaviruses/).

<sup>32</sup> Gao, George F. “For a better world: Biosafety strategies to protect global health.” *Biosafety and Health*, June 2019, 1(1): 1-3. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7147920/>



33

Entitled, “Current status and future challenges of high-level biosafety laboratories in China,” the article discusses at length the construction of the WNBL. Yuan identifies multiple key issues, including inadequate biosafety management systems, insufficient resources for efficient laboratory operation, and deficiency of professional capacity. With a surprising level of transparency, Yuan admits that the enforcement of pathogen, waste, and laboratory animal management regulations “needs to be strengthened.”<sup>34</sup> Discussing the insufficient level of resources being provided by the PRC government, he stated:

**The maintenance cost is generally neglected; several high-level BSLs have insufficient operational funds for routine yet vital processes. Due to the limited resources, some BSL-3 laboratories run on extremely minimal operational costs or in some cases none at all.**<sup>35</sup>

Yuan also raised concerns about a lack of specialized biosafety managers and engineers to run the labs.<sup>36</sup> It is important to note that researchers at the WIV had previously conducted gain-of-function research on coronaviruses at the BSL-2 and BSL-3 levels. This is important given that both the head of the China CDC and the head of the WIV’s BSL-4 labs had expressed concern about the safety of this research and the labs in which it was being conducted.

Interestingly, there appears to have been ongoing maintenance and repairs projects occurring at the WIV in 2019, before Yuan published his article raising these concerns. It is important to note that at the time of the hazardous waste treatment system renovation project, the WNBL had been operational for less than two years. Such a significant renovation so soon after the facility began operation appears unusual. Procurement announcements published on the PRC’s government procurement website provide evidence of ongoing work at what appears to be both WIV locations.

Project Name	Location	Date	Budget (USD)
Maintenance Project of P3 Laboratory and Laboratory Animal Center in Zhengdian Park <sup>37</sup>	WNBL	March 1, 2019	\$401,284.10
Procurement of Positive Pressure Protective Clothing <sup>38</sup>	WNBL	March 21, 2019	\$177,161.40
Hazardous Waste Treatment System Renovation Project <sup>39</sup>	WNBL	July 31, 2019	\$1,521,279.28

<sup>33</sup>Yuan Zhinming. “Current status and future challenges of high-level biosafety laboratories in China.” *Journal of Biosafety and Biosecurity*, Sept. 2019, 1(2): 123-127. <https://www.sciencedirect.com/science/article/pii/S2588933819300391#b0080>

<sup>34</sup>*Ibid.*

<sup>35</sup>*Ibid.*

<sup>36</sup>*Ibid.*

<sup>37</sup>“Announcement of Competitive Consultation on Maintenance Project of P3 Laboratory and Laboratory Animal Center in Zhengdian Park, Wuhan Institute of Virology, Chinese Academy of Sciences.” *China Government Procurement Network*, 1 March 2019, <https://archive.is/7eCPU#selection-229.0-229.185>

<sup>38</sup>“Announcement of a single source for the purchase of positive pressure protective clothing project by Wuhan Institute of Virology, Chinese Academy of Sciences.” *China Government Procurement Network*, 21 March 2019, <https://archive.is/VUcNA#selection-229.0-229.157>

<sup>39</sup>“Announcement on the transaction of the hazardous waste treatment system renovation project in Zhengdian Park, Wuhan Institute of Virology, Chinese Academy of Sciences.” *China Government Procurement Network*, 31 July 2019, <https://archive.is/3CW03#selection-229.0-229.166>



Procurement Project of The Environmental Air Disinfection System and The Scalable Automated Sample Storage Management System <sup>40</sup>	Unclear	August 14, 2019	\$132,200,025.47
Security Service Procurement Project <sup>41</sup>	WNBL	September 12, 2019	\$1,281,022.33
Central Air Conditioning Renovation Project <sup>42</sup>	Unclear	September 16, 2019	\$606,382,986.11
Procurement of Air Incinerator and Testing Service <sup>43</sup>	Unclear	December 3, 2019	\$49,388.81

Table 2: WIV Procurement Projects in 2019

The references to maintenance at the BSL-3 and animal center at the WNBL, the procurement of an environmental air disinfection system, and renovations to the hazardous waste treatment system and central air conditioning system all raise questions about how well these systems were functioning in the months prior to the outbreak of COVID-19.

### The Disappearing Database

On September 12, 2019 the WIV's online, public database of samples and virus sequences was taken offline in the middle of the night between 2:00AM and 3:00AM local time.<sup>44</sup> The database contained more than 22,000 entries consisting of sample and pathogen data collected from bats and mice. The database contained key information about each sample, including what type of animal it was collected from, where it was collected, whether the virus was successfully isolated, the type of virus collected, and its similarity to other known viruses.

<sup>40</sup>Announcement of winning the bid for the procurement project of the environmental air disinfection system and the scalable automated sample storage management system of the Wuhan Institute of Virology, Chinese Academy of Sciences." *China Government Procurement Network*, 14 Aug. 2019, <https://archive.is/InXLD#selection-229.0-229.228>

<sup>41</sup>Competitive consultation on the procurement project of security services in Zhengdian Science Park, Wuhan Institute of Virology, Chinese Academy of Sciences." *China Government Procurement Network*, 12 Sept. 2019, <https://archive.is/tUi75#selection-229.0-229.156>

<sup>42</sup>Competitive Consultation on Central Air Conditioning Renovation Project of Wuhan Institute of Virology, Chinese Academy of Sciences." *China Government Procurement Network*, 16 Sept. 2019, <https://archive.is/bfoTD#selection-229.0-229.131>

<sup>43</sup>The Wuhan Institute of Virology of the Chinese Academy of Sciences plans to use a single-source procurement method to publicize the procurement of air incineration devices and test service projects." *China Government Procurement Network*, 3 Dec. 2019, <https://archive.is/Jifqr#selection-229.0-229.197>

<sup>44</sup>Status breakdown of the database of characteristic wild animals carrying virus pathogens (September 2019)." *Scientific Database Service Monitoring & Statistics System*, <https://archive.is/AGtFv#selection-1553.0-1567.2>

Table 1 Virus data display of bat samples

Data element name	Example
Sample ID	162387A
Sample tissue type	Anal
Animal type	bat
Source species	<i>Rousettus leschenaultii</i>
Species molecular identification	<i>Rousettus</i> sp.
Collection date	2016-08-21
country	China
province	Yunnan
city	Miaoxin village, Mengna county, Sipsongpanna
GPS information	101.51944,21.78127
Whether high-throughput sequencing	No
Whether the virus is isolated	No
publishing	Luo Y, Li B, Jiang RD, et al. <i>Virology</i> . 2018;33(1):87–95. doi:10.1007/s12250-018-0017-2
Remarks	
Detection method	PCR-based
Virus name	Coronaviridae
Test results	Positive
blast result	btcov HKU9
Virus classification	HKU9
Virus sequence	See references for details
Similarity	94%
Sequence length	398bp
Sequence-encoded gene	Partial RdRp

Fig. 6: Example Database Entry<sup>45</sup>

To date, there has been no consistent answer provided as to why the database was removed or when or if it will be put back online.

Shi is listed as the data correspondence author for the project. When questioned about the database being taken offline, Shi has given several conflicting answers. During a December 2020 interview with *BBC*, Shi said the database was taken offline for “security reasons” after cyberattacks against the work and personal emails of WIV staff. She also insisted that WIV virus sequences were saved in the GenBank database, run by the National Center for Biotechnology Information. Shi stated, “It’s completely transparent. We have nothing to hide.”<sup>46</sup>

In a January 26, 2021 email to someone inquiring about the database, however, Shi stated the database was taken down due to cyberattacks “during [the] COVID-19 pandemic.”<sup>47</sup> She also claimed that researchers had “only entered a limit[ed] data in this database” despite it having more than 22,000 entries.

45 “Database of pathogens of bat and murine viruses.” *Wikisource*, <https://zh.wikisource.org/zh-hant/%E8%9D%99%E8%9D%A0%E6%BA%90%E5%92%8C%E9%BC%A0%E6%BA%90%E7%97%85%E6%AF%92%E7%97%85%E5%8E%9F%E6%95%B0%E6%8D%AE%E5%BA%93>

46 Sudworth, John. “Covid: Wuhan Scientist Would ‘Welcome’ Visit Probing Lab Leak Theory.” *BBC News*, 21 Dec. 2020, [www.bbc.com/news/world-asia-china-55364445](http://www.bbc.com/news/world-asia-china-55364445).

47 Cleary, Tommy. “Prof Zheng-Li Shi Replied to Me, to CNRI,中文DOI运维 I Can Only Conclude @PeterDaszak & the Rest of the @WHO Organisation Were given the Same Information Access Ultimatum:No Trust, No Conversation.@SciDiplomacyUSA Has Its Work Cut Out.Data Hostage? Pic.twitter.com/KhiFs42U7j.” *Twitter*, 10 Mar. 2021, [https://twitter.com/tommy\\_cleary/status/1369689088790425602?s=20](https://twitter.com/tommy_cleary/status/1369689088790425602?s=20).

In an apparent contradiction of her *BBC* interview, Shi admitted that “access to the visitors is limited,”<sup>48</sup> but maintains:

...all our work regarding the different type of bat coronavirus (partial sequences or full-length genome sequences) have been published and the sequence and sample information have been submitted to GenBank.<sup>49</sup>

At the end of her email, Shi writes, “I’ll not answer any of your questions if your curiosity is based on the conspiracy of ‘man made or lab leak of SARS-CoV-2’ or some non-sense questions based on your suspicion. **No trust, no conversation**”<sup>50</sup> (emphasis added).

### New Leadership and PLA Involvement

The WIV’s website indicates that Yuan Zhiming serves as the Dean of the Wuhan Branch of the Chinese Academy of Sciences and director of the WNBL BSL-4 lab.<sup>51</sup> However, news posted on Weibo Douban, a PRC website, on February 7th, 2020 stated that PLA officials were dispatched to assume control of the response. The report says PLA Major General Chen Wei, an expert in biology and chemical weapon defenses, was deployed to Wuhan in January 2020 and took control of the WNBL BSL-4 lab. The posting of this information to Douban is significant given the website’s history of censoring posts critical of the CCP, including censoring words related to the Tiananmen Square Massacre.<sup>54</sup> The post’s survival on a heavily CCP censored site confirms its legitimacy.



<sup>48</sup> Sudworth.

<sup>49</sup> *Ibid.*

<sup>50</sup> *Ibid.*

<sup>51</sup> “Yuan Zhiming.” *Wuhan Institute of Virology*, [http://www.whiov.cas.cn/sourcedb\\_whiov\\_cas/zw/rck/200907/t20090718\\_2100080.html](http://www.whiov.cas.cn/sourcedb_whiov_cas/zw/rck/200907/t20090718_2100080.html)

<sup>52</sup> Gertz, Bill. “Chinese Maj. Gen. Chen Wei TAKES Leading Role in Coronavirus Fight.” *The Washington Times*, 16 Feb. 2020, [www.washingtontimes.com/news/2020/feb/16/chinese-maj-gen-chen-wei-takes-leading-role-in-cor/](http://www.washingtontimes.com/news/2020/feb/16/chinese-maj-gen-chen-wei-takes-leading-role-in-cor/).

<sup>53</sup> Guli. “Major General Chen Wei, China’s Chief Biochemical Weapons Expert, Takes Over Wuhan P4 Virus Laboratory.” *Radio France Internationale*, <https://www.rfi.fr/cn/%E4%B8%AD%E5%9B%BD/20200208-%E4%B8%AD%E5%9B%BD%E9%A6%96%E5%B8%AD%E7%94%9F%E5%8C%96%E6%AD%A6%E5%99%A8%E4%B8%93%E5%AE%B6%E9%99%88%E8%96%87%E5%B0%91%E5%B0%86%E6%8E%A5%E7%AE%A1%E6%AD%A6%E6%B1%89p4%E7%97%85%E6%AF%92%E5%AE%9E%E9%AA%8C%E5%AE%A4>

<sup>54</sup> Honorof, Marshall. “China Marks Tiananmen Massacre with ‘Internet Maintenance Day.’” *NBC News*, 4 June 2013, <https://www.nbcnews.com/id/wbna52096871>

Committee Minority Staff have also received testimony from a former senior U.S. official that Gen. Chen actually took control of the WNBL BSL-4 lab in late 2019, not January 2020 as was publicly reported. Gen. Chen taking over part of the WIV demonstrates the CCP was concerned about the activity happening there as news of the virus was spreading. If she took control in 2019, it would mean the CCP knew about the virus earlier, and that the outbreak began earlier – a topic discussed further in this section.

Gen. Chen is a researcher at the Academy of Military Medical Sciences in Beijing, and served as a delegate to the 12th National People’s Congress.<sup>55</sup> In January 2018, Gen. Chen was made a member of the 13th National Committee of the Chinese People’s Political Consultative Conference (CPPCC). According to the U.S.-China Economic Security Review Commission, the CPPCC is a “critical coordinating body that brings together representatives of China’s other interest groups and is led by a member of China’s highest-level decision-making authority, the CCP’s Politburo Standing Committee.”<sup>56</sup>

According to a January 15, 2021 fact sheet published by the State Department, in the years leading up to the pandemic, researchers at the WIV were engaged in classified research, including experiments on animals, on behalf of the PLA.<sup>57</sup> Dr. Shi has repeatedly denied any involvement of the PLA at the WIV. During a lecture hosted only by Rutgers Medical School, Shi stated:

We—our work, our research is open, and we have a lot of international collaboration. And from my knowledge, all our research work is open, is transparency. So, at the beginning of COVID-19, we heard the rumors that it’s claimed in our laboratory we have some project, blah blah, with army, blah blah, these kinds of rumors. But this is not correct because I am the lab’s director and responsible for research activity. I don’t know any kind of research work performed in this lab. This is incorrect information.<sup>58</sup>

This statement is demonstrably false. The WIV had multiple connections to PLA researchers prior to the COVID-19 pandemic; several were listed on the WIV’s English language website. The Academic Committee of State Key Laboratory of Virology at the WIV included a Deputy Director from the Second Military Medical University and a member from the 302 Military Hospital of China. The Scientific Advisory Committee for the Center for Emerging Infectious Diseases had among its members a researcher from the Institute of Military Veterinary at the Academy of Military Medical Sciences.<sup>59</sup> This website was scrubbed on May 28, 2020, and the lists of committee members removed. However, archived copies of the website are available online.

<sup>55</sup> “List of Deputies to the Twelfth National People’s Congress of the People’s Republic of China.” *Sohu*, <http://news.sohu.com/20130227/n367313787.shtml>

<sup>56</sup> Bowe, Alexander. “China’s Overseas United Front Work: Background and Implications for the United States.” *U.S.-China Economic and Security Review Commission*, 24 Aug. 2018, [https://www.uscc.gov/sites/default/files/Research/China%27s%20Overseas%20United%20Front%20Work%20-%20Background%20and%20Implications%20for%20US\\_final\\_0.pdf](https://www.uscc.gov/sites/default/files/Research/China%27s%20Overseas%20United%20Front%20Work%20-%20Background%20and%20Implications%20for%20US_final_0.pdf)

<sup>57</sup> United States, Department of State. “Fact Sheet: Activity at the Wuhan Institute of Virology.” 15 Jan. 2021, <https://2017-2021.state.gov/fact-sheet-activity-at-the-wuhan-institute-of-virology/index.html>

<sup>58</sup> Eban, Katherine. “The Lab-Leak Theory: Inside the Fight to Uncover COVID-19’s Origins.” *Vanity Fair*, 3 June 2021, [www.vanityfair.com/news/2021/06/the-lab-leak-theory-inside-the-fight-to-uncover-covid-19s-origins](http://www.vanityfair.com/news/2021/06/the-lab-leak-theory-inside-the-fight-to-uncover-covid-19s-origins).

<sup>59</sup> “Committees.” *Wuhan Institute of Virology*, [https://web.archive.org/web/20200527045823/http://english.wiv.ac.cn/about\\_us2016/Committees/](https://web.archive.org/web/20200527045823/http://english.wiv.ac.cn/about_us2016/Committees/)

**Academic Committee of State key laboratory of virology, WIV, CAS**

Director: Zihe RAO, Tsinghua University, China.

Deputy Directors: Hongyang WANG, The Second Military Medical University, China.

Hongbin SHU, Wuhan University, China.

**Members:**

Jianfang GUI, Institute of Hydrobiology, Chinese Academy of Sciences, China.

Fusheng WANG, 302 Military Hospital of China, China.

Hualan CHEN, Harbin Veterinary Research Institute, Chinese Academy of Agricultural Sciences, China.

Zhenghong YUAN, Fudan University, China.

Ningshao XIA, Xiamen University, China.

Linqi ZHANG, Tsinghua University, China.

Musheng ZENG, Sun Yat-sen University, China.

Jianguo WU, Wuhan University, China.

Xinwen CHEN, Wuhan Institute of Virology, Chinese Academy of Sciences, China.

Ke LAN, Wuhan University, China.

Fig. 3: Archived Versions of the WIV Committees Page

This raises the obvious question of why Shi, who served on one of the committees, would lie about military researchers working with the WIV. **Her denial and the scrubbing of the website appear to be obvious attempts to obfuscate the PLA's involvement with the WIV.**

**Geospatial Analysis of Traffic Patterns at Wuhan Hospitals Near the WIV**

Around the time the WIV's virus database went offline, car traffic at hospitals in downtown Wuhan began to increase. Researchers from Boston University School of Public Health, Boston Children's Hospital, and Harvard Medical School used satellite imagery to examine parking lot volume of hospitals in Wuhan for the two and a half years prior to December 2019. They found that five of six hospitals analyzed had the highest relative daily volume of cars in the parking lot in September and October 2019, before the first reported cases of COVID-19.

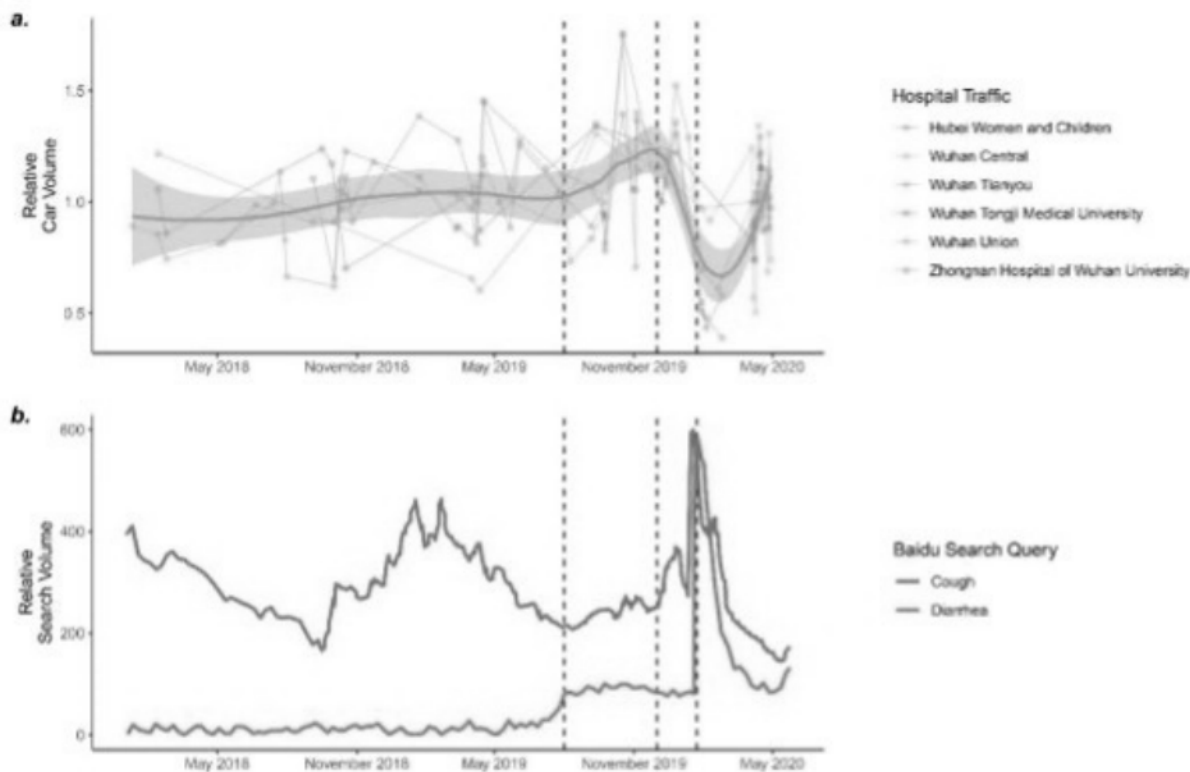


Fig. 7: Time-series of Different Influenza-like Illnesses, Symptoms and Surveillance signal<sup>62</sup>

This peak corresponded with an increase in searches for “cough” and “diarrhea” in Wuhan on Baidu, a Chinese search engine.<sup>60</sup> According to the CDC, both cough and diarrhea are symptoms of COVID-19.<sup>61</sup> This study suggests a virus with similar symptoms as COVID-19 was circulating in Wuhan in September and October.

### The Initial Outbreak’s Proximity to the WIV

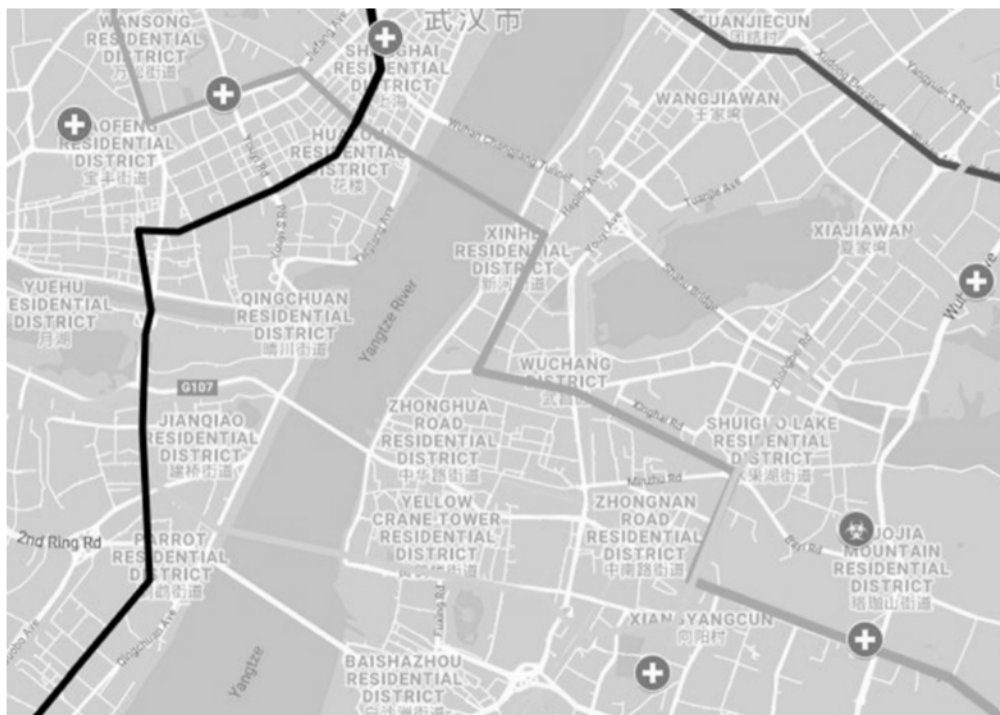
When people get sick, they are likely to seek healthcare near their home or work. Each of the hospitals that saw a rise in traffic with patients complaining of COVID-19 symptoms are located within 6.5 miles of the WIV Headquarters and are connected by public transit lines. The below map shows the location of the WIV Headquarters (in red) and the six hospitals (in blue) which experienced increase vehicle traffic in September and October 2019. When plotted on a map, these six hospitals are clustered around the WIV Headquarters in Wuchang, Wuhan, and are connected to that facility via the Wuhan Metro – various lines are shown in black, yellow, pink, and green on the map. The pink line represents Line 2, whose daily passenger volume exceeded one million trips in 2017.<sup>63</sup>

<sup>60</sup> Nsoesie, Elaine Okanyene, et. al. “Analysis of hospital traffic and search engine data in Wuhan China indicates early disease activity in the Fall of 2019 (2020).” *Digital Access to Scholarship at Harvard*, 2020. <http://nrs.harvard.edu/urn-3:HUL.InstRepos:42669767>

<sup>61</sup> “Symptoms of COVID-19.” *Centers for Disease Control and Prevention*. <https://www.cdc.gov/coronavirus/2019-ncov/symptoms-testing/symptoms.html>

<sup>62</sup> Nsoesie

<sup>63</sup> “Wuhan Metro is bursting with passengers, breaking records for two consecutive days.” 5 April 2017, <https://web.archive.org/web/20170825184909/http://ctjb.cnhubei.com/html/ctjb/20170405/ctjb3089625.html>



Map 1: Harvard Study Hospitals in Relation to the WIV Headquarters

It is also important to note, according to an Australian scientist who worked in the BSL-4 lab, a daily shuttle bus transfers WIV researchers from the Wuhan Branch of the Chinese Academy of Sciences to the WNBL facility and back again.<sup>64</sup> According to public mapping data, the shuttle pick up and drop off point is less than 500 meters from the WIV Headquarters. As such, it is likely that researchers from both the WIV Headquarters, as well as the WNBL, used the Wuhan metro and/or the WNBL shuttle bus, as part of their daily work commute.

Therefore, it is reasonable to conclude, based on the WIV's extensive sample library and history of genetically manipulating coronaviruses, that in early September, one or more researchers became infected with SARS-CoV-2 in the lab and carried it out into the city. Based on the WIV's publications, researchers could have been exposed while experimenting with a natural virus collected from the wild or infected with a virus they genetically manipulated. Those researchers likely traveled to and from the WIV via the Wuhan metro or via the shuttle service, providing a vector for the virus to spread. This corresponds with the first signs of a growing wave of ill people in Wuhan centered around the WIV's Wuchang facility.

### The 2019 Military World Games and Sick Athletes

The 7th International Military Sports Council Military World Games (MWGs) opened in Wuhan on October 18, 2019. The games are similar to the Olympic games but consist of military athletes with some added military disciplines. The MWGs in Wuhan drew 9,308 athletes, representing 109 countries, to compete in 329 events across 27 sports. Twenty-five countries sent delegations of more than 100 athletes, including Russia, Brazil, France, Germany, and Poland.<sup>65</sup>

<sup>64</sup> Cortez, Michelle Fay. "The Last—And Only—Foreign Scientist in the Wuhan Lab Speaks Out." *Bloomberg*, 27 June 2021, [www.bloomberg.com/news/features/2021-06-27/did-covid-come-from-a-lab-scientist-at-wuhan-institute-speaks-out](http://www.bloomberg.com/news/features/2021-06-27/did-covid-come-from-a-lab-scientist-at-wuhan-institute-speaks-out).

<sup>65</sup> "Military Games to Open Friday in China." *China Daily*, 17 Oct. 2019, [www.china.org.cn/sports/2019-10/17/content\\_75311946.htm](http://www.china.org.cn/sports/2019-10/17/content_75311946.htm).

The PRC government recruited 236,000 volunteers for the games, which required 90 hotels, three railroad stations, and more than 2,000 drivers.<sup>66</sup> An archived version of the competition’s website from October 20, 2019, lists the more than thirty venues that hosted events for the MWGs across Wuhan and the broader Hubei province.<sup>67</sup> The live website is no longer accessible – it is unclear why it was removed.

During the games, many of the international athletes became sick with what now appear to be symptoms of COVID-19. In one interview, an athlete from Luxembourg described Wuhan as a “ghost town,”<sup>68</sup> and recalls having his temperature taken upon arriving at the city’s airport. In an interview with *The Financial Post*, a Canadian newspaper, one member of the Canadian Armed Forces who participated in the games said (emphasis added):

**This was a city of 15 million people that was in lockdown. It was strange, but we were told this was to make it easy for the Games’ participants to get around. [I got] very sick 12 days after we arrived, with fever, chills, vomiting, insomnia.... On our flight to come home, 60 Canadian athletes on the flight were put in isolation [at the back of the plane] for the 12-hour flight. We were sick with symptoms ranging from coughs to diarrhea and in between.**<sup>69</sup>

The service member also revealed his family members became ill as his symptoms increased,<sup>70</sup> a development that is consistent with both human-to-human transmission of a viral infection and COVID-19. Similar claims about COVID-19 like symptoms have been made by athletes from Germany, France, Italy,<sup>71</sup> and Sweden.<sup>72</sup>

By cross referencing the listed MWG venues with publicly available mapping data, it is possible to visualize the venues (in black) in relation to the WIV Headquarters (in red) and the above-mentioned hospitals (in blue). The green figures represent athletes who have publicly expressed their belief they contracted COVID-19 while in Wuhan and are mapped at the venues which hosted the events in which they competed. Some of these athletes resided in the military athletes’ village.

“  
[I got] very sick 12 days after we arrived, with fever, chills, vomiting, insomnia.... On our flight to come home, 60 Canadian athletes on the flight were put in isolation [at the back of the plane] for the 12-hour flight. We were sick with symptoms ranging from coughs to diarrhea and in between.

- Canadian Athlete

”

<sup>66</sup> “2019 Military World Games Kicks off in Central China’s Wuhan.” *CISION*, 17 Oct. 2019, [www.prnewswire.com/news-releases/2019-military-world-games-kicks-off-in-central-chinas-wuhan-300940464.html](http://www.prnewswire.com/news-releases/2019-military-world-games-kicks-off-in-central-chinas-wuhan-300940464.html).

<sup>67</sup> “Competition Venues.” *Wuhan 2019 Military World Games*, [https://web.archive.org/web/20191020154108/en.wuhan2019mwg.cn/html/Competition\\_venues/](https://web.archive.org/web/20191020154108/en.wuhan2019mwg.cn/html/Competition_venues/).

<sup>68</sup> Houston, Michael. “More athletes claim they contracted COVID-19 at Military World Games in Wuhan.” *Inside the Games*, 17 May 2020, <https://www.insidethegames.biz/articles/1094347/world-military-games-illness-covid-19>.

<sup>69</sup> Francis, Diane. “Diane Francis: Canadian Forces Have Right to Know If They Got COVID at the 2019 Military World Games in Wuhan.” *Financial Post*, 25 June 2021, <https://financialpost.com/diane-francis/diane-francis-canadian-forces-have-right-to-know-if-they-got-covid-at-the-2019-military-world-games-in-wuhan>.

<sup>70</sup> *Ibid.*

<sup>71</sup> Houston.

<sup>72</sup> Liao, George. “Coronavirus May Have Been Spreading since Wuhan Military Games Last October.” *Taiwan News*, 13 May 2020, [www.taiwannews.com.tw/en/news/3932712](http://www.taiwannews.com.tw/en/news/3932712).





Map 2: WIV Headquarters, Hospitals, MWG Venues, and Sick Athletes

At least four countries who sent delegations to the MWGs have now confirmed the presence of SARS-CoV-2 or COVID-19 cases within their borders in November and December 2019, before the news of an outbreak first became public.

**1. Italy.** In February 2021, researchers from Italy published a research letter in the CDC’s *Emerging Infectious Diseases* journal describing a case involving a 4-year-old boy from Milan. A retrospective analysis of samples taken in 2019 identified the boy, who developed a cough on November 21, 2019, as having been infected with SARS-CoV-2 three months before Italy’s first reported case. The boy had no reported travel history.<sup>73</sup>

**2. Brazil.** A March 2021 article by researchers in Brazil examined wastewater samples from October to December 2019. Previous studies have confirmed that humans infected with the virus can experience prolonged viral shedding via their gastrointestinal tract. A sample from November 27th tested positive for SARS-CoV-2 RNA, confirming the virus was circulating in Santa Catarina, Brazil months before January 21, 2020, when the first case in the Americas was reported.<sup>74</sup>

**3. Sweden.** Sweden’s Public Health Agency said it is likely that individuals in the country were infected with SARS-CoV-2 as early as November 2019.<sup>75</sup>

73 Amendola, Antonella, et. al. “Evidence of SARS-CoV-2 RNA in an Oropharyngeal Swab Specimen, Milan, Italy, Early December 2019.” *Emerging Infectious Diseases*, Feb. 2021, 27(2). <https://doi.org/10.3201/eid2702.204632>

74 Fongaro, Gislaine et al. “The presence of SARS-CoV-2 RNA in human sewage in Santa Catarina, Brazil, November 2019.” *The Science of the Total Environment*, 8 March 2021, 778: 146198. <https://dx.doi.org/10.1016%2Fj.scitotenv.2021.146198>

75 “Coronavirus May Have Arrived in Sweden in November: Public Health Agency.” *The Local*, 5 May 2020, [www.thelocal.se/20200505/the-coronavirus-may-have-arrived-in-sweden-in-november/](http://www.thelocal.se/20200505/the-coronavirus-may-have-arrived-in-sweden-in-november/).

**4. France.** Researchers in France also re-tested samples from late 2019 in an effort to identify early COVID-19 cases. They identified a 42-year-old male who presented to the emergency room on December 27th with an influenza-like illness. He had no connection to the PRC and no recent travel history. Upon re-testing, the patient’s samples were positive for SARS-CoV-2. It should be noted that one of his children also had similar symptoms before the man became sick, suggesting that the first case in France was likely earlier than December 27th.<sup>76</sup>

As stated above, athletes from France, Italy, and Sweden also complained of illnesses with symptoms similar to COVID-19 while at the MWGs in Wuhan. **The presence of SARS-CoV-2 in four countries, on two separate continents, suggests a common source. If, as presumed, SARS-CoV-2 first infected humans in Wuhan before spreading to the rest of the world, the 2019 Military World Games in Wuhan appears to be a key vector in the global spread – in other words, potentially one of the first “super spreader” events.**

### Conclusion

While much of the public debate was initially focused on the Huanan seafood market in Wuhan as the origin of the pandemic, the preponderance of evidence now suggests that the virus leaked from the Wuhan Institute of Virology. Given the WIV’s demonstrated history of conducting gain-of-function experiments on coronaviruses, including genetically manipulating viruses specifically to make them infectious to humans in BSL-2 labs, as well as their possession of one of the world’s largest collections of coronaviruses, it is completely plausible that one or more researcher(s) was accidentally infected and carried the virus out of the lab. The evidence outlined above, combined with the cover-up conducted by CCP authorities, strongly suggest the Wuhan Institute of Virology as the source of the current pandemic.

### III. EVIDENCE OF GENETIC MODIFICATION

The other topic of debate is whether the virus could have been genetically modified. The WIV was conducting gain-of-function research on coronaviruses and testing them against human immune systems in the months leading up to the emergence of SARS-CoV-2, however the scientific community has claimed it is not possible it was anything but a naturally occurring virus. But, as this report lays out, we believe it is a viable hypothesis that the virus could have been modified.

“You can engineer a virus without leaving any trace. The answers you are looking for, however, can only be found in the archives of the Wuhan laboratory.”

– Dr. Ralph Baric

<sup>76</sup> Deslandes, A et al. “SARS-CoV-2 was already spreading in France in late December 2019.” *International Journal of Antimicrobial Agents*, 3 May 2020, 55(6): 106006. <https://dx.doi.org/10.1016%2Fj.ijantimicag.2020.106006>

<sup>77</sup> Stahl, Lesley. “What Happened In WUHAN? Why Questions Still Linger on the Origin of the Coronavirus.” *CBS News*, 28 Mar. 2021, [www.cbsnews.com/news/covid-19-wuhan-origins-60-minutes-2021-03-28/](http://www.cbsnews.com/news/covid-19-wuhan-origins-60-minutes-2021-03-28/).

### Research Regarding SARS Like Coronaviruses from 2004-2017

The WIV's work on bat coronaviruses dates back to the aftermath of SARS in the early 2000s. Shi met Peter Daszak, an American citizen, in 2004 during an effort to find the origins of the 2002 SARS pandemic. Daszak is the CEO of EcoHealth Alliance, a New York-based NGO that funds scientific research around the world.<sup>78</sup> For the last year and a half, questions have been raised about how and why EcoHealth Alliance provided the WIV with U.S. taxpayer dollars. Those funds were provided to EcoHealth Alliance in



the form of grants from the Department of Health and Human Services (HHS), National Institutes of Health (NIH), National Science Foundation (NSF), and the United States Agency for International Development (USAID).

Beginning in 2005, and continuing over the next 16 years, Shi and Daszak have collaborated on coronavirus research. Together, they “led dozens of expeditions to caves full of bats, to collect samples and analyze them.”<sup>79</sup> They have identified more than 500 novel coronaviruses, including roughly 50 related to SARS or MERS, and they have repeatedly engaged in gain-of-function research on coronaviruses designed to make them more infectious in humans.<sup>80</sup> As discussed below, the vast majority of the most relevant scientific publications that have emerged from the WIV regarding coronaviruses was conducted with funding provided by Peter Daszak through EcoHealth Alliance.

**Article and Publication:** “Bats Are Natural Reservoirs of SARS-Like Coronaviruses,” in *Science* (2005).

**Participants:** Li Wendog, primary author; Shi, second author and one of three corresponding authors; Peter Daszak; additional scientists from Australia and China.

**Funding:** The paper was supported in part by funding from the PRC government, who provided a special grant for Animal Reservoirs of SARS-CoV from the State Key Program for Basic Research (grant no. 2005CB523004) and the State High Technology Development Program (grant no. 2005AA219070) from the Ministry of Science and Technology.

<sup>78</sup> Zaugg, Julie. “In Wuhan with Bat Woman, at the origins of the Covid-19.” *L’Illustré*, 22 Jan. 2021, <https://www.illustré.ch/magazine/a-wuhan-avec-bat-woman-aux-origines-du-covid-19>

<sup>79</sup> *Ibid.*

<sup>80</sup> *Ibid.*

It was also funded by the U.S. government, through the NIH and NSF, who provided funding in the form of an ‘Ecology of Infectious Diseases’ award (no. R01-TW05869) from the John E. Fogarty International Center and the V. Kann Rasmussen Foundation.

**Purpose:** The scientists hoped to identify the origins of SARS by identifying species of bats which are a natural host for SARS-like coronaviruses.

**Conclusion:** “These findings on coronaviruses, together with data on henipaviruses (23–25, 28), suggest that genetic diversity exists among zoonotic viruses in bats, increasing the possibility of variants crossing the species barrier and causing outbreaks of disease in human populations. It is therefore essential that we enhance our knowledge and understanding of reservoir host distribution, animal-animal and human-animal interaction (particularly within the wet-market system), and the genetic diversity of bat-borne viruses to prevent future outbreaks.”<sup>81</sup>

**Relevance:** This conclusion would drive the next fifteen years of collaboration between the WIV and Peter Daszak, with Shi directing the laboratory work.

In 2006, Shi and Daszak collaborated with a researcher in Australia to publish “Review of bats and SARS” in *Emerging Infectious Diseases*, a peer-reviewed journal published monthly by the U.S. Centers for Disease Control and Prevention. Shi was again listed as the second author, and the work was funded by the same PRC and NIH/NSF grants referenced above. The following year, these grants supported the publication of “Evolutionary Relationships between Bat Coronaviruses and Their Hosts” in *Emerging Infectious Diseases*. Shi is listed as the sixth author, followed by another WIV researcher, and Peter Daszak is listed as one of two corresponding authors.<sup>82</sup>

In 2007, Shi and several other WIV researchers joined additional scientists in publishing another paper on coronaviruses.

**Article and Publication:** “Difference in Receptor Usage between Severe Acute Respiratory Syndrome (SARS) Coronavirus and SARS-Like Coronavirus of Bat Origin” in *Journal of Virology*.

**Participants:** WIV researchers and Linfa Wang. Shi is listed as the corresponding author.

**Funding:** This work was funded by the PRC government and grants from Australia and the European Commission.

**Purpose:** This study focused on the receptors used by the spike protein of SARS-like coronaviruses, which are the major surface structures that enable coronaviruses to bind to receptors on cells. To test this, researchers created multiple chimeric viruses by inserting different sequences of the SARS-CoV spike protein into the spike protein of the SARS-like virus being examined, and tested them against bat, civet, and human ACE2 expressing cells.

**Conclusion:** One of these chimeric viruses was able to enter cells through the human ACE2 receptor. ACE2 is an abbreviation for angiotensin converting enzyme-2, which is a protein found on the surface of cells and tissues throughout the human body,

<sup>81</sup> *Ibid.*

<sup>82</sup> Wang L-F, Shi Z, Zhang S, Field H, Daszak P, Eaton BT. “Review of bats and SARS.” *Emerg Infect Dis*, Dec. 2006; 12(12): 1834-1840., <http://dx.doi.org/10.3201/eid1212.060401>

<sup>83</sup> Cui J, et. al. “Evolutionary relationships between bat coronaviruses and their hosts.” *Emerg Infect Dis.*, Oct. 2007; 13(10):1526-32. [https://wwwnc.cdc.gov/eid/article/13/10/07-0448\\_article](https://wwwnc.cdc.gov/eid/article/13/10/07-0448_article)

including the nose, mouth, and lungs. “In the lungs, ACE2 is highly abundant on type 2 pneumocytes, an important cell type present in chambers within the lung called alveoli, where oxygen is absorbed and waste carbon dioxide is released.”<sup>84</sup> ACE2 is also the location where SARS-CoV-2’s spike protein binds to human cells. Researchers concluded that “a minimal insert region” is “sufficient to convert the SL-COV S [SARS-like coronavirus spike protein] from non-ACE2 binding to human ACE2 binding.”<sup>85</sup>

**Relevance:** In other words, WIV researchers were able to take a SARS-like coronavirus that does not infect humans and modify it so it was able to do so. Also importantly, this work was done under BSL-2 conditions.

Shi and Daszak do not appear as coauthors on a paper again until 2013.

**Article and Publication:** “Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor” in *Nature*.<sup>86</sup>

**Participants:** WIV and EcoHealth researchers, including Hu, Shi, Daszak, and Wang who are credited for designing the experiments. Shi and Daszak listed as corresponding authors.

**Funding:** The study was funded by grants from the PRC government (including grant no. 2013FY113500), as well as the National Institute of Allergy and Infectious Diseases (NIAID) (no. R01AI079231), a NIH/NSF “Ecology and Evolution of Infectious Diseases” award (no. R01TW005869), an award from the NIH Fogarty International Center supported by International Influenza Funds from the Office of the Secretary of the Department of Health and Human Services (no. R56TW009502), and USAID’s Emerging Pandemic Threats PREDICT program.<sup>87</sup>

**Purpose:** This work marked “the first recorded isolation of a live SL-CoV” [SARS-live coronavirus], which researchers isolated from bat fecal samples and named WIV1. Additionally, they identified two novel bat coronaviruses (SCH014 and Rs3367) and reported “the first identification of a wild-type bat SL-CoV capable of using ACE2 as an entry receptor.”<sup>88</sup>

**Conclusion:** “Finally, this study demonstrates the public health importance of pathogen discovery programs targeting wildlife that aim to identify the ‘known unknowns’—previously unknown viral strains closely related to known pathogens. These programs, focused on specific high-risk wildlife groups and hotspots of disease emergence, may be a critical part of future global strategies to predict, prepare for, and prevent pandemic emergence.”<sup>90</sup>

**Relevance:** By isolating a wild-type (common strain in nature) SARS-like coronavirus that binds to ACE2, and testing it in human lung tissue, the authors proved that bat coronaviruses are capable of infecting humans directly, without having to pass through an intermediate host.

<sup>84</sup> Sriram, Krishna, et al. “What Is the ACE2 Receptor, How Is It Connected to Coronavirus and Why Might It Be Key to Treating COVID-19? The Experts Explain.” *The Conversation*, 25 May 2021, <https://theconversation.com/what-is-the-ace2-receptor-how-is-it-connected-to-coronavirus-and-why-might-it-be-key-to-treating-covid-19-the-experts-explain-136928>.

<sup>85</sup> Ren.

<sup>86</sup> Ge, Xing-Yi et al. “Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor.” *Nature*, 30 Oct. 2013, 503(7477): 535-8, <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5389864/>

<sup>87</sup> *Ibid.*

<sup>88</sup> *Ibid.*

<sup>89</sup> *Ibid.*

<sup>90</sup> *Ibid.*

In 2014, Shi and Daszak coauthored two more joint WIV-EcoHealth Alliance papers. The lead author for one of the papers, entitled “Detection of diverse novel astroviruses from small mammals in China,” was Ben Hu, a WIV researcher who was a coauthor of earlier Shi/Daszak papers. Shi is listed as the corresponding author, and the paper was again jointly funded by the PRC government (including grant no. 2013FY113500) and USAID’s PREDICT program.<sup>91</sup>

The next year, in 2015, Shi provided Ralph Baric and other researchers at the University of North Carolina at Chapel Hill with spike protein sequences and plasmids of SHC014, one of the viruses Shi, Daszak, and WIV researchers identified in bat feces samples in 2013. American researchers used those samples to create “a chimeric virus expressing the spike of bat coronavirus SHC014 in a mouse-adapted SARS-CoV backbone.”<sup>92</sup> **In other words, they removed the spike protein from SHC014 and inserted it into a SARS coronavirus that was genetically manipulated to better infect mice.** This work was done under BSL-3 conditions. The newly created virus was then shown to bind to ACE2 in humans, replicate “efficiently”<sup>93</sup> in primary human airways cells, and withstand antibodies and vaccines. Researchers concluded that the work “suggests a potential risk of SARS-CoV re-emergence from viruses currently circulating in bat populations.”<sup>94</sup> This research was funded by NIAID and the NIH under multiple awards (nos. U19AI109761, U19AI107810, AI085524, F32AI102561, K99AG049092, DK065988), USAID’s PREDICT program via EcoHealth Alliance, and the PRC government. Baric was the corresponding author.<sup>95</sup>

2015 also saw the publication of another Shi/Hu/Wang/Daszak paper. Entitled “Isolation and Characterization of a Novel Bat Coronavirus Closely Related to the Direct Progenitor of Severe Acute Respiratory Syndrome Coronavirus,” it was published in the *Journal of Virology*. Nine of the twelve authors were WIV researchers, including Hu and Shi, who was the corresponding author. Here the WIV reported the successful isolation of a second novel coronavirus, WIV16. The SARS-like coronavirus was isolated from a single sample of bat fecal matter collected in Kunming, Yunnan Province of the PRC in July 2013. Like previous papers, this work was supported by a NIAID grant (no. R01AI110964) and by grants from the PRC government (including grant no. 2013FY113500).<sup>96</sup>

In addition to her aforementioned work with researchers at UNC Chapel Hill, Shi also provided them with additional bat coronavirus sequences and plasmid of WIV1’s spike protein. The resulting paper, “SARS-like WIV1-CoV poised for human emergence,” was published in the Proceedings of the National Academy of Sciences of the United States of America in March 2016. While neither Shi nor Daszak (nor any WIV researcher) are listed as coauthors, Baric was the corresponding author.

<sup>91</sup> Hu, Ben, et. al. “Detection of diverse novel astroviruses from small mammals in China.” *J Gen Virol*. Nov 2014, 95(Pt 11): 2442-2449. <https://pubmed.ncbi.nlm.nih.gov/25034867/>

<sup>92</sup> Menachery, Vineet, et. al. “A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence.” *Nat Med*, 9 Nov. 2015, 21:1508–1513. <https://doi.org/10.1038/nm.3985>

<sup>93</sup> Menachery

<sup>94</sup> *Ibid.*

<sup>95</sup> *Ibid.*

<sup>96</sup> Yang, Xing-Lou et al. “Isolation and Characterization of a Novel Bat Coronavirus Closely Related to the Direct Progenitor of Severe Acute Respiratory Syndrome Coronavirus.” *Journal of Virology*, 30 Dec. 2015, 90(6): 3253-6. <https://dx.doi.org/10.1128%2FJVI.02582-15>

This paper is significant because the authors discuss moving from disease surveillance to creating chimeric viruses as a means of pandemic preparedness; “this manuscript describes efforts to extend surveillance beyond sequence analysis, constructing chimeric and full-length zoonotic coronaviruses to evaluate emergence potential.”<sup>97</sup>

During this work, researchers produced chimeric viruses created by inserting the spike protein from WIV1 into a strain of SARS-CoV adapted to infecting mice. They subsequently tested this chimeric virus in human airway epithelial cells as well as in mice.<sup>98</sup> In addition to standard BALB/c mice (a strain of albino, lab-breed house mice used in experimentation<sup>99</sup>), researchers genetically manipulated the mice to create a strain of mice expressing the human ACE2 (hACE2) receptor. While hACE2 was found primarily in the lungs of the mice, it was also present in the brain, liver, kidneys, and gastrointestinal tract. The WIV1 chimeric virus was then tested in these hACE2 expressing mice, proving that the chimeric virus could infect humans. This work was funded by NIAID and NIH awards (nos. U19AI109761, U19AI107810, AI1085524, F32AI102561, K99AG049092, DK065988, AI076159, and AI079521).<sup>100</sup>

In 2016, Shi and Daszak also coauthored two additional papers focused on infectious diseases that year. One, entitled “Bat Severe Acute Respiratory Syndrome-Like Coronavirus WIV1 Encodes an Extra Accessory Protein, ORFX, Involved in Modulation of the Host Immune Response,” was coauthored by Wang and represents a major step forward in the WIV’s work. While working on this project, WIV researchers created a reverse genetics system and used it to genetically modify WIV1, the live coronavirus that was successfully isolated in 2013 and that UNC researchers manipulated months earlier. WIV researchers created multiple versions of this virus by deleting or adding genetic information to the virus’ RNA. According to the paper, all experiments with live virus for this paper were done under BSL-2 conditions, which does not require respirators or biological safety cabinets. Nine of the eleven authors are WIV researchers, and Shi is the corresponding author. The experimentation for the paper was supported by a grant from NIAID (no. R01AI110964) and funding from the PRC government.<sup>101</sup>

The following year, Ben Hu was the lead author of a paper entitled “Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus.” As with previous papers, the overwhelming majority (14 out of 17) of the authors worked at the WIV. Daszak, Shi, and Wang are all listed as coauthors. Hu is the lead author and Shi is one of two corresponding authors. Daszak is credited for “funding acquisition.”<sup>102</sup>

Additionally, using the reverse genetics system they debuted the previous year, WIV researchers created eight separate chimeric viruses by inserting the spike protein of various SARS-like coronaviruses into WIV1. Two of these chimeric viruses (WIV1-Rs4231S and WIV1-Rs7327S), and one natural virus, Rs4874, all replicated within hACE2 expressing cells.<sup>103</sup>

<sup>97</sup> Menachery, Vineet, et al. “SARS-like WIV1-CoV poised for human emergence.” *Proceedings of the National Academy of Sciences of the United States of America*, 14 March 2016, 113(11): 3048-53. <https://dx.doi.org/10.1073/pnas.1517719113>

<sup>98</sup> *Ibid.*

<sup>99</sup> “Inbred Strains: BALB.” MGI, [www.informatics.jax.org/inbred\\_strains/mouse/docs/BALB.shtml](http://www.informatics.jax.org/inbred_strains/mouse/docs/BALB.shtml).

<sup>100</sup> Menachery 2016.

<sup>101</sup> Zeng, Lei-Ping et al. “Bat Severe Acute Respiratory Syndrome-Like Coronavirus WIV1 Encodes an Extra Accessory Protein, ORFX, Involved in Modulation of the Host Immune Response.” *Journal of Virology*, 24 June 2016, 90(14): 6573-6582. <https://dx.doi.org/10.1128/JVI.03079-15>

<sup>102</sup> Hu, Ben et al. “Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus.” *PLOS Pathogens*, 30 Nov. 2017, 13(11). <https://dx.doi.org/10.1371/journal.ppat.1006698>

<sup>103</sup> Hu, 2017.



To reiterate, WIV researchers created chimeric coronaviruses able to infect humans in 2017, before the WNBL BSL-4 lab became operational. This work was jointly funded by NIAID (no. R01AI110964), USAID’s PREDICT program, and the PRC government (including grant no. 2013FY113500).

### Research Regarding SARS-Like Coronaviruses at the WIV or in Conjunction with WIV Scientists from 2018-2019

While Shi and Daszak coauthored several additional papers in 2018 and 2019 regarding coronaviruses, none include gain-of-function research on SARS-like coronaviruses designed to make them more infectious to humans. This is especially odd given that in 2018 the Chinese Academy of Science launched a new special project titled “Pathogen Host Adaption and Immune Intervention.”<sup>104</sup> One of the five subprojects was titled “Research on Virus Traceability, Cross-Species Transmission, and Pathogenic Mechanism,” – Shi is listed as one of the two scientists in charge.<sup>105</sup> This subproject had three areas of focus: 1) the traceability, evolution and transmission mechanism of new pathogens; 2) molecular mechanisms of viral cross-species infection and pathogenicity, and 3) the interaction mechanism between virus and host.

A second WIV scientist, Cui Zongqiang, was one of two researchers in charge of another subproject entitled, “New methods and new technologies for infection and immune research.”<sup>106</sup> This project focused on, among other things, evaluating new vaccines and establishing “humanized small animal models”<sup>107</sup> for in vitro pathogen testing.<sup>108</sup>

In January 2018, Shi was appointed Principal Investigator for a new Strategic Priority Research Program of the Chinese Academy of Sciences (grant no. XBD29010101, \$1.35 million USD),<sup>109</sup> investigating “genetic evolution and transmission mechanism of important bat-borne viruses.” This project, especially with its focus on transmission mechanisms, aligns with the first focus area mentioned above. That same month, Shi began work on a project titled “Study on the evolutionary mechanism of bat SARS-like coronavirus adapted to host receptor molecules and the risk of cross-species infection.”<sup>110</sup> The project was funded at a value of roughly \$850,000 USD (grant no. 31770175) and is slated to run until December 2021.<sup>111</sup> This grant aligns with the second focus area, the description of which specifically mentions replicating and modifying coronaviruses (emphasis added):

For important emerging emergencies and virulent viruses (influenza virus, Ebola virus, coronavirus, Marburg virus, arenavirus, etc.), by studying **their ability to invade different host cells and their ability to replicate in different host cells**, analyze the key molecules affecting their cross-species infections and their pathogenic mechanisms. Including: virus invasion, virus replication and assembly, and infection model.<sup>112</sup>

<sup>104</sup> “Guidelines for the application of the ‘Pathogen Host Adaptation and Immune Intervention’ project of the Chinese Academy of Sciences Strategic Leading Technology.” Chinese Academy of Sciences, 6 Sept. 2018, <https://archive.is/spmNg#selection-3389.0-3389.160>

<sup>105</sup> *Ibid.*

<sup>106</sup> *Ibid.*

<sup>107</sup> *Ibid.*

<sup>108</sup> *Ibid.*

<sup>109</sup> Shi, Zheng-li. “Curriculum Vitae.” <https://www.ws-virology.org/wp-content/uploads/2017/11/Zhengli-Shi.pdf>

<sup>110</sup> “Study on the evolutionary mechanism of bat SARS-like coronavirus adapted to host receptor molecules and the risk of cross-species infection.”

<sup>110</sup> *MedSci*, <https://archive.is/g35C6#selection-1425.0-1425.139>

<sup>111</sup> *Ibid.*

<sup>112</sup> “Guidelines for the application of the ‘Pathogen Host Adaptation and Immune Intervention’ project of the Chinese Academy of Sciences Strategic Leading Technology.” *Chinese Academy of Sciences*, 6 Sept. 2018, <https://archive.is/spmNg#selection-3389.0-3389.160>



Shi did not publish any papers funded by this grant before the start of the pandemic. As such, it is impossible to know what experiments she was conducting in the months prior to the pandemic.

Further evidence expands on Shi's work in 2018 and 2019. In January 2019, Shi and several other scientists were awarded a National Natural Science Award Second Prize for a project entitled, "Research on Important Viruses Carried by Chinese Bats."<sup>113</sup> Five out of the six researchers on the award were coauthors of the previously discussed 2013 paper entitled, "Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor."

In January 2019, Ben Hu, was awarded \$385,850 in grant money (grant no. 31800142) by the Youth Science Fund Project (YSFP) of the National Natural Science Foundation of China.<sup>114</sup> The YSFP "supports the young researchers to independently select topics within the scope of the scientific funding and carry out basic research."<sup>115</sup> This project, selected by Ben Hu, was titled, "Pathogenicity of two new bat SARS-related coronaviruses to transgenic mice expressing human ACE2."<sup>116</sup> To date, the two novel SARS-related coronaviruses have not been identified, and the grant money has only been cited in papers published about SARS-CoV-2.

WIV researchers confirmed to the WHO investigative team that they were conducting experimentations testing chimeric coronaviruses in 2018 and 2019.<sup>117</sup> According to an interview with Shi published by *Science*, all coronavirus experimentation, including infecting hACE2 mice and civets, was done at the BSL-2 and BSL-3 levels – "the coronavirus research in our laboratory is conducted in BSL-2 or BSL-3 laboratories."<sup>118</sup>

This ongoing work appears to coincide with Peter Daszak's stated goal of developing a broad-spectrum coronavirus vaccine. In a May 19, 2020, interview with "This Week in Virology," Daszak discussed the goal of the gain-of-function work he funded on coronaviruses with the WIV (emphasis added):

Coronaviruses are pretty good – I mean you're a virologist, you know all this stuff – but the... you can... um manipulate them in the lab pretty easily. The spike protein drives a lot of what happens with the coronavirus – zoonotic risk. So, you can get the sequence, you can build the protein, and we work with Ralph Baric at UNC to do this, insert it into a backbone of another virus, and do some work in the lab. So, you can get more predictive when you find a sequence – you've got this diversity. Now, the logical progression for vaccines is, if you're going to develop a vaccine for SARS, people are going to use pandemic SARS, but let's try to insert some of these other related [viruses] and get a better vaccine.

113 "Catalogue and introduction of the 2018 National Natural Science Award winning projects." *Ministry of Science and Technology*, 8 Jan. 2019, <https://archive.is/jKq7B#selection-187.0-187.86>

114 "Pathogenicity of two new bat SARS-related coronaviruses to transgenic mice expressing human ACE2." *MedSci*, <https://archive.is/shrM2#selection-1545.0-1558.0>

115 "[Good News] 100% winning bid! All applications of the National Natural Science Foundation of China(NSFC) were approved." *Faculty of Economics and Management, ECNU Academy of Statistics and Interdisciplinary Sciences*, 11 May 2020, <http://asis.ecnu.edu.cn/asisenglish/64/ba/c23635a287930/page.htm>

116 "Pathogenicity of two new bat SARS-related coronaviruses to transgenic mice expressing human ACE2." *MedSci*, <https://archive.is/shrM2#selection-1545.0-1558.0>

117 Joint Report – ANNEXES.

118 Shi, Zheng-li. "Reply to Science Magazine." *Science Magazine*, <https://www.sciencemag.org/sites/default/files/Shi%20Zhengli%20Q%26A.pdf>

119 Racaniello, Vincent. "TWiV 615: Peter Daszak of EcoHealth Alliance." YouTube, interview by Vincent Racaniello, 19 May 2020, [https://www.youtube.com/watch?v=IdYDL\\_RK--w](https://www.youtube.com/watch?v=IdYDL_RK--w)

Shi, Hu, and others at the WIV were the ones collecting, identifying, genetically modifying, and testing these novel coronaviruses against human immune systems for Peter Daszak.

**In sum, in the years leading up to the emergence of SARS-CoV-2, there was:**

- **Research by Shi and others at the WIV on how to alter the spike protein of non-infectious SARS-like coronaviruses so that they can bind to human ACE2 receptors;**
- **Repeated collaboration between Shi, Hu, Daszak, Wang, and other researchers on genetically manipulating coronaviruses to increase their infectiousness in humans;**
- **A new PRC Strategic Priority Research Program, run by Shi, that was actively manufacturing chimeric viruses in BSL-2 and BSL-3 conditions and seeking out novel viruses;**
- **Evidence of ongoing collaboration between Shi and the other scientists who first isolated a live coronavirus in 2013;**
- **A second grant awarded to Hu to test novel coronaviruses against human immune systems in BSL-2 and BSL-3 conditions;**
- **A stated effort to develop a broad-spectrum coronavirus vaccine.**

**Given the above, it is self-evident that Shi and her colleagues, with funding and support from Daszak, were actively genetically manipulating coronaviruses and testing them against human immune systems in 2018 and 2019, before the beginning of the pandemic.**

### Unusual Features of SARS-CoV-2

Committee Minority Staff interviews with scientists and current and former U.S. government officials raised several questions about the natural origins of SARS-CoV-2, including:

1. The highly infectious nature of SARS-CoV-2, which they consider as infectious as measles;
2. The lack of an identified intermediate host (found 4 months after the outbreak of SARS and 9 months after MERS); and
3. The highly efficient binding to human ACE2.

The highly contagious nature of SARS-CoV-2 has been a hot topic of conversation since the virus began to spread around the world. Some scientists and other experts point to the incredibly high case numbers as evidence that SARS-CoV-2 is inherently different from known natural betacoronaviruses. For example, MERS first appeared in 2012 and has infected less than 4,000 people. SARS first appeared in 2002 and infected less than 10,000. At the time of writing, less than two years from when it has first appeared, SARS-CoV-2 has infected more than 196.4 million people.

SARS-CoV-2 also has a highly unusual affinity for binding to human ACE2 receptors over other hosts. In February 2020, American researchers examined this issue closely. They found that SARS-CoV-2's spike protein "binds at least 10 times more tightly than the corresponding spike protein of severe acute respiratory syndrome (SARS)-CoV to their common host cell receptor."<sup>120</sup> In other words, SARS-CoV-2 binds more than 10 times more tightly to human ACE2 than the virus that causes SARS. The researchers found this likely explains why the virus is so contagious.<sup>121</sup>

120 Wrapp, Daniel et al. "Cryo-EM structure of the 2019-nCoV spike in the prefusion conformation." *Science*, 13 March 2020, 367(6483): 1260-1263. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7164637/>

121 *Ibid.*

Australian and British researchers also examined how SARS-CoV-2 binds to the ACE2 of various animals, publishing their research in *Scientific Reports* on June 24, 2021. The scientists found that SARS-CoV-2's spike protein binds the strongest to human ACE2. They reported (emphasis added):

This finding was surprising as a **zoonotic virus typically exhibits the highest affinity initially for its original host species**, with lower initial affinity to receptors of new host species until it adapts. As the virus adapts to its new host, mutations are acquired that increase the binding affinity for the new host receptor. Since **our binding calculations were based on SARS-CoV-2 samples isolated in China from December 2019**, at the very onset of the outbreak, the extremely high affinity of S protein for human ACE2 was unexpected.<sup>122</sup>

The first preprint version of this paper went further, concluding, “the data indicates that SARS-CoV-2 is uniquely adapted to infect humans, **raising important questions as to whether it arose in nature by a rare chance event or whether its origins might lie elsewhere**” emphasis added.<sup>123</sup> **This research provides evidence that SARS-CoV-2 is uniquely well adapted to humans, suggesting a non-zoonotic source of the outbreak.**

### The Furin Cleavage Site

One of the most discussed questions centers around the furin cleavage site (FCS) of SARS-CoV-2. The FCS is part of the virus' spike protein, which enables it to bind to and enter human cells. In February 2020, French and Canadian scientists reported SARS-CoV-2 contains an FCS that is absent in other coronaviruses of the same clade, or branch of viruses believed to have a similar common ancestor. The scientists also reported that when a bronchitis virus was modified by inserting a similar cleavage site, the virus' pathogenicity was increased.<sup>124</sup> While some scientists have noted that other coronaviruses contain furin cleavage sites, phylogenetic analysis shows that SARS-CoV-2 is the only identified sarbecovirus (a subsection of *betacoronaviruses*) with this feature.<sup>125</sup>

In January 2021 a group of American researchers published “Loss of furin cleavage site attenuates SARS-CoV-2 pathogenesis” in *Nature*. In the article, researchers reported the FCS “may have facilitated the emergence of SARS-CoV-2 in humans.”<sup>126</sup> Using a reverse genetic system, they created a mutant strain of SARS-CoV-2 which lacked the FCS. The result was a virus that was weakened in human respiratory cells and that exhibited reduced development in hACE2 expressing mice. This demonstrates the importance of the FCS in the rapid spread of COVID-19.

122 Piplani, S., et. al. “In silico comparison of SARS-CoV-2 spike protein-ACE2 binding affinities across species and implications for virus origin.” *Scientific Reports*, 24 June 2021, 11(13063) <https://www.nature.com/articles/s41598-021-92388-5>

123 Piplani, S., et. al. Preprint of “In silico comparison of SARS-CoV-2 spike protein-ACE2 binding affinities across species and implications for virus origin.” *ArXiv*, 13 May 2020, <https://arxiv.org/abs/2005.06199v1>

124 Coutard, B et al. “The spike glycoprotein of the new coronavirus 2019-nCoV contains a furin-like cleavage site absent in CoV of the same clade.” *Antiviral Research*, Feb. 2020, 176: 104742 <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7114094/>

125 Wu, Yiran, and Suwen Zhao. “Furin cleavage sites naturally occur in coronaviruses.” *Stem Cell Research*, 9 Dec. 2020, 50:102115. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7836551/>

126 Johnson, B.A., et. al. “Loss of furin cleavage site attenuates SARS-CoV-2 pathogenesis.” *Nature*, 25 Jan. 2021, 591: 293-299. <https://www.nature.com/articles/s41586-021-03237-4>

In other words, did the FCS develop naturally, or was it added in via genetic manipulation? Part of the genetic sequence for the FCS includes a CGG double codon (CGG-CGG). This group of six nucleotides (a group of three nucleotides is also known as a codon) is half of the 12 nucleotides that create the FCS. SARS-CoV-2 is the only identified coronavirus within its class to feature this combination. Some believe this is evidence of genetic manipulation, arguing this double codon is a telltale sign of the FCS being artificially inserted into the virus.<sup>127</sup>

### The “No-See-Um” Method

Critics of the theory that the virus was genetically modified or man-made have repeatedly pointed to the apparent lack of telltale signs of genetic manipulation in the SARS-CoV-2 genome. They claim this is “proof” the virus was not only naturally occurring, but that the COVID-19 pandemic could only be the result of a zoonotic spillover event. Such arguments ignore key pieces of evidence to the contrary.

In 2005, Ralph Baric, one of the researchers at UNC Chapel Hill with whom Shi would later collaborate with between 2014 and 2016, published a paper entitled, “Development of mouse hepatitis virus and SARS-CoV infectious cDNA constructs.”<sup>128</sup> In this paper, Baric references using a novel genetic engineering system he developed with other UNC colleagues to engineer full-length SARS-CoV genomes via a “no-see-um” method. This method allows for the assembly of various partial genomic sequences into a full-length genome, creating a new and infectious coronavirus.<sup>129</sup> The publication includes the below figure, which is titled, “Systemic Assembly Strategy for the SARS-CoV infectious clone.” It clearly shows the various SARS fragments and how they were used to create a full-length, custom genomic sequence.

**Molecularly cloned viruses were indistinguishable from wild type.**

**– Dr. Ralph Baric**

127 Quay, Steven, and Richard Muller. “The Science Suggests a Wuhan Lab Leak.” *The Wall Street Journal*, 6 June 2021, [www.wsj.com/articles/the-science-suggests-a-wuhan-lab-leak-11622995184](https://www.wsj.com/articles/the-science-suggests-a-wuhan-lab-leak-11622995184).

128 Baric R.S., Sims A.C. “Development of Mouse Hepatitis Virus and SARS-CoV Infectious cDNA Constructs.” *Curr Top Microbiol Immunol*, 2005; 287:229-52. [https://doi.org/10.1007/3-540-26765-4\\_8](https://doi.org/10.1007/3-540-26765-4_8)

129 *Ibid.*

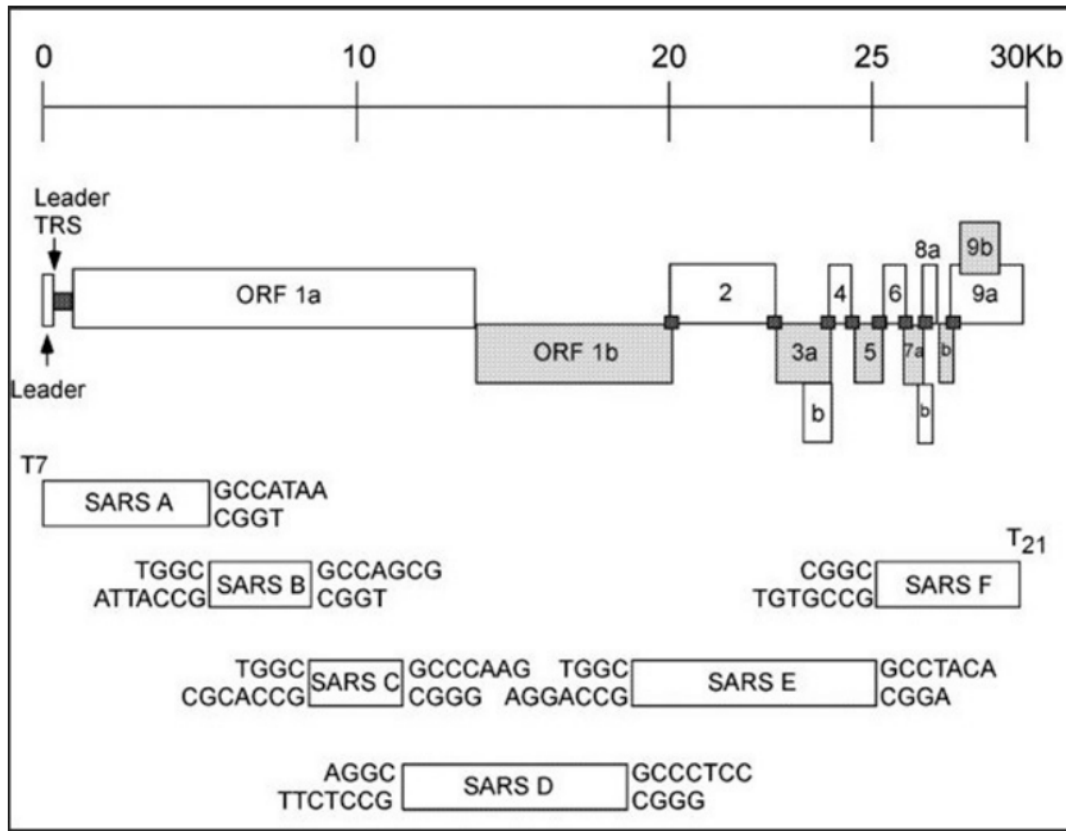


Fig. 5: Baric's "No-See-Um" System

The paper stated these viruses were "indistinguishable from wild type,"<sup>130</sup> meaning that it is impossible to tell they were synthetically created.

Baric himself confirmed this interpretation in a September 2020 interview, where he stated, "You can engineer a virus without leaving any trace. The answers you are looking for, however, can only be found in the archives of the Wuhan laboratory."<sup>131</sup> Referring to chimeric viruses he generated in 2015 with WIV researchers, Baric said his team intentionally left signature mutations to show that it was genetically engineered. "Otherwise there is no way to distinguish a natural virus from one made in the laboratory."<sup>132</sup>

Shi and Baric have collaborated on multiple papers regarding coronaviruses. The most recent of which was in May 2020, when they joined other researchers in publishing "Pathogenesis of SARS-CoV-2 in Transgenic Mice Expressing Human Angiotensin-Converting Enzyme 2."<sup>133</sup> One year later, Baric signed onto a May 14, 2021, letter published in *Science* which argued that the lab leak theory must be taken seriously and should be fully evaluated.<sup>134</sup>

<sup>130</sup> *Ibid.*

<sup>131</sup> Renda, Silvia. "Possibile Creare Un Virus in Laboratorio Senza Lasciare Traccia? La Risposta Dell'autore Della Chimera Del 2015 Di Cui Parlò Tg Leonardo." *L'HuffPost*, 14 Sept. 2020, [www.huffingtonpost.it/entry/e-possibile-creare-un-virus-in-laboratorio-senza-lasciare-traccia-la-risposta-dellesperto\\_it\\_5f5f3993c5b62874bc1f7339](https://www.huffingtonpost.it/entry/e-possibile-creare-un-virus-in-laboratorio-senza-lasciare-traccia-la-risposta-dellesperto_it_5f5f3993c5b62874bc1f7339).

<sup>132</sup> *Ibid.*

<sup>133</sup> Jiang, Ren-Di et al. "Pathogenesis of SARS-CoV-2 in Transgenic Mice Expressing Human Angiotensin-Converting Enzyme 2." *Cell*, 21 May 2020, 182(1): 50-58.e8, <https://dx.doi.org/10.1016%2Fj.cell.2020.05.027>.

<sup>134</sup> Bloom, Jesse D., et. al. "Investigate the origins of COVID-19." *Science*, 14 May 2021; 372(6543): 694. <https://science.sciencemag.org/content/372/6543/694.1>

In 2017, a dissertation was submitted to the University of Chinese Academy of Sciences by Zeng Leiping, a doctoral student working at the WIV, entitled “Reverse Genetic System of Bat SARS-like Coronaviruses and Function of ORFX.”<sup>135</sup> The referenced reverse genetic system is the same that was used by the WIV in 2016 to create genetically modified viruses and conduct experiments with live viruses under BSL-2 conditions. In his dissertation, Zeng stated that he and other WIV researchers used this system to “construct an S gene chimeric recombinant viral infectious BAC clone with WIV1 as the backbone and without leaving any trace sequences (e.g. incorporated enzymatic sites) in the recombinant viral genome” (emphasis added).

In an end-of-chapter discussion in the dissertation, Zeng reiterates this lack of evidence of genetic manipulation, stating:

We established a reverse genetics system for coronaviruses, and based on the genomic backbone of WIV1, we **established a scheme to replace the S gene without traces**, constructed infectious BAC clones of 12 S-gene chimeric recombinant viruses, and successfully rescued. Four of these recombinant viral strains (including Rs4231, Rs4874, Rs7327, and SHC014) were tested for ACE2 utilization by these strains in humans, civets, and bats.

Zeng was employed at the WIV when he submitted his dissertation, and Shi was his advisor. **As such, it is clear that Shi and others at the WIV not only possessed the capability to genetically modify coronaviruses “without traces,” but were actively doing so in the years leading up to the current pandemic.** It appears Zeng Leiping is currently a postdoctoral research fellow in bioengineering at Stanford University.

#### IV. EVIDENCE OF A LAB LEAK COVER-UP

In addition to the events previously discussed (sequence database taken offline, road closures during the MWG, etc.), there are several additional incidents that suggest the PRC, WIV researchers, and others were actively working to suppress and discredit early conversations that the virus could have been man-made or that it could have leaked from a WIV facility.

In April 2012, six miners working in a copper mine located in Yunnan province of the PRC fell ill. Between the ages of 30 and 63, the workers presented to a hospital in Kunming with “persistent coughs, fevers, head and chest pains and breathing difficulties.”<sup>139</sup> Three of the six eventually died. Researchers from the WIV were asked to investigate and test samples from the sick miners. They also began collecting samples from bats in the cave that housed the mine, which led to the discovery of several new coronaviruses. As a result, the WIV began a long-term study of the mine, collecting samples each year. Despite this, Shi maintains the miners were killed by a fungus growing on bat feces not from a virus.<sup>140</sup>

<sup>135</sup> Leiping, Zeng. *Reverse Genetic System of Bat SARS-like Coronaviruses and Function of ORFX*. 2017. The University of Chinese Academy of Sciences, PhD dissertation. English translation first made available by @TheSeeker268 on Twitter, <https://twitter.com/TheSeeker268/status/1392575597772107776?s=20>

<sup>136</sup> *Ibid.*

<sup>137</sup> *Ibid.*

<sup>138</sup> “Leiping Zeng.” *Stanford*, <https://profiles.stanford.edu/leiping-zeng>

<sup>139</sup> Stanway, David. “Explainer: China's Mojiang Mine and Its Role in the Origins of COVID-19.” *Reuters*, 9 June 2021, [www.reuters.com/business/healthcare-pharmaceuticals/chinas-mojang-mine-its-role-origins-covid-19-2021-06-09/](http://www.reuters.com/business/healthcare-pharmaceuticals/chinas-mojang-mine-its-role-origins-covid-19-2021-06-09/).

<sup>140</sup> Qiu, Jane. “How China's 'Bat Woman' Hunted Down Viruses from SARS to the New Coronavirus.” *Scientific American*, 1 June 2020, [www.scientificamerican.com/article/how-chinas-bat-woman-hunted-down-viruses-from-sars-to-the-new-coronavirus/](http://www.scientificamerican.com/article/how-chinas-bat-woman-hunted-down-viruses-from-sars-to-the-new-coronavirus/)

ID4991 vs. RaTG13: SARS-CoV-2's "Closest Relative"

A 2016 paper published by PRC researchers (most of whom are affiliated with the WIV) describes these efforts as researchers conducting “surveillance of coronaviruses in bats in an abandoned mineshaft in Mojiang County, Yunnan Province, China, from 2012–2013.”<sup>141</sup> Shi and Hu are listed as coauthors. WIV researchers identified two new betacoronaviruses – HiBtCoV/3740-2 and RaBtCoV/4991. The study concluded, “RaBtCoV/4991 showed more divergence from human SARS-CoV than other bat SL-CoVs and could be considered as a new strain of this virus lineage.”<sup>142</sup> Shi designed and coordinated the study, drafted the manuscript, and is listed as the corresponding author.

Four years later and after the initial reports of an unknown SARS-like coronavirus in Wuhan, Shi and 28 other PRC scientists submitted an article to *Nature* for publication entitled, “A pneumonia outbreak associated with a new coronavirus of probably bat origin,”<sup>143</sup> on January 20, 2020. It was published in early February. It should be noted that this manuscript was submitted on the same day the PRC’s National Health Commission first issued a statement confirming human-to-human transmission – one month after local health officials warned the CCP human-to-human transmissions were occurring.<sup>144</sup> It is highly unlikely Shi and her coauthors would have written this paper the same day they submitted it, meaning they were aware for days or perhaps weeks that the virus was spreading via from human-to-human transmission and did not alert the world. According to a study by researchers at the University of Southampton, implementing appropriate restrictions based on human-to-human transmission just one week before this paper was published would have reduced the number of cases in Wuhan by 66%.<sup>145</sup> This would have made a significant difference in the spread of the virus, especially in conjunction with the significant travel that occurred during the Spring Festival, which ran from January 10 to January 23, 2020, when the city of Wuhan was locked down.

Shi is listed as the corresponding author for the article, which states that COVID-19 “has now progressed to be transmitted by human-to-human contact.”<sup>146</sup> The researchers conclude that RaTG13, an allegedly naturally occurring bat coronavirus, is the closest relative to SARS-CoV-2 (emphasis added):

**We then found that a short region of RNA-dependent RNA polymerase (RdRp) from a bat coronavirus (BatCoV RaTG13)—which was previously detected in *Rhinolophus affinis* from Yunnan province—showed high sequence identity to 2019-nCoV. We carried out full-length sequencing on this RNA sample (GISAID accession number EPI\_ISL\_402131). Simplot analysis showed that 2019-nCoV was highly similar throughout the genome to RaTG13 (Fig. 1c), with an overall genome sequence identity of 96.2%. Using the aligned genome sequences of 2019-nCoV, RaTG13, SARS-CoV and previously reported bat SARSr-CoVs, no evidence for recombination events was detected**

<sup>141</sup> Ge, Xing-Yi et al. “Coexistence of multiple coronaviruses in several bat colonies in an abandoned mineshaft.” *Virologica Sinica*, 3 Feb. 2016; 31(1): 31-40. <https://dx.doi.org/10.1007%2Fs12250-016-3713-9>

<sup>142</sup> Ibid.

<sup>143</sup> Zhou, P., et al. “A pneumonia outbreak associated with a new coronavirus of probable bat origin.” *Nature*, 3 Feb 2020, 579: 270–273. <https://doi.org/10.1038/s41586-020-2012-7>

<sup>144</sup> Wang, Yanan. “Human-to-Human Transmission Confirmed in China Coronavirus.” *AP NEWS*, 20 Jan. 2020. <https://apnews.com/14d7dcffa205d9022fa9ea593bb2a8c5>

<sup>145</sup> Lai, Shengjie, et al. “Effect of Non-Pharmaceutical Interventions for Containing the COVID-19 Outbreak in China.” *MedRxiv*, 2020, <https://www.medrxiv.org/content/10.1101/2020.03.03.20029843v3>.

<sup>146</sup> Zhou (2020).



in the genome of 2019-nCoV. Phylogenetic analysis of the full-length genome and the gene sequences of RdRp and spike (S) showed that—for all sequences—**RaTG13 is the closest relative of 2019-nCoV and they form a distinct lineage from other SARSr-CoVs (Fig. 1d and Extended Data Fig. 2)...The close phylogenetic relationship to RaTG13 provides evidence that 2019-nCoV may have originated in bats.**<sup>147</sup>

A close examination of the paper, and the corrections published months later, reveal inconsistencies in the researchers' claims. Several of the statements made in the above quotation are simply false. After months of criticism and questioning about RaTG13, Shi and the other researchers were forced to publish an addendum on November 17, 2020. **That addendum reveals that RaTG13 was actually ID4991, the sample collected years prior in 2012 or 2013, and that the full-length genomic sequence was obtained in 2018, not in January 2020 as the paper originally stated.**<sup>148</sup>

Unfortunately, no other labs can confirm the genomic sequence of RaTG13 – Shi said in an interview published in *Science Magazine* that the entire sample was used up after genomic sequencing.<sup>149</sup> The inability of outside researchers to verify the genome of RaTG13, and the above efforts to obfuscate when the WIV collected and sequenced RaTG13, raises multiple questions:

- Why leave out of the February 2020 article that the virus sequence was renamed?
- Why lie about when the full-length sequence was obtained?
- Why only issue a correction almost ten months later?
- Why was this sample destroyed via testing when others weren't?

In December 2020, reporters from *BBC News* attempted to visit the cave in Yunnan where RaTG13 was collected. They found themselves followed by plain-clothes police officers and stopped at checkpoints where they were told to stay out of the area.<sup>150</sup> A French publication, *Envoye Special*, produced a video in which they reported conversations with villagers who lived near the mine. According to one of those villagers, the mine was closed and monitored via surveillance cameras. That villager also alleged several people were arrested for venturing too close to the mine.<sup>151</sup>

It is important to note that in March 2020, American, British, and Australian researchers published “The proximal origin of SARS-CoV-2” in *Nature Magazine*.<sup>152</sup> Regarding RaTG13, they found, “Although RaTG13, sampled from a *Rhinolophus affinis* bat, is ~96% identical overall to SARS-CoV-2, its spike diverges in the RBD, which suggests that it may not bind efficiently to human ACE2.” “RBD” is an abbreviation for receptor-binding domain, part of the virus' spike protein. **This is the same part of the virus' genome that Shi, Hu, and other WIV researchers were genetically modifying and replacing as far back as 2015.**

<sup>147</sup> *Ibid.*

<sup>148</sup> Zhou, P., et al. “Addendum: A pneumonia outbreak associated with a new coronavirus of probable bat origin.” *Nature*, 17 Nov. 2020, 588: E6. <https://doi.org/10.1038/s41586-020-2951-z>

<sup>149</sup> Shi, Zheng-li. “Reply to Science Magazine.” *Science Magazine*, <https://www.sciencemag.org/sites/default/files/Shi%20Zhengli%20Q%20Q%26A.pdf>

<sup>150</sup> Sudworth, John. “Covid: Wuhan Scientist Would ‘Welcome’ Visit Probing Lab Leak Theory.” *BBC News*, 21 Dec. 2020, [www.bbc.com/news/world-asia-china-55364445](http://www.bbc.com/news/world-asia-china-55364445).

<sup>151</sup> Asis, Francisco de. “Quite Important the Conversation with Danaoshan Inhabitant.- He Pointed towards the Location We Already Knew for the Mine.- The Roadblocks Are Probably the Diverted Traffic We Already Observed Too.Rest of the Story Is Just Incredible! Pic.twitter.com/kzHz7v5rSg.” *Twitter*, Twitter, 12 Mar. 2021, <https://twitter.com/franciscocodeasis/status/1370183826731888641?s=20>.

<sup>152</sup> Andersen, Kristian G et al. “The proximal origin of SARS-CoV-2.” *Nature Medicine*, 17 March 2022, 26(4):450-452. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7095063/>

<sup>153</sup> *Ibid.*



If SARS-CoV-2 was genetically modified, this could represent a viable model for how. RaTG13's RBD, or full spike protein, could be replaced using the WIV's reverse genetic system. If one of the many unpublished coronaviruses in the WIV's possession was modified, and the resulting chimeric virus was then exposed to hACE2 expressing mice or civets, the resulting virus could become better adapted to infecting humans – just like SARS-CoV-2.

According to scientists – including those working at the WIV – ID4991/RaTG13 is more closely related to SARS-CoV-2 than any other publicly identified virus. It's now clear WIV researchers had this virus as early as 2013, several years before the WIV began genetically modifying other coronaviruses found in the wild. **Given the largest difference between RaTG13 and SARS-CoV-2 is at the spike protein – precisely where the WIV modified various coronaviruses for years – and that WIV researchers renamed the virus and lied about when they sequenced, ID4991/RaTG13 could be a source of genetic material if SARS-CoV-2 was indeed genetically modified.**

According to emails obtained by *Buzzfeed News*, it appears Kristian G. Andersen, the lead and corresponding author of the abovementioned article, initially considered this a viable theory. In a January 31, 2020 email to Dr. Anthony Fauci, the director of NIAID, Andersen stated that parts of the virus were possibly engineered and inconsistent with evolutionary theory:

**From:** Kristian G. Andersen (b) (6) >  
**Sent:** Friday, January 31, 2020 10:32 PM  
**To:** Fauci, Anthony (NIH/NIAID) [E] (b) (6)  
**Cc:** Jeremy Farrar (b) (6) >  
**Subject:** Re: FW: Science: Mining coronavirus genomes for clues to the outbreak's origins

Hi Tony,

Thanks for sharing. Yes, I saw this earlier today and both Eddie and myself are actually quoted in it. It's a great article, but the problem is that our phylogenetic analyses aren't able to answer whether the sequences are unusual at individual residues, except if they are completely off. On a phylogenetic tree the virus looks totally normal and the close clustering with bats suggest that bats serve as the reservoir. 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.

We have a good team lined up to look very critically at this, so we should know much more at the end of the weekend. I should mention that after discussions earlier today, Eddie, Bob, Mike, and myself all find the genome inconsistent with expectations from evolutionary theory. But we have to look at this much more closely and there are still further analyses to be done, so those opinions could still change.

Best,  
 Kristian

154

Fig. 8: Andersen Email Suggesting SARS-CoV-2 was Genetically Modified

The WIV's intentionally misleading February 2020 paper regarding RaTG13 was uploaded as a preprint on January 23rd<sup>155</sup>. Given that Andersen and his coauthors cited it in their March 2020 paper, it is all but certain that Andersen, Dr. Fauci, and the others would have seen it before Andersen sent this email. The day after Anderson emailed Dr. Fauci on February 1, 2020, Dr. Fauci, Andersen, and others debated this issue via teleconference. Previously, they had agreed to keep the debate confidential. Following this discussion, Andersen abandoned his claims that the virus was genetically modified.<sup>156</sup> It is unclear what was said on this call that led to Anderson doing so.

<sup>154</sup> Andersen, Kristian G. Email to Anthony Fauci and Jeremy Farrar. 31 Jan. 2020.

<https://s3.documentcloud.org/documents/20793561/leopold-nih-foia-anthony-fauci-emails.pdf>

<sup>155</sup> Zhou, Peng, et. al. Preprint of "Discovery of a novel coronavirus associated with the recent pneumonia outbreak in humans and its potential bat origin." 23 Jan. 2020, *bioRxiv*, <https://www.biorxiv.org/content/10.1101/2020.01.22.914952v2>

<sup>156</sup> Young, Alison. "I Remember It Very Well": Dr. Fauci Describes a Secret 2020 Meeting to Talk about COVID Origins." *USA Today*, 18 June 2021, [www.usatoday.com/story/opinion/2021/06/17/anthony-fauci-2020-meeting-covid-origins/7737494002/](https://www.usatoday.com/story/opinion/2021/06/17/anthony-fauci-2020-meeting-covid-origins/7737494002/).

### Additional Cover-Up Activities by Scientists at the WIV

As more investigative work continues on the type of research being conducted at the WIV, CCP censors and WIV researchers have been deleting or scrubbing references to coronavirus research that could be related to the origins of the COVID-19 pandemic. As previously discussed, Ben Hu received a Youth Science Fund Project award to test the pathogenicity of two novel SARS-related coronaviruses beginning in 2019. In some publicly facing PRC websites, Hu's name has now been struck from the grant.




C010802	To study the mechanism of baculovirus Ac34 protein inhibiting the nuclear pathway of mammalian CRM1	Mu Jingfang	Wuhan Institute of Virology, Chinese Academy of Sciences 
C010802	Pathogenicity of two new bat SARS-related coronaviruses to transgenic mice expressing human ACE2		Wuhan Institute of Virology, Chinese Academy of Sciences 
H1904	Study on the mechanism of enterovirus 71 type 3A protein antagonizing RNAi antiviral immunity	Qiu Yang	Wuhan Institute of Virology, Chinese Academy of Sciences 

Fig. 9: Ben Hu's Name Removed From 2019 Grant <sup>157</sup>

Of the almost 80 WIV grants listed in the database, the one awarded to Ben Hu is the only one that does not identify the principal investigator.

A December 12, 2017, interview with Hu was pulled offline after it began circulating on Twitter. In the article, Hu discusses monitoring and collecting samples from the bat cave in Yunnan and his work using the reverse genetic system to insert spike proteins into live coronaviruses. Interestingly, he discusses how Shi Zheng-li “often personally leads the team to take samples.” <sup>158</sup> It is likely that this article was pulled down for drawing attention to the cave where RaTG13 was collected.

Similarly, a 2018 article written by Hu and published <sup>159</sup> on the website for the Wuhan Branch of the Chinese Academy of Sciences has also been removed. While the article broadly discusses the work of Shi and other researchers at the WIV, it does not offer any unique insight or evidence of dangerous research. So why was it removed?

<sup>157</sup> 2019 Natural Science Foundation Query and Analysis System. <https://journal.medsci.cn/m/nsfc.do?u=%E4%B8%AD%E5%9B%BD%E7%A7%91%E5%AD%A6%E9%99%A2%E6%AD%A6%E6%B1%89%E7%97%85%E6%AF%92%E7%A0%94%E7%A9%B6%E6%89%80>

<sup>158</sup> “Hunting bat viruses, tracking the origin of SARS, an interview with Dr. Hu Ben, Wuhan Institute of Virology, Chinese Academy of Sciences.” *First Author*, 12 Dec. 2017, <https://archive.vn/sVHmq#selection-45.79-45.215>

<sup>159</sup> Hu, Ben. “The Wuhan Institute of Virology's “Research on Chinese Bats Carrying Important Viruses” won the first prize of the 2018 Hubei Provincial Natural Science Award.” *Wuhan Branch, Chinese Academy of Sciences*, 13 April 2018, archived: [https://web.archive.org/web/20210107222832/http://whb.ac.cn/xw/kyjz/201811/t20181122\\_5191050.html](https://web.archive.org/web/20210107222832/http://whb.ac.cn/xw/kyjz/201811/t20181122_5191050.html)

Perhaps most incriminating are Shi's repeated lies about activities taking place at the WIV. In August 2020, after the publication of the Committee Minority Staff's interim report, the China Global Television Network interviewed Shi about our work. In the resulting article, Shi denied that Major General Chen Wei took over the BSL-4 lab:

Liu Xin: The report actually went further and said that the lab has been taken over by the Chinese military. It says that Major General Chen Wei has succeeded Yuan Zhiming as the Director of the WIV and Chen Wei is a Chinese military medical sciences expert.

Shi Zhengli: This is a rumor; there is no such thing.

Liu Xin: You absolutely deny that the Chinese military has taken over the WIV.

Shi Zhengli: Yes, it is a rumor.<sup>160</sup>

This is demonstrably false. As previously discussed, posts made on CCP-controlled forums announcing Chen's arrival acknowledged her takeover of the lab. The report stated, "PLA Maj. Gen. Chen Wei has been in Wuhan for more than 10 days. She took over the P4 lab as if it were a 'reassurance pill.'"<sup>161</sup>

During the same interview, and in response to Committee Minority Staff raising questions about a possible lab leak, Shi again lied, claiming that all of the WIV's research has been published and their samples available for review:

Another piece of evidence that I can give you is that our lab has been doing research for 15 years, and all our work has been published. We also have a library of our own genetic sequences, and we have experimental records of all our work related to the virus, which are accessible for people to check.<sup>162</sup>

This, again, is demonstrably false. The WIV's sequence library was taken offline in September 2019 and is not "accessible for people to check." Given the previously discussed undisclosed coronavirus research and military activities at the WIV, it is obvious that not "all" of the WIV's work has been published. Daszak confirmed this in an interview with *Nature*: "we have data that we've gathered over 15 years of working in China — 5 years under a previous grant from the NIH — which haven't been published yet."<sup>163</sup>

In a June 2021 interview, Shi told the *New York Times*, "my lab has never conducted or cooperated in conducting GOF experiments that enhance the virulence of viruses."<sup>164</sup> This is a bizarre claim given the years of published research, often designed and led by Shi, that explicitly sought to make coronaviruses more infectious to humans. In the same interview, Shi lied about WIV researchers falling ill in the fall of 2019 – "The Wuhan Institute of Virology has not come across such cases." This is despite the State Department's January 15th 2021 fact sheet and confirmation from a Dutch virologist on the WHO's investigative team that several researchers were sick.<sup>165</sup>

<sup>160</sup> Xin, Liu. "Exclusive Interview: CGTN's Liu Xin Talks to China's 'Bat Woman'." *CGTN*, 26 Aug. 2020,

<https://news.cgtn.com/news/2020-08-22/Can-politics-be-put-aside-while-looking-for-origins-of-coronavirus--T9HgctyKv6/index.html>.

<sup>161</sup> Guli.

<sup>162</sup> Xin.

<sup>163</sup> Subbaraman, Nidhi. "Heinous!: Coronavirus Researcher Shut down for Wuhan-Lab Link Slams New Funding Restrictions." *Nature News*, 21 Aug. 2020, [www.nature.com/articles/d41586-020-02473-4](http://www.nature.com/articles/d41586-020-02473-4).

<sup>164</sup> Qin, Amy, and Chris Buckley. "A Top Virologist in China, at Center of a Pandemic Storm, Speaks Out." *The New York Times*, 14 June 2021, [www.nytimes.com/2021/06/14/world/asia/china-covid-wuhan-lab-leak.html](http://www.nytimes.com/2021/06/14/world/asia/china-covid-wuhan-lab-leak.html)

<sup>165</sup> Gordon, Michael R., et al. "WSJ News Exclusive | Intelligence on Sick Staff at Wuhan Lab Fuels Debate on Covid-19 Origin." *The Wall Street Journal*, 23 May 2021, [www.wsj.com/articles/intelligence-on-sick-staff-at-wuhan-lab-fuels-debate-on-covid-19-origin-11621796228](http://www.wsj.com/articles/intelligence-on-sick-staff-at-wuhan-lab-fuels-debate-on-covid-19-origin-11621796228).

### Cover-Up Activities by the Chinese Communist Party

According to a WHO internal document from August 2020, the PRC put little effort into determining the source of the SARS-CoV-2 after January 2020:

Following extensive discussions with and presentation from Chinese counterparts, it appears that little had been done in terms of epidemiological investigations around Wuhan since January 2020. The data presented orally gave a few more details than what was presented at the emergency committee meetings in January 2020. No PowerPoint presentations were made and no documents were shared.<sup>166</sup>

Given the large amount of financial resources devoted by the PRC in the years prior for locating, sampling, identifying, and experimenting with coronaviruses, it is odd that little effort would be put into determining the source of the virus, if the source was unknown. In mid-February 2020, the PRC's Ministry of Science and Technology issued new guidelines for laboratory research in the PRC. Official PRC sources stressed:

The mention of biosafety at labs by the ministry has nothing to do with some saying that the coronavirus leaked from the Wuhan Institute of Virology of the Chinese Academy of Sciences.<sup>167</sup>

Experts interviewed in February 2020 by *The Global Times* stated that PRC labs paid "insufficient attention to biological disposal."<sup>168</sup> This included disposing of lab materials into sewage systems.<sup>169</sup>

Given that these new guidelines were issued after the PRC stopped searching for the source of the outbreak, it raises questions as to what prompted the PRC to stop its search.

Shortly thereafter, on February 25, 2020, the Chinese Center for Disease Control and Prevention issued supplementary regulations affecting how PRC scientists work on research related to COVID-19. The guidelines prohibit researchers from sharing data or samples and requires them to receive permission prior to conducting research or publishing the results.

**3. No one can, under their own name or in the name of their research team, provide other institutions and individuals with information related to the COVID-19 epidemic on their own, including data, biological specimens, pathogens, culture, etc.**

**4. Before publishing papers and research results related to the COVID-19 epidemic, you must first report them to the Science and Technology Group/Department for preliminary review, and if necessary, submit it to the Emergency Leading Group or the Department of Science and Education of the National Health Commission for approval.**

**Papers that have been submitted but not yet reviewed by the Science and Technology Group/Department should be withdrawn as soon as possible and redone according to these regulations.**

*Fig. 10: Excerpt from China CDC Regulations Issued on February 25th*<sup>170</sup>

<sup>166</sup> Kirchgaessner, Stephanie. "China Did 'Little' to Hunt for Covid Origins in Early Months, Says WHO Document." *The Guardian*, 23 Feb. 2021, [www.theguardian.com/world/2021/feb/23/china-did-little-hunt-covid-origins-early-months-says-who-document](http://www.theguardian.com/world/2021/feb/23/china-did-little-hunt-covid-origins-early-months-says-who-document)

<sup>167</sup> Caiyu, Liu, and Leng Shumei. "Biosafety Guideline Issued to Fix Chronic Management Loopholes at Virus Labs." *Global Times*, 16 Feb. 2020, [www.globaltimes.cn/content/1179747.shtml](http://www.globaltimes.cn/content/1179747.shtml).

<sup>168</sup> *Ibid.*

<sup>169</sup> *Ibid.*

A full copy of the regulations is included in the Appendix.

On February 27, 2020, *Health Times*, published remarks from an interview with Yu Chuanhua, who referenced health data from February 25th. Yu is the Vice President of the Hubei Health Statistics and Information Society and Professor of Epidemiology and Health Statistics at Wuhan University, and was running a database of confirmed COVID-19 cases in early 2020. In the interview, Yu stated he had evidence of COVID-19 cases as early as September 2019:

Professor Yu Chuanhua said, “For example, there is data on a patient who became ill on September 29. The data shows that the patient has not undergone nucleic acid testing. The clinical diagnosis (CT diagnosis) is a suspected case. The patient has died. This data has not been confirmed and there is no time to death. It may also be wrong data.” With the research of the database, Professor Yu Chuanhua found more and more case data before December 8. There were two cases in November, and the onset time was November 14 and November 21, 2019. Before December 8, there were also five or six cases. Among them, one patient who became ill at the end of November was hospitalized on December 2 and was clinically diagnosed with pneumonia.<sup>171</sup>

Before the interview was published on February 27th, Yu called the reporter and tried to retract the information regarding the two sick patients in November.<sup>172</sup> It is likely that this was done to comply with the China CDC gag order that was issued two days prior.

Nine days later, on March 5, 2020, the Joint Prevention and Control Mechanism (JPCM) of the State Council Novel Coronavirus Pneumonia Scientific Research Group issued a confidential memo, obtained by the *Associated Press*, entitled, “Notice on the Standardization of the Management and Publication of Novel Coronavirus Scientific Research.”<sup>173</sup> The notice announced the research group was taking control of all publication work related to the pandemic for “coordinated deployment.”<sup>174</sup> It also required units publishing research to notify the JPCM’s propaganda team, which was tasked to work with a special public opinion team to coordinate publication of research with public opinion and “social concerns.”<sup>175</sup>

170 Chinese Center for Disease Control and Prevention. “On the Supplementary Regulations on Strengthening the Management of Science and Technology During the Emergency Response to the Novel Coronavirus.” 25 Feb. 2020.

<https://www.documentcloud.org/documents/7340336-China-CDC-Sup-Regs.html>

171 Wang, Zhenya. “Experts Judge the Source of the New Crown: December 8 Last Year May Not Be the Earliest Time of Onset.” *Health Times*, 27 Feb. 2020, [www.jksb.com.cn/index.php?m=wap&a=show&catid=629&id=160018](http://www.jksb.com.cn/index.php?m=wap&a=show&catid=629&id=160018).

172 *Ibid.*

173 Joint Prevention and Control Mechanism of the State Council Novel Coronavirus Pneumonia Scientific Research Group. “Notice on the Standardization of the Management and Publication of Novel Coronavirus Scientific Research.” 3 Mar. 2020.

<https://www.documentcloud.org/documents/7340337-State-Research-regulations.html>

174 *Ibid.*

175 *Ibid.*

Each member work unit of the scientific research team will gather scientific research information within their own unit and systems, review and check the content and form of its publication, and report it to the scientific research team for approval in a timely manner. The scientific research group's dedicated teams of professionals and various experts are responsible for reviewing the publication's content and format and giving expert opinions, and when necessary, arranging expert assessment. After the scientific research group approves, the publishing work unit should, according to work requirements, arrange publication via press conferences, official websites, state social media, news media and other platforms, and notify the propaganda and scientific research teams of the Joint Prevention and Control Mechanism of the State Council. In principle, COVID-19 scientific research should be published first in the form of an official authoritative publication. The special group on public opinion should strengthen communication with the propaganda team, take into account the trend of public opinion and social concerns, and strengthen guidance of the publication of scientific research and information.

*Fig. 11: Excerpt from JPCM Memo*

The memo concludes with a warning: “Those who fail to apply for approval in accordance with the prescribed procedures and publish unconfirmed false information on scientific research, thereby causing serious adverse social impacts, shall be held accountable.”<sup>176</sup> A full copy of the memo is included in the Appendix. These documents are clear evidence of the CCP's effort to restrict research on SARS-CoV-2, so that the only research published supports the Party's official story on the origins and emergence of COVID-19.

After the release of the Committee Minority Staff's interim report on the origins of COVID-19, *China Global Television Network*, a PRC state-owned media outlet, released a propaganda video aimed at undermining this investigation. Entitled, “Clearing up confusion in McCaul report on COVID-19,” the approximately 45-minute video labels the report “misinformation.”<sup>177</sup> It also discusses what they call the “tired old theory that the virus could have leaked from a lab”<sup>178</sup> and reveals that Shi Zheng-li was interviewed about our report. The piece also claims the BSL-4 lab space at the WIV was never taken over by Maj. Gen. Chen Wei.<sup>180</sup> As discussed earlier, this statement is demonstrably untrue.

In June 2021, Jesse Bloom published a preprint entitled, “Recovery of deleted deep sequencing data sheds more light on the early Wuhan SARS-CoV-2 epidemic.” Bloom is a Principal Investigator and Associate Professor for Basic Sciences and the Herbold Computational Biology Program at Fred Hutch, a cancer research center. Bloom was able to recover multiple deleted viral sequences collected from patients in Wuhan in early December 2020. These sequences were originally uploaded to the NIH's Sequence Read Archive by researchers in Wuhan, but later deleted at their request.

<sup>176</sup> *Ibid.*

<sup>177</sup> “The Point: Clearing up Confusion in the McCaul Report On Covid-19.” *CCTV News*, 25 July 2020, [www.youtube.com/watch?v=n5qYogMTZOW](https://www.youtube.com/watch?v=n5qYogMTZOW).

<sup>178</sup> *Ibid.*

<sup>179</sup> *Ibid.*

<sup>180</sup> *Ibid.*

Oddly, these samples more greatly diverge from SARS-CoV-2's bat coronavirus ancestor – “the earliest SARSCoV-2 sequences were collected in Wuhan in December, but these sequences are more distant from RaTG13 than sequences collected in January from other locations in China or even other countries.”<sup>181</sup> Bloom concludes (emphasis added):

**The fact that this informative data set was deleted suggests implications beyond those gleaned directly from the recovered sequences.** Samples from early outpatients in Wuhan are a gold mine for anyone seeking to understand spread of the virus. Even my analysis of 13 partial sequences is revealing, and it clearly would have been more scientifically informative to fully sequence all 34 samples rather than delete the partial sequence data. **There is no obvious scientific reason for the deletion:** the sequences are concordant with the samples described in Wang et al. (2020a,b), there are no corrections to the paper, the paper states human subjects approval was obtained, and the sequencing shows no evidence of plasmid or sample-to-sample contamination.... Even though the sequencing data were on the Google Cloud (as described above) and the mutations were listed in a table in the Small paper by Wang et al. (2020b), **the practical consequence of removing the data from the SRA was that nobody was aware these sequences existed.** Particularly in light of the directive that labs destroy early samples (Pingui 2020) and multiple orders requiring approval of publications on COVID-19 (China CDC 2020; Kang et al. 2020a), **this suggests a less than wholehearted effort to maximize information about viral sequences from early in the Wuhan epidemic.**<sup>182</sup>

The PRC's efforts to obfuscate the origins of COVID-19 were not limited to destroying samples and silencing doctors, but featured a sustained disinformation campaign as well. As discussed in our previous report, Lijian Zhao, an official within the PRC's Foreign Ministry, shared an article on Twitter that claimed the virus was brought to the PRC by the U.S. military.<sup>183</sup> The article was from the *Global Times* research.ca, a website that pushes pro-Putin propaganda and has reported ties to Russian state media.<sup>184</sup> His tweet was amplified by the Chinese Embassy in South Africa.<sup>185</sup>

181 Bloom, Jesse D. Preprint: “Recovery of deleted deep sequencing data sheds more light on the early Wuhan SARS-CoV-2 epidemic.” *bioRxiv*, 29 June 2021, <https://www.biorxiv.org/content/10.1101/2021.06.18.449051v2>

182 *Ibid.*

183 Zhao, Lijian. “This Article Is Very Much Important to Each and Every One of Us. Please Read and Retweet It. COVID-19: Further Evidence That the Virus Originated in the US. <https://t.co/LPanIo40MR>.” *Twitter*, 13 Mar. 2020, [www.twitter.com/zlj517/status/1238269193427906560](https://www.twitter.com/zlj517/status/1238269193427906560)

184 Thomas, Elise, and Aspi. “Chinese Diplomats and Western Fringe Media Outlets Push the Same Coronavirus Conspiracies.” *The Strategist*, 30 Mar. 2020, [www.aspistrategist.org.au/chinese-diplomats-and-western-fringe-media-outlets-push-the-same-coronavirus-conspiracies/](http://www.aspistrategist.org.au/chinese-diplomats-and-western-fringe-media-outlets-push-the-same-coronavirus-conspiracies/).

185 Chinese Embassy in South Africa. “More Evidence Suggests That the Virus Was Not Originated at the Seafood Market in Wuhan at All, Not to Mention the so Called ‘Made in China’.” <https://t.co/8cRxsZB3z>.” *Twitter*, 16 Mar. 2020, [www.twitter.com/ChineseEmbSA/status/1239453193689587712](https://www.twitter.com/ChineseEmbSA/status/1239453193689587712)





Fig. 12: PRC Spokesman Tweet Suggesting COVID-19 Arrived in Wuhan via the Military World Games

To further drive this narrative, CCP-controlled media outlets accused Maatje Benassi, a member of the U.S. Army Reserve, as being “patient zero.” Benassi competed at the Military World Games without becoming ill, yet has been repeatedly targeted for harassment. Videos pushing the theory have been uploaded to WeChat, Weibo, and Xigua – PRC based sites. Two weeks after Zhao tweeted that the U.S. army brought the virus to Wuhan, the *Global Times* amplified the narrative, urging the U.S. government to release athletes’ health info and repeated the claim about Benassi.<sup>186</sup>

Another tweet by Zhao actually suggests the pandemic did start in September, as is suggested in this addendum, but that it began in the United States.<sup>187</sup>

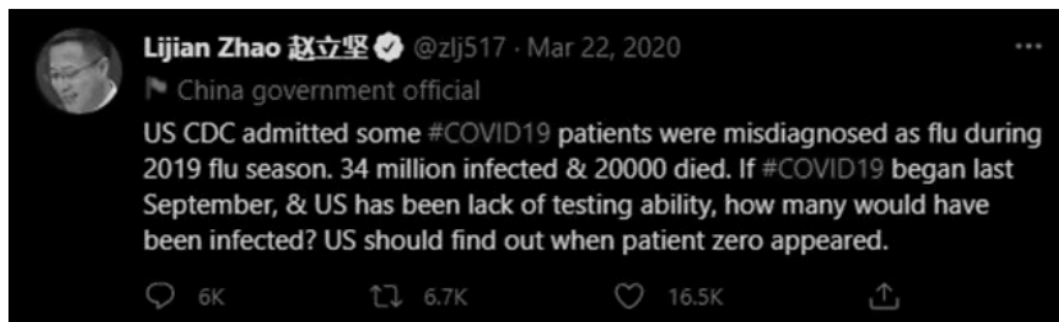


Fig. 13: PRC Spokesman Tweet Suggesting the COVID-19 Pandemic Started in September 2019.

<sup>186</sup> Shumei, Leng, and Wan Lin. “US Urged to Release Health Info of Military Athletes Who Came to Wuhan in October 2019.” *Global Times*, 25 Mar. 2020, [www.globaltimes.cn/content/1183658.shtml](http://www.globaltimes.cn/content/1183658.shtml).

<sup>187</sup> Zhao, Lijian. *US CDC Admitted Some #COVID19 Patients Were Misdiagnosed as Flu during 2019 Flu Season. 34 Million Infected & 20000 Died. If #COVID19 Began Last September, & US Has Been Lack of Testing Ability, How Many Would Have Been Infected? US Should Find out When Patient Zero Appeared.* Twitter, 22 Mar. 2020, <https://twitter.com/zlj517/status/1241723635964039168?s=20>.



It is important to note that this tweet was sent in March 2020. The previously discussed Harvard study suggesting the pandemic began in September was not published until the second half of 2020. This accusation came ten days after Zhao repeated his theory that the U.S. military brought COVID-19 to Wuhan. If the CCP realized an investigation would show an uptick in visits of patients with symptoms similar to COVID-19 in September, October, and November of 2019, this would likely be the actions they would take to coverup the source of those illnesses.

### WIV Disinformation Campaign Involving Peter Daszak

As we have previously explained, Peter Daszak was heavily involved in the gain-of-function research taking place at the WIV, including research that was done at BSL-2 levels and that was done while the United States had a moratorium in place on funding gain-of-function research. In addition, we have uncovered strong evidence that suggests Peter Daszak is the public face of a CCP disinformation campaign designed to suppress public discussion about a potential lab leak. Emails obtained by a third-party organization show that Daszak organized a February 19, 2020, statement in the *Lancet* “condemn[ing] conspiracy theories suggesting that COVID-19 does not have a natural origin.”<sup>188</sup> The statement continued, “Conspiracy theories do nothing but create fear, rumours, and prejudice that jeopardise our global collaboration in the fight against this virus.”<sup>189</sup> The emails show Daszak’s effort to organize a large group of scientists to sign onto a statement that he personally drafted. One email concludes with Daszak stating, “Please note that this statement will not have EcoHealth Alliance logo on it and will not be identifiable as coming from any one organization or person, the idea is to have this as a community supporting our colleagues.”<sup>190</sup>

The emails, sent from Daszak’s EcoHealth Alliance email account, also reveal the statement was drafted in response to a request by WIV researchers with whom Daszak had worked (emphasis added):

You should know that the conspiracy theorists have been very active, targeting our collaborators with some extremely unpleasant web pages in China, and some have now received death threats to themselves and their families. **They have asked for any show of support we can give them.**<sup>191</sup>

In a separate email, Daszak states that Linfa Wang (who did not sign the statement) pushed for Daszak and Baric to not sign the statement, effectively hiding their involvement. As previously discussed, Linfa Wang, who is copied on several other emails about the statement, was a coauthor of multiple Daszak/Shi/Hu papers. Wang is currently the Director and Professor of the Program in Emerging Infectious Diseases at the Duke-NUS Graduate Medical School in Singapore. He is a PRC national who received his B.S. in biochemistry from the East China Normal University in Shanghai, PRC<sup>192</sup> before completing a Ph.D. in molecular biology at the University of California, Davis in the United States.

<sup>188</sup> Calisher, Charles et al. “Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19.” *Lancet*, 7 Mar. 2020, 395(10226): e42-e43. <https://pubmed.ncbi.nlm.nih.gov/32087122/>

<sup>189</sup> *Ibid.*

<sup>190</sup> Daszak, Peter. Email to Linda Saif, Hume Field, JM Hughe, Rita Colweel, Alison Andrew, Aleksei Chmura, Hongying Li, William B. Karesh, and Robert Kessler. 6 Feb. 2020. [https://usrtk.org/wp-content/uploads/2020/11/The\\_Lancet\\_Emails\\_Daszak-2.6.20.pdf](https://usrtk.org/wp-content/uploads/2020/11/The_Lancet_Emails_Daszak-2.6.20.pdf)

<sup>191</sup> Daszak, Peter. Email to Rita Colwell. 8 Feb. 2020. [https://usrtk.org/wp-content/uploads/2020/11/The\\_Lancet\\_Emails\\_Daszak-2.8.20.pdf](https://usrtk.org/wp-content/uploads/2020/11/The_Lancet_Emails_Daszak-2.8.20.pdf)

<sup>192</sup> Wang, Linfa. “Curriculum Vitae.” [https://globalhealth.duke.edu/sites/default/files/cv/cv-linfa\\_wang-jan2017.pdf](https://globalhealth.duke.edu/sites/default/files/cv/cv-linfa_wang-jan2017.pdf)

In January 2020, Wang was at the WIV in Wuhan, visiting researchers he worked with. Given his previous publications, this likely included a visit with Hu and Shi, with whom he has authored dozens of papers. He departed the city on January 18th,<sup>192</sup> less than three weeks before Daszak externally circulated his draft *Lancet* statement. Wang is included on the email soliciting cosigners.<sup>193</sup>

In the email, Daszak states, (emphasis added):

I spoke with Linfa last night about the statement we sent round. He thinks, and I agree with him, that **you, me and him should not sign this statement, so it has some distance from us** and therefore doesn't work in a counterproductive way... **We'll then put it out in a way that doesn't link it back to our collaboration so we maximize an independent voice.**<sup>194</sup>

Copies of these emails are included in the Appendix.

**While pushing for Daszak and Baric, the WIV's most prominent American collaborators, to hide their efforts to organize this statement, Wang was serving as the Chair of the Scientific Advisory Board for the Center for Emerging Diseases at the Wuhan Institute of Virology, of which Shi Zheng-li is the Director.**<sup>195</sup>

Baric agreed and chose not to sign. It is unclear why Daszak ultimately changed his mind and signed the statement. Despite Daszak's role as the organizer of the *Lancet* statement, Charles Calisher is listed as the corresponding author. Oddly, the email address listed for Calisher is a generic one (COVID19statement@gmail.com)<sup>196</sup> that appears to have been created specifically for this statement, an unusual practice for scientific publications.

The February 2021 *Lancet* statement declared the authors had “no competing interest,” despite Daszak organizing the letter on behalf of WIV researchers who he funded and with whom he collaborated. In June 2020, after public concerns regarding Daszak's connection to the WIV, “the *Lancet* invited the 27 authors of the letter to re-evaluate their competing interests.”<sup>197</sup> **Daszak submitted a revised disclosure statement which, while transparent about his prior work with PRC researchers, fails to reference the WIV or disclose that he drafted the statement at the request of PRC researchers.**<sup>198</sup>

The emails also reveal that Daszak helped edit a letter sent on February 6, 2020 by the Presidents of the U.S. National Academies of Sciences, Engineering, and Medicine to the White House Office of Science and Technology Policy regarding the origins of COVID-19.

192 Kupferschmidt, Kai. “This Biologist Helped Trace SARS to Bats. Now, He's Working to Uncover the Origins of COVID-19.” *Science*, 9 Sept. 2020. [www.sciencemag.org/news/2020/09/biologist-helped-trace-sars-bats-now-hes-working-uncover-origins-covid-19](http://www.sciencemag.org/news/2020/09/biologist-helped-trace-sars-bats-now-hes-working-uncover-origins-covid-19).

193 Daszak (6 Feb.)

194 Daszak, Peter. Email to Ralph Baric, Toni Baric, Alison Andre, and Aleksei Chmura. 6 Feb. 2020. [https://usrtk.org/wp-content/uploads/2021/02/Baric\\_Daszak\\_email.pdf](https://usrtk.org/wp-content/uploads/2021/02/Baric_Daszak_email.pdf)

195 Wang.

196 Calisher.

197 Editors of The *Lancet*. “Addendum: competing interests and the origins of SARS-CoV-2.” *The Lancet*, 26 June 2021, 397: 2449-50. <https://www.thelancet.com/action/showPdf?pii=S0140-6736%2821%2901377-5>

198 *Ibid*.

199 McNutt, Marcia, et al. “NASEM Response to OSTP Re Coronavirus\_February 6, 2020.” Received by Kelvin Droegemeier, National Academies of Science, Engineering, and Medicine, 6 Feb. 2020, Washington, District of Columbia. [https://www.nationalacademies.org/documents/link/LDA8FF8BAB7F1D4A98AC250C7916649E610A15AD51C6/fileview/DA215521A660F40FD8D752FFB82A8E21FA8D3C29976D/NASEM%20Response%20to%20OSTP%20re%20Coronavirus\\_February%206%2C%202020.pdf?hide=thumbs+breadcrumbs+favs+props+nextprev+sidebar+pin+actions&scheme=light&fitwidth](https://www.nationalacademies.org/documents/link/LDA8FF8BAB7F1D4A98AC250C7916649E610A15AD51C6/fileview/DA215521A660F40FD8D752FFB82A8E21FA8D3C29976D/NASEM%20Response%20to%20OSTP%20re%20Coronavirus_February%206%2C%202020.pdf?hide=thumbs+breadcrumbs+favs+props+nextprev+sidebar+pin+actions&scheme=light&fitwidth)

While not included in the final version, the last draft edited by Daszak and the other experts who were consulted included a line stating, “The initial views of the experts is that the available genomic data are consistent with natural evolution and that there is currently no evidence that the virus was engineered to spread more quickly among humans.” Daszak actually pushed for broader language, as he believed “this is a bit too specific, because there are other conspiracy theories out there.” It is unclear why the sentence was removed by the Presidents of the U.S. National Academies before the letter was sent to the White House. Daszak specifically sought to time the publication of his statement in *The Lancet* for after this letter was released. And the statement references the letter as proof of the virus’ natural origin, without disclosing that Daszak helped edit it. It is highly likely that senior government officials, including Dr. Fauci, would have seen both the letter from the U.S. National Academies of Sciences, Engineering, and Medicine and the statement published in *The Lancet*, shaping their opinion and stifling debate within the U.S. federal government regarding the origins of COVID-19.

Sixteen months after sending this initial letter, the Presidents of the U.S. National Academies of Sciences, Engineering, and Medicine released an updated statement on June 15, 2021, titled, “Let Scientific Evidence Determine Origin of SARS-CoV-2, Urge Presidents of the National Academies.”<sup>199</sup> This updated statement acknowledges there are scenarios that the origin of the pandemic could have resulted from a lab leak, stating (emphasis added):

However, misinformation, unsubstantiated claims, and personal attacks on scientists surrounding the different theories of how the virus emerged are unacceptable, and are sowing public confusion and risk undermining the public’s trust in science and scientists, including those still leading efforts to bring the pandemic under control... In the case of SARS-CoV-2, there are multiple scenarios that could, in principle, explain its origin with varying degrees of plausibility based on our current understanding. **These scenarios range from natural zoonotic spillover (when a virus spreads from non-human animals to humans) to those that are associated with laboratory work.**<sup>200</sup>

Unlike the letter to the White House, this statement does not state which, if any, outside experts were consulted when drafting the statement.

Interestingly, three weeks later, in July 2021, Daszak and his colleagues released an update to their February 2020 statement with a very similar title: “Science, not speculation, is essential to determine how SARS-CoV-2 reached humans.” The second statement was signed by 24 of the original 27 authors and reflects a major step back from those authors’ original position (emphasis added):

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<sup>200</sup> *Ibid.*

Interestingly, three weeks later, in July 2021, Daszak and his colleagues released an update to their February 2020 statement with a very similar title: “Science, not speculation, is essential to determine how SARS-CoV-2 reached humans.” The second statement was signed by 24 of the original 27 authors and reflects a major step back from those authors’ original position (emphasis added):

**The second intent of our original Correspondence was to express our working view that SARS-CoV-2 most likely originated in nature and not in a laboratory, on the basis of early genetic analysis of the new virus and well-established evidence from previous emerging infectious diseases, including the coronaviruses that cause the common cold as well as the original SARS-CoV and MERS-CoV. Opinions, however, are neither data nor conclusions.** Evidence obtained using the scientific method must<sup>201</sup> inform our understanding and be the basis for interpretation of the available information.

This is quite different from Daszak’s words in the first border-line propaganda statement “condemn[ing] conspiracy theories suggesting that COVID-19 does not have a natural origin.”<sup>202</sup>

Despite this softening, the authors continue to accuse those who seek to investigate the lab leak hypothesis of being the source of the PRC’s unwillingness to cooperate with an international investigation:

Allegations and conjecture are of no help, as they do not facilitate access to information and objective assessment of the pathway from a bat virus to a human pathogen that might help to prevent a future pandemic. Recrimination has not, and will not, encourage international cooperation and collaboration.<sup>203</sup>

Whereas the first statement cited the letter from the Presidents of the U.S. National Academies of Sciences, Engineering, and Medicine (which Daszak helped edit), the second cites the Presidents’ statement released just weeks prior. This raises the question of whether Daszak, or any of the authors, assisted in drafting or editing the June 15th statement issues by the National Academies.

It should also be noted that Daszak was the only representative of the United States on the WHO-China Joint Study team in early 2021. The United States put forth a list of experts to be considered, none of whom were chosen. Daszak was not on that list but was nevertheless selected and approved by the CCP.<sup>204</sup> The annexes of the WHO’s report on the origins of COVID-19, issued in March 2021, include multiple examples of CCP disinformation that have been repeated by Daszak. This include a discussion of “conspiracy theories,”<sup>205</sup> which include the lab leak hypothesis and questions regarding the possible genetically modified nature of SARS-CoV-2. It also<sup>206</sup> refers to the WIV’s sequence database that was taken offline as a “rumour about missing data.” This is similar language to that which Daszak used during his Chatham House interview – despite the database remaining offline.<sup>207</sup> Committee Minority Staff was unable to determine whether Daszak assisted in the drafting or editing of the WHO report.

201 Calisher, Charles H et al. “Science, not speculation, is essential to determine how SARS-CoV-2 reached humans.” *Lancet*, 5 July 2021, 398:209-211. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8257054/>

202 Calisher (Feb.)

203 Calisher (July)

204 Testimony from former senior U.S. official received by Committee Minority Staff.

205 Joint Report - ANNEXES.

206 *Ibid.*

207 *Ibid.*

Peter Daszak has taken several additional concerning actions in regard to the origins of COVID-19, including inexplicably lying about the work conducted by EcoHealth Alliance in the months following the emergence of SARS-CoV-2. In an August 21, 2020, interview with *Nature*, after the NIH suspended the grants he was using to fund research at the WIV, Daszak claimed “The grant isn’t used to fund work on SARS-CoV-2. Our organization has not actually published any data on SARS-CoV-2.”<sup>208</sup> This is despite the fact that four days later *Nature* Communications published “Origin and cross-species transmission of bat coronaviruses in China.”<sup>209</sup> Daszak, Shi, Hu, and Wang are all listed as authors, with Shi and Daszak both being listed as corresponding authors. The preprint for the article was uploaded on May 31, 2020, almost three months before Daszak’s interview with *Nature*. The paper includes a<sup>210</sup> phylogenetic analysis “suggesting a likely origin for SARS-CoV-2 in *Rhinolophus* spp. bats.” Daszak, Shi, three EcoHealth Alliance affiliated researchers, and Linfa Wang are credited with designing the study, conducting fieldwork, and establishing collection and testing protocols.

The research was funded by the NIH (grant no. R01AI110964) and USAID’s PREDICT project (cooperative agreement number GHN-A-OO-09-00010-00), as well as the Strategic Priority Research Program of the Chinese Academy of Sciences (grant no. XDB29010101) that Shi was directing. It also received support from the National Natural Science Foundation of China (grants no. 31770175 and 31830096). The paper notes:

All work conducted by EcoHealth Alliance staff after April 24th 2020 was supported by generous funding from The Samuel Freeman Charitable Trust, Pamela Thye, The Wallace Fund, & an Anonymous Donor c/o Schwab Charitable.<sup>211</sup>

April 24th was the day the NIH terminated the project Understanding the Risk of Bat Coronavirus Emergence, which was funded under grant R01AI110964,<sup>212</sup> which is cited in the paper as funding this work.<sup>213</sup> The grant Daszak told *Nature* was not being used to fund work on SARS-CoV-2 is cited in a paper presenting research on SARS-CoV-2.

Earlier, in March 2020, Peter Daszak and two other EcoHealth Alliance affiliated researchers published “A strategy to prevent future epidemics similar to the 2019-nCoV outbreak.”<sup>214</sup> While the paper lacked lab experimentation, it discussed SARS-CoV-2 and claimed that “wildlife trade has clearly played a role in the emergence of”<sup>215</sup> the virus. This work was also funded by the same NIH grant (grant no. R01AI110964), as well as the same cooperative agreement with USAID’s PREDICT Project.

In December 2020, Daszak stated in a tweet that the suspension of the aforementioned NIH grant directly prevented him from accessing samples at the WIV. If the grant did not support EcoHealth Alliance’s work on SARS-CoV-2, how could it be related to their inability to access SARS-CoV-2 samples?

208 Subbaraman.

209 Latinne, Alice et al. “Origin and cross-species transmission of bat coronaviruses in China.” *Nature Communications*, 25 Aug. 2020, 11(1):4235, <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7447761/>

210 *Ibid.*

211 *Ibid.*

212 Lauer, Michael. Email to Peter Daszak. 24 April 2020.

<https://www.sciencemag.org/sites/default/files/Lauer.Daszak.NIH%20grant%20killed.partial%20email%20transcripts.April%202020.pdf>

213 Latinne

214 Daszak, Peter et al. “A strategy to prevent future epidemics similar to the 2019-nCoV outbreak.” *Biosafety and Health*, March 2020, 2(1): 6-8.

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7144510/>

215 *Ibid.*

Why did Daszak claim the NIH grant “isn’t used to fund work on SARS-CoV-2” when his own published research and statements show that it was?

Another concerning example of Daszak’s behavior comes from a March 10, 2021 discussion with Chatham House. In response to a question about the WIV taking down its viral sequence and sample database in September 2019 and whether the WHO investigative team requested to see the data, Peter Daszak stated (emphasis added):

I asked the question in front of the whole team, both sides, while we were at the Wuhan Institute of Virology, about the **so-called missing database**. And what we were told, by Shi Zheng-li, was that there had been hacking attempts on it, about 3,000 hacking attempts, and they took down this excel spreadsheet-based database. Absolutely reasonable. **We did not ask to see the data**, and as you know, a lot of this work is work that has been conducted with EcoHealth Alliance, and I’m also part of those data, and we **do basically know what’s in those databanks**. And I shared, **I gave a talk to both sides about the work we’ve done with the Wuhan Institute of Virology and explained what’s there. There is no evidence of viruses closer to SARS-CoV-2 than RaTG13 in those databases. It’s as simple as that.**<sup>217</sup>

This is a stunning claim given the database contained more than 22,000 samples and was inaccessible by anyone outside of the WIV after September 2019. It was physically impossible for Daszak to remotely access the database after the SARS-CoV-2 genome was released in January 2020 in order to compare the genome to samples in the database. **If not, given that no one outside of the WIV knew RaTG13 was closely related to SARS-CoV-2 prior to publication in February 2020, how could Daszak claim to know there is not a closer match in one of the 22,000 plus samples when he could not access the data? This raises the question of whether he has copy of the database.**

Daszak has also been, at best, incorrect about how the WIV handed RaTG13. In an April 21, 2020 interview with the *New York Times*, he stated (emphasis added):

We found the closest relative to the current SARS-CoV-2 in a bat in China in 2013. We **sequenced a bit of the genome, and then it went in the freezer**; because it didn’t look like SARS, we thought it was at a lower risk of emerging. With the Virome project, we could have sequenced the whole genome, discovered that it binds to human cells and upgraded the risk. And maybe then when we were designing vaccines for SARS, those could have targeted this one too, and we would have had something in the freezer ready to go if it emerged.<sup>218</sup>

This is, of course, untrue. Researchers at the WIV fully sequenced RaTG13’s genome in 2018.<sup>219</sup> Either Daszak knew this was untrue, and lied to the *New York Times*, or he was being kept in the dark about the work being conducted at the WIV. If the later is true, it raises more questions about Daszak’s March 2021 claim to know everything in the WIV’s database that was taken offline.

216 Subbaraman.

217 “Sustaining the Response: Inside the WHO-China Mission.” *Chatham House*, 10 March 2021, <https://www.youtube.com/watch?v=GMIIIEF58944&t=3249s>.

218 Kahn, Jennifer. “How Scientists Could Stop the Next Pandemic Before It Starts.” *The New York Times*, 21 Apr. 2020, [www.nytimes.com/2020/04/21/magazine/pandemic-vaccine.html](http://www.nytimes.com/2020/04/21/magazine/pandemic-vaccine.html).

219 Zhou, (Nov. 2020).

## V. HYPOTHESIS: A LAB LEAK THAT CAUSED A PANDEMIC

Having examined the evidenced discussed in this addendum, Committee Minority Staff has put together the following hypothesis that could reasonably represent what could have occurred in the early months of the COVID-19 pandemic.

In the months leading up to an accidental release of SARS-CoV-2, the hazardous waste treatment system at the WNBL was undergoing renovation. The central air conditioning system at one of the facilities needed to be renovated, which likely resulted in lower than ideal air circulation and enabling viral particles to remain suspended in the air longer. After the July 4, 2019 notice from the Ministry of Science and Technology, and prior to the September 30th deadline, researchers at the WIV were reviewing samples collected under grant 2013FY113500, held by Yuan Zhiming, the Director of the WNBL BSL-4.<sup>220</sup>

This is the same grant which funded:

- The 2013 paper reporting the first isolation of a live SARS-like coronavirus after sampling at the cave in Kunming.<sup>221</sup>
- The 2014 paper, which was the result of collecting 986 samples from 39 species of small mammals in Guangxi and Yunnan provinces.
- The 2016 paper, where a second live coronavirus was successfully isolated.
- The 2017 paper, where a third live SARS-like coronavirus was isolated and WIV researchers created eight chimeric coronaviruses with altered spike proteins.

Hu, Shi, and others at the WIV were actively testing novel and genetically manipulated coronaviruses against hACE2 expressing mice and civets at BSL-2 and BSL-3 conditions, including viruses collected from the cave in Yunnan where the miners fell ill. A defective hazardous waste treatment system and central air conditioning system would increase the likelihood of a lab employee (or several) becoming infected with SARS-CoV-2, as viral particles would be more likely to remain in the air for longer periods of time. As previously discussed, the WIV provides a shuttle for employees, transporting individuals from near the old WIV facility in Wuchang to the WNBL and back. The infected employees (whether from the WNBL or the WIV Headquarters) then traveled throughout central Wuhan, likely by the metro, spreading the virus.

In early September, it became known that an accidental release occurred. Initially, not knowing SARS-CoV-2 spreads via human-to-human transmission or that asymptomatic people are responsible for a large number of new cases, concern was low. Concern was additionally tempered by the knowledge that previous accidental releases from labs resulted in only a small number of infections. Still, measures are ordered in response. At midnight local time on the morning of September 12th, the Wuhan University, which sits less than a mile from the WIV Headquarters and whose medical school houses a BSL-3 lab accredited to experiment on animals,<sup>222</sup> issues a notice for laboratory inspections in late September.<sup>223</sup> It is likely that officials issued similar orders to other labs in the area. Between two and three hours later, the WIV's viral sequence database is taken offline in the middle of the night.<sup>224</sup>

Roughly 17 hours later, at 7:09 p.m. local time, the WIV publishes a procurement announcement for “security services” at the WNBL, to include gatekeepers, guards, video surveillance, security patrols, and people to handle the “registration and reception of foreign personnel.”<sup>225</sup> The budget provided was in excess of \$1.2 million.<sup>226</sup>



In order to prevent national embarrassment, the decision was made to allow the 2019 Military World Games to continue. No spectators were allowed to attend the games, but international athletes and some of the 236,000 volunteers still become infected, spreading the virus in the city. Dozens of athletes fall ill with symptoms. Since COVID-19 can infect humans without causing symptoms, an untold number of athletes and volunteers become infected, but are asymptomatic and unaware they are infectious.

The athletes return to their home countries in late October, carrying SARS-CoV-2 across the world. Just as was the case in 2002 with SARS,<sup>227</sup> the CCP sought to hide the outbreak, wasting precious time that could have been used to prevent the global pandemic. By the time the world was alerted to the virus spreading in Wuhan, it had already begun to spread around the world.

In December, as cases begin to overload local hospitals, it became impossible to hide the outbreak. At some point in late 2019, Major General Chen Wei is brought in to take over the BSL-4 lab at the WNBL and lead the response efforts. The Wuhan Branch of the China CDC set a case definition for COVID-19 that only included those who have visited the Huanan Seafood Market, meaning that only people who had a link to the market were identified as having COVID-19. This further obscured the true origins of the virus.

Linfa Wang, a scientist with ties to the WIV and who has worked with Shi, Hu, and Daszak on the genetic modification of coronaviruses, was in Wuhan in early January 2020. While there he visited the WIV and likely met with Shi, Hu, and others. Sometime after his departure on January 18th and before February 6th, WIV researchers asked Peter Daszak to organize a public statement suppressing debate regarding the lab as the origin of SARS-CoV-2. On January 20th, WIV researchers submitted the February 2020 article where ID4991 was renamed as RaTG13 and which contained false information about when the genomic sequence for the virus was obtained.

At 12:43am on February 6th, Daszak sent the draft statement to Wang, Baric, and others asking them to join as cosigners. Sometime before Daszak went to bed that night, Wang called him and requested that he, Daszak, and Baric not sign the statement in order to obfuscate their connections to the WIV. Baric agreed, and neither him nor Wang signed the statement. The statement was published on February 19th, declaring discussion of a lab leak a conspiracy theory, and suppressing public debate on the origins of COVID-19.

220 "Notice of the Resource Allocation and Management Department of the Basic Research Department of the Ministry of Science and Technology on the Comprehensive Performance Evaluation of Special Projects of Basic Science and Technology Work." *Ministry of Science and Technology*, 4 July 2019, <https://archive.is/pIwh4#selection-703.7-711.34>

221 Ge.

222 "About Wuhan University School of Medicine (WUSM)." *Wuhan University School of Medicine*, 23 Apr. 2013, [https://wsm70.whu.edu.cn/English\\_Site/About.htm](https://wsm70.whu.edu.cn/English_Site/About.htm)

223 "Notice on the implementation of laboratory safety inspections in 2019." *Wuhan University*, <http://simlab.whu.edu.cn/info/1107/1018.htm>

224 "Status breakdown of the database of characteristic wild animals carrying virus pathogens (September 2019)." *Scientific Database Service Monitoring & Statistics System*. <https://archive.is/AGtFv#selection-1553.0-1567.2>

225 "Competitive consultation on the procurement project of security services in Zhengdian Science Park, Wuhan Institute of Virology, Chinese Academy of Sciences." *China Government Procurement Network*, 12 Sept. 2019, [https://web.archive.org/web/20210716170719/http://www.ccgp.gov.cn/cggg/dfgg/jzxc/201909/t20190912\\_12900712.htm](https://web.archive.org/web/20210716170719/http://www.ccgp.gov.cn/cggg/dfgg/jzxc/201909/t20190912_12900712.htm)

226 *Ibid.*

227 Epstein, Gady A. "Chinese Admit to SARS Mistakes." *Baltimoresun.com*, Baltimore Sun, 1 Apr. 2003, [www.baltimoresun.com/bal-te.sars21apr21-story.html](http://www.baltimoresun.com/bal-te.sars21apr21-story.html).



## V. RECOMMENDATIONS

In the previously issued report, Committee Minority Staff provided several recommendations for actions to be taken by the United States in response to COVID-19, including seeking new leadership at the WHO, pursuing Taiwan's re-admittance to the WHO as an observer, engaging in an international investigation with likeminded WHO Member States regarding the early stages of COVID-19, and supporting concrete reforms to the International Health Regulations. These recommendations remain relevant.

In response to the new information laid out in this addendum, there are additional steps that can be taken by the Committee, Congress more broadly, and the Executive Branch on this issue. Given the previously detailed inconsistencies and CCP disinformation campaign regarding a possible lab leak, Peter Daszak must be subpoenaed to appear before the House Foreign Affairs Committee and Senate Foreign Relations Committee as material witness to this investigation. Committee Minority Staff attempted, on multiple occasions, to contact Daszak with a list of questions relevant to this report. He never responded. In contrast, Ralph Baric provided answers to a list of questions from Committee Minority Staff. His assistance was appreciated, and we believe his testimony would also be useful. Daszak and Baric should provide expert testimony, including but not limited to the following questions:

- What was the extent of genetic manipulation of coronaviruses and their testing against human immune systems at the WIV in 2018 and 2019?
- Who requested the statement of support published in the *Lancet*?
- Did this request include labeling discussion of a possible lab leak as a conspiracy theory?
- What was the nature and content of Wang's call to Daszak in the early hours of February 6th, 2020?
- Why did Daszak make conflicting, and apparently false, statements regarding the NIH grant terminated in 2020?
- How could Daszak confirm RaTG13 is the closest match to SARS-CoV-2 in the WIV's database if it was taken offline in September 2019?
- Does Daszak have a copy of the WIV's database that was taken offline?
- Who put forth Daszak's name to join the joint WHO-China investigative team?
- Was Daszak aware the funding he was providing directly supported gain-of-function research by paying for the collection of viruses the WIV later experimented with, even though the federal government had a moratorium on such research from 2014 through 2017?
- Do they believe SARS-CoV-2 could possibly be a genetically modified virus created via a system similar to Baric's "no-see-um" method and the system used by WIV researchers in 2016, thus leaving no evidence of manipulation?

Committee Minority Staff also recommends Congress pursue legislation to implement the following restrictions and sanctions in response to the pandemic:

- Institute a ban on conducting and funding any work that includes gain-of-function research until an international and legally binding standard is set, and only where that standard is verifiably being followed.
- Authorize and fund a public-private partnership for pandemic prevention, warning, and early detection.

- Sanction the Chinese Academy of Sciences and affiliated entities.
- List the Wuhan Institute of Virology and its leadership on the Specially Designated Nationals and Blocked Persons List and apply additional, appropriate secondary sanctions.
- Expand statutory and administrative sanctions regimes to curb the abuse of dual-use technology.
- Authorize new sanctions for academic, governmental, and military bioresearch facilities that fail to ensure the appropriate levels of safety and information sharing.
- Review all H-2B visas of Chinese nationals engaged in biological, chemical, or related research in the United States for possible revocation.
- Review all student visas of Chinese nationals studying at U.S. academic institutions for possible revocation.

Additionally, the Executive Branch should engage in international negotiations to establish a legally binding international standard for laboratory biosafety, to include certification and inspections by an international organization similar to the International Atomic Energy Agency.

Foreign governments facing economic contraction that have entered into agreements under the PRC's Belt and Road Initiative are encouraged to examine bilateral agreement terms. In particular, agreements or memoranda of understanding that promote joint scientific and academic research wherein the Chinese government has access to natural resources, minerals, plant life, and animals unique to the nation state. Agreements that promote adaptation of governing structures that centralize control over all local, municipal, or provincial levels increase the risk of creating national governing structures that manipulate, misinform, misdirect and gaslight their own citizens to protect centralized governing structures.

Foreign governments considering entering into bilateral agreements with the PRC are advised to be aware that based on the information presented within this report, the PRC conducts scientific research without regard for adequate safety protocols in place, in a manner that does not comport with international safety standards, and without adequate assessment of the risks scientific research may pose to the environment, test subjects, or humanity. It is the recommendation of the Committee Minority Staff that such agreements be avoided.

## VII. CONCLUSION

The Intelligence Community 90-day review report on the origins of COVID-19, ordered by President Biden, is due no later than August 24, 2021. While based on open source information, it is the hope of Committee Minority Staff that the collection and analysis contained within this addendum, produced at the direction of Ranking Member Michael T. McCaul, will help inform the public debate about the viability of a laboratory accident being the source of SARS-CoV-2. It is vital the public discourse surround the Wuhan Institute of Virology is transparent, honest, and detailed.

**It is the opinion of Committee Minority Staff, based on the preponderance of available information; the documented efforts to obfuscate, hide, and destroy evidence; and the lack of physical evidence to the contrary; that SARS-CoV-2 was accidentally released from a Wuhan Institute of Virology laboratory sometime prior to September 12, 2019. The virus, which may be natural in origin or the result of genetic manipulation, was likely collected in the identified cave in Yunnan province, PRC, sometime between 2012 and 2015. Its release was due to poor lab safety standards and practices, exacerbated by dangerous gain-of-function research being conducted at inadequate biosafety levels, including BSL-2. The virus was then spread throughout central Wuhan, likely via the Wuhan Metro, in the weeks prior to the Military World Games. Those games became an international vector, spreading the virus to multiple continents around the world.**

It is incumbent on the parties identified in this report to respond to the issues raised herein and provide clarity and any new or additional evidence as soon as possible. As always, Committee Minority Staff stands ready to receive such evidence or testimony that supports or contradicts this report. Until such time as the Chinese Communist Party lifts its self-imposed veil of secrecy, explains its lies regarding the early stages of the pandemic, and provides access to the WIV's archives and sample database, questions will remain as to the origins of SARS-CoV-2 and the COVID-19 pandemic. Until that day, it is incumbent upon the United States and likeminded countries around the world to ensure accountability, and implement the reforms necessary to prevent the CCP's malfeasance from giving rise to a third pandemic during the 21st century.

## VII. APPENDIX

### Timeline of the WIV Lab Leak and the Start of the COVID-19 Pandemic

**April 2012:** Six miners working in a copper mine located in a cave in Yunnan province of the PRC fall ill. Between the ages of 30 and 63, the workers presented to a hospital in Kunming with persistent coughs, fevers, head and chest pains, and breathing difficulties.” Three of the six died.

**Late 2012 – 2015:** Researchers from the WIV collect samples from bats in the cave.

**2015 - 2017:** Shi Zheng-li, Ben Hu, Peter Daszak, and Linfa Wang jointly publish research on the isolation of novel coronaviruses. They conduct gain-of-function research, testing novel and genetically manipulated coronaviruses against mice and other animals expressing human immune systems. At times they collaborate with Ralph Baric.

**2018 – 2019:** Shi, Hu, and other researchers at the WIV infect transgenic mice and civets expressing human immune systems with unpublished novel and genetically modified coronaviruses.

**July 4, 2019:** The PRC’s Ministry of Science and Technology orders a review of several grants, including grant no. 2013FY113500. This is the grant which funded the collection of hundreds of coronaviruses and bat samples from the cave in Yunnan province.

**July 16, 2019:** The WIV publishes a tender requesting bids to conduct renovation on the hazardous waste treatment system at the Wuhan National Biosafety Lab (WNBL). The closing date was July 31st.

**Late August/Early September 2019:** One or more researchers become accidentally infected with SARS-CoV-2, which was either collected in the Yunnan cave, or the result of gain-of-function research at the WIV. They travel by metro in central Wuhan, spreading the virus.

**September 12, 2019:** At 12:00am local time, the Wuhan University issues a statement announcing lab inspections. Between 2:00am and 3:00am, the WIV’s viral sequence and sample database is taken offline. At 7:09pm, the WIV publishes a tender requesting bids to provide security services at the WNBL.

**September – October 2019:** Car traffic at hospitals surrounding the WIV Headquarters, as well as the shuttle stop for the WNBL, show a steady increase before hitting its highest levels in 2.5 years. Baidu search terms for COVID-19 related symptoms increase in a corresponding manner.

**Late October – Early November 2019:** The international athletes return home, carrying SARS-CoV-2 around the world.

- November 21, 2019:** A 4-year-old boy from Milan, Italy develops a cough. His samples will later test positive for COVID-19.
- November 27, 2019:** Samples of wastewater are collected in Brazil that will later test positive for the presence of SARS-CoV-2 RNA.
- December 1, 2019:** The CCP's first "official" case of COVID-19 become infected.
- Late 2019:** Major General Chen Wei arrives in Wuhan, taking over the WNBL BSL-4 lab.
- Dec. 27, 2019:** A Chinese genomic company reportedly sequenced most of the virus in Wuhan and results showed a similarity to SARS. Zhang Jixian, a doctor from Hubei Provincial Hospital of Integrated Chinese and Western Medicine, tells PRC health authorities that a novel disease affecting some 180 patients was caused by a new coronavirus.
- Dec. 29, 2019:** Wuhan Municipal CDC organized an expert team to investigate after the Hubei Provincial Hospital of Integrated Chinese and Western Medicine and other hospitals find additional cases.
- Dec. 30, 2019:** Doctors in Wuhan report positive tests for "SARS Coronavirus" to local health officials. Under the 2005 International Health Regulations, the PRC is required to report these results to the WHO within 24 hours. They do not.
- Dec. 31, 2019:** WHO officials in Geneva become aware of media reports regarding an outbreak in Wuhan and direct the WHO China Country Office to investigate.
- Jan. 2020:** Linfa Wang meets with collaborators at the WIV, likely including Shi and Hu.
- Jan. 1, 2020:** Hubei Provincial Health Commission official orders gene sequencing companies and labs who had already determined the novel virus was similar to SARS to stop testing and to destroy existing samples. Dr. Li Wenliang is detained for "rumor mongering."
- Jan. 2, 2020:** The Wuhan Institute of Virology (WIV) completes gene sequencing of the virus, but the CCP does not share the sequence or inform the WHO. PRC aggressively highlights the detentions of the Wuhan doctors.
- Jan. 3, 2020:** China's National Health Commission ordered institutions not to publish any information related to the "unknown disease" and ordered labs to transfer samples to CCP controlled national institutions or destroy them.
- Jan. 11-12, 2020:** After a researcher in Shanghai leaks the gene sequence online, the CCP transmits the WIV's gene sequencing information to the WHO that was completed 10 days earlier. The Shanghai lab where the researcher works is ordered to close.

**Jan. 14, 2020:** Xi Jinping is warned by a top Chinese health official that a pandemic is occurring.

**Jan. 18, 2020:** Linfa Wang departs Wuhan.

**Jan. 20, 2020:** WIV researchers submitted an article claiming that SARS-CoV-2 is natural in origin. The article renames ID4991 as RaTG13 and contained false information about when the genomic sequence for the virus was obtained.

**Jan. 23, 2020:** The CCP institutes a city-wide lockdown of Wuhan. However, before the lockdown goes into effect, an estimated 5 million people leave the city.

**Last Week of January 2020:** Daszak and other outside experts edit a letter to be sent by the Presidents of the National Academies of Sciences, Engineering, and Medicine to the White House Office of Science and Technology Policy. Daszak pushes for language to address “conspiracy theories.”

**Jan. 30, 2020:** One week after declining to do so, Tedros declares a Public Health Emergency of International Concern.

**Late Jan. – Early Feb. 2020:** PRC researchers, likely those at the WIV, request Peter Daszak’s assistance in responding to suggestions of a lab leak or genetic manipulation of SARS-CoV-2. Daszak helps edit the National Academies of Sciences, Engineering, and Medicine’s response to the White House Office of Science and Technology Policy on the origins of COVID-19.

**Feb. 3, 2020:** The WIV researchers’ paper submitted on January 20th is published by *Nature* online.

**Feb. 6, 2020 at 12:43:40 am:** Daszak sends the draft Lancet statement, which cites the Feb. 3 WIV paper, to Wang, Baric, and others asking them to join as cosigners. Within hours, Wang calls him, informs Daszak that he will not sign, and requests that neither Daszak or Baric sign.

**Feb. 6, 2020 (Afternoon):** At 3:16pm, Daszak send a High Important email to Baric, forwarding Wang’s request, and informing Baric the statement will be “put out in a way that doesn’t link it back to our collaboration.” At 4:01:22 pm, Baric agrees to not sign the statement.

**Feb. 7, 2020:** Dr. Li, who first shared the positive SARS test results with his classmates via WeChat, dies from COVID-19.

**Feb. 9, 2020:** The death toll for COVID-19 surpasses that of SARS.

**Feb. 15, 2020:** First death from COVID-19 outside of Asia occurs, in France.

- **Feb. 16, 2020:** WHO and PRC officials begin a nine-day “WHO-China Joint Mission on Coronavirus Disease 2019” and travel to the PRC to examine the outbreak and origin of COVID-19. Many team members, including at least one American, were not allowed to visit Wuhan.
- **Feb. 18, 2020:** Daszak statement is published by the *Lancet* online, which references the letter from the U.S. National Academies of Sciences, Engineering, and Medicine he helped write and the WIV’s February 3rd paper on the origins of COVID-19. Despite drafting the letter, Daszak is not listed as the corresponding author.
- **Feb. 25, 2020:** For the first time, more new cases are reported outside of PRC than within.
- **Feb. 26, 2020:** The WHO-China Joint Mission issues its findings, praising the PRC for its handling of the outbreak.
- **Feb. 29, 2020:** The first reported COVID-19 death in the United States occurs.
- **March 11, 2020:** The WHO officially declares the COVID-19 outbreak a pandemic after 114 countries had already reported 118,000 cases including more than 1,000 in the United States.
- **Nov. 17, 2020:** As a result of public pressure, Shi, Hu, and other WIV researchers publish an addendum to their February 3rd paper, confirming that RaTG13 was ID4991 collected from the cave in Yunnan, and revealing they collected 293 coronaviruses from the cave between 2012 and 2015.
- **June 15, 2021:** The Presidents of the U.S. National Academies of Sciences, Engineering, and Medicine release a statement saying, “let scientific evidence determine origin of SARS-CoV-2.”
- **June 21, 2021:** After public pressure, Daszak updates his public disclosure form for the *Lancet* statement. He does not mention the WIV or that the statement was drafted at the request of PRC researchers.
- **July 5, 2021:** Daszak and 23 of the original 27 authors release an update to their February 2021 statement, walking back their labeling of public debate around the source of the virus as “conspiracy theories.”

China Center for Disease and Control Memo on Supplementary Regulations

# 中国疾控中心处(室)便函

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科技处便函〔2020〕16号

## 关于加强新型冠状病毒肺炎应急响应期间有关 科技管理的补充规定

中心直属各单位，机关各处室：

为进一步加强我中心新型冠状病毒肺炎应急响应期间科研管理，根据上级有关文件精神，特制定《加强新型冠状病毒肺炎应急响应期间有关科技管理的补充规定》，请各单位和各处室负责人务必高度重视，层层传达，必须通知到每个人。如有违反有关规定者，将追究单位和违规者的责任。

附件：加强新型冠状病毒肺炎应急响应期间有关科技管理的补充规定

中国疾控中心科技处

2020年2月25日

抄送：高福、李新华、刘剑君、冯子健。

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附件

## 加强新型冠状病毒肺炎应急响应期间有关科技管理的补充规定

根据《国家卫生健康委办公厅关于在重大突发传染病防控工作中加强生物样本资源及相关科研活动管理工作的通知》（国卫办科教函〔2020〕3号）、《科技部办公厅关于加强新型冠状病毒肺炎科技攻关项目管理有关事项的通知》等文件精神，为有力抗击新型冠状病毒肺炎（简称“新冠肺炎”）疫情，严格规范科研管理，进一步加强科研管理制度的落实，现对《加强新型冠状病毒感染的肺炎应急响应期间有关科技管理规定》（中疾控科技便函〔2020〕128号）制定本补充规定。

一、坚持国家和人民利益至上，以做好新冠肺炎疫情防控为首要任务。疫情应急响应期间，要集中优势力量，分清轻重缓急，将主要精力放在疫情防控中，把论文“写在祖国大地上”，把研究成果应用到战胜疫情中，在疫情防控任务完成之前不应将精力放在论文发表上。

二、开展新冠肺炎疫情相关科研项目，必须经科技组/科技处进行初审，根据研究内容组织专家进行科学论证和伦理审查，必要时提请应急领导小组或国家卫生健康委科教司审批。上级委托的科研项目必须经科技组/科技处请示应急领导小组审定并备案。

三、任何人不能以个人或研究团队名义擅自向其他机构和个人提供新冠肺炎疫情相关信息，包括数据、生物标本、病原体、培养物等。

四、在发表与新冠肺炎疫情相关的论文和成果前，必须先报科技组/科技处初审，必要时提请应急领导小组或国家卫生健康委科教司审批。

未经科技组/科技处审核的已投稿的论文，尽快撤稿并执行本规定。

五、科研项目进展报告原则上按月报科技组/科技处，或根据上级要求的时限进行报告。

六、要严格遵循医学伦理、科研诚信和学风建设等相关规定。

七、有违反上述规定者，依纪依法依规进行严肃处理。

八、本规定发布之日执行，由科技组/科技处解释。

中国疾控中心科技处

2020年2月25日

## Memo to the Offices of the Chinese Center for Disease Control and Prevention

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Memo (2020) No. 16 of the Science and Technology Department

### **On the Supplementary Regulations on Strengthening the Management of Science and Technology During the Emergency Response to the Novel Coronavirus Pneumonia**

All units and offices directly under the center:

In order to further strengthen scientific research management in our center during the emergency response to the novel coronavirus pneumonia, and in accordance with the spirit of relevant documents issued by the higher authorities, the "Supplementary Regulations on Strengthening the Management of Science and Technology During the Emergency Response to the Novel Coronavirus Pneumonia" has been formulated. Every unit and office, please attach great importance to it and spread it through all levels - everyone must be notified. In case of any violation of relevant regulations, the offender and their unit will be held accountable.

Attachment: Supplementary Regulations on Strengthening the Management of Science and Technology During the Emergency Response to the Novel Coronavirus Pneumonia

Chinese Center for Disease Control and Prevention  
February 25, 2020

CC: Gao Fu, Li Xinhua, Liu Jianjun, Feng Zijian.

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## Annex

## **Supplementary Regulations on Strengthening the Management of Science and Technology During the Emergency Response to the Novel Coronavirus Pneumonia**

According to the spirit of the "Notice of the General Office of the National Health Commission on Strengthening the Management of Biological Sample Resources and Related Scientific Research Activities during the Prevention and Control of Major Infectious Diseases" (National Health Commission Science and Technology Memo [2020] No. 3), the "Notice of the General Office of the Ministry of Science and Technology on Strengthening the Management of New Coronavirus Pneumonia Science and Technology Research Projects" and other documents, and in order to effectively combat the new coronavirus pneumonia ("COVID-19") epidemic, to strictly standardize scientific research management, and to further strengthen the implementation of scientific research management systems, these supplementary "Regulations on Strengthening the Management of Science and Technology During the Emergency Response to the Novel Coronavirus Pneumonia" (Chinese Center for Disease Control Science and Technology Memo [2020] No. 128) have been formulated.

1. Prioritize the interests of the country and the people and take the prevention and control of the COVID-19 epidemic as the primary task. During the emergency response against the epidemic, we must concentrate our forces, distinguish our priorities, focus our main energies on controlling the epidemic, write papers "on the land of the motherland", apply research results to the fight against the epidemic, and not focus on publishing papers until the epidemic is under control.

2. The launch of scientific research projects related to the COVID-19 epidemic must undergo preliminary review by the Science and Technology Group/Department. According to the research subject, experts should be organized to conduct scientific and ethical reviews, and, if necessary, the project must be submitted to the emergency

leading group or the Department of Science and Education of the National Health Commission for approval. The research projects authorized by higher authorities must be examined and approved by the emergency leading group via the Science and Technology Group/Department and be kept on record.

3. No one can, under their own name or in the name of their research team, provide other institutions and individuals with information related to the COVID-19 epidemic on their own, including data, biological specimens, pathogens, culture, etc.

4. Before publishing papers and research results related to the COVID-19 epidemic, you must first report them to the Science and Technology Group/Department for preliminary review, and if necessary, submit it to the Emergency Leading Group or the Department of Science and Education of the National Health Commission for approval.

Papers that have been submitted but not yet reviewed by the Science and Technology Group/Department should be withdrawn as soon as possible and redone according to these regulations.

5. In principle, progress reports on scientific research projects should be reported to the Science and Technology Group/Department on a monthly basis, or according to the time period stipulated by higher authorities.

6. Strictly follow relevant regulations on medical ethics, scientific research integrity and academic spirit.

7. Anyone who violates the above regulations shall be dealt with severely in accordance with discipline, laws and regulations.

8. The date of the implementation of this regulation will be explained by the Science and Technology Group/Department.

Chinese Center for Disease Control and Prevention

February 25, 2020

JCPM Confidential Notice on the Standardization of the Management of Publication of Novel  
Coronavirus Pneumonia Scientific Research

## 国务院应对新型冠状病毒肺炎疫情联防联控机制科研攻关组

### 关于规范新冠肺炎科研攻关成果 信息发布管理的通知

国务院应对新型冠状病毒肺炎疫情联防联控机制科研攻关组成员单位  
办公厅(室), 有关单位:

为深入贯彻国务院应对新型冠状病毒肺炎疫情联防联控机制(以下  
简称国务院联防联控机制)会议的有关要求, 切实规范科研攻关成  
果信息发布管理, 现就有关事项通知如下。

#### 一、全面加强科研攻关成果信息发布管理

按照“依法依规、科学客观、归口管理、精准发布”的原则,  
把新冠肺炎治疗药物、疫苗、病毒溯源、病毒传播途径、检测试剂等  
各类疫情防控科研成果信息的发布工作, 纳入国务院应对新型冠状病毒  
肺炎疫情联防联控机制科研攻关组(以下简称科研攻关组)的统一部  
署。科研攻关组统筹协调科研应急攻关成果信息发布, 指导、协调各  
地各单位科研成果信息发布。

## 二、建立规范的科研攻关成果信息发布机制

科研攻关组各成员单位及时汇总本单位、本系统科研攻关成果信息，就发布内容、发布形式进行审核把关，并及时报科研攻关组批准。科研攻关组按业务归口组织各专班负责对发布内容、发布形式提出专业性审核意见，必要时组织专家论证。科研攻关组同意后，发布单位应根据工作需要选择新闻发布会、官方网站、政务新媒体、新闻媒体等平台发布，并通报国务院联防联控机制宣传组、科研攻关组。原则上，新冠肺炎科研成果信息首发采用官方权威发布形式。舆论专班加强与宣传组沟通，结合舆情动态和社会关切，强化对科研成果信息发布的指导。

## 三、严格要求各科研单位做好科研成果信息发布

联防联控机制科研攻关组各成员单位要按照归口管理原则，严格本单位本系统相关科研成果信息的发布审批程序，加强对本单位本系统归口管理的高等院校、研究机构、企业的管理，将本通知要求传达至从事新冠肺炎研究的各相关单位。各成果信息发布单位是发布内容的第一责任人，要综合考虑实际工作进展、疫情防治态势、社会关切问题、预期发布成效等方面，精准确定发布内容，合理引导社会预期。各高等院校、研究机构、医疗机构、企业及其人员在疫情防控期间，未经审批不得擅自发布疫情防控相关科研成果信息。在中华医学会平台交流的论文仍按原备案机制办理。

#### 四、加强科研攻关成果信息发布工作统筹

疫情防控期间，各地各单位要认真贯彻落实习近平总书记关于疫情防控工作的一系列重要指示精神，进一步强化大局意识、责任意识，加强审核把关，主动沟通协调，形成新冠肺炎科研成果信息发布全国“一盘棋”格局。重要敏感科研成果信息要反复核实，把握不准的要及时按程序向科研攻关组及相关部门请示。

#### 五、强化监督问责

对未按规定程序报批，发布未经证实的虚假科研成果信息，造成严重不良社会影响的，要追究责任。

联系人：赵婧， [REDACTED]、[REDACTED]  
 吴运高， [REDACTED]、[REDACTED]  
 传真： [REDACTED]， 联系邮箱： [REDACTED]

NOT NIH REDACTIONS

国务院应对新型冠状病毒肺炎  
 疫情联防联控机制科研攻关组  
 （代章）

2020年3月3日

（此件不公开）

抄送：国务院联防联控机制宣传组。

科学技术部办公厅

2020年3月3日印发



## Joint Prevention and Control Mechanism of the State Council in Response to the Novel Coronavirus Pneumonia Scientific Research Group

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### Notice on the Standardization of the Management of Publication of Novel Coronavirus Pneumonia Scientific Research

To the Joint Prevention and Control Mechanism of the State Council in Response to the Novel Coronavirus Pneumonia member work units and offices, and other relevant work units:

In order to thoroughly implement relevant requirements from the meeting of the Joint Prevention and Control Mechanism of the State Council in Response to the Novel Coronavirus Pneumonia (hereinafter referred to as the "Joint Prevention and Control Mechanism of the State Council"), and to effectively standardize the management of the publication of scientific research, the following is issued below.

#### **1. Comprehensively strengthen the management of publication of scientific research**

In accordance with the principles of "following laws and regulations, being scientific and objective, centralized management, and precise publications", all publication work on epidemic prevention research and information related to COVID-19, including medication, vaccines, virus origins, virus transmission routes, testing reagents, etc. will be taken over by the Joint Prevention and Control Mechanism of the State Council's scientific research group (hereinafter referred to as "the scientific research group") for coordinated deployment. The scientific research group will coordinate the publication of information on emergency scientific research, and guide and coordinate the publication of information on scientific research by all work units in all locations.

#### **2. Establish a standardized publication mechanism for scientific research**

Each member work unit of the scientific research team will gather scientific research information within their own unit and systems, review and check the content and form of its publication, and report it to the scientific research team for approval in a timely manner. The scientific research group's dedicated teams of professionals and various experts are responsible for reviewing the publication's content and format and giving expert opinions, and when necessary, arranging expert assessment. After the scientific research group approves, the publishing work unit should, according to work requirements, arrange publication via press conferences, official websites, state social media, news media and other platforms, and notify the propaganda and scientific research teams of the Joint Prevention and Control Mechanism of the State Council. In principle, COVID-19 scientific research should be published first in the form of an official authoritative publication. The special group on public opinion should strengthen communication with the propaganda team, take into account the trend of public opinion and social concerns, and strengthen guidance of the publication of scientific research and information.

### **3. Strictly require all scientific research units to do a good job on the publication of scientific research**

The member work units of the scientific research team of the Joint Prevention and Control Mechanism shall follow the principle of centralized management, strictly enforce their own system's publication approval procedures for relevant scientific research, strengthen the management of universities, research institutions, and enterprises under the centralized management of their work unit systems, and communicate the requirements of this notice to all relevant units engaged in research on COVID-19. The publishing work unit is the one primarily responsible for the research content they publish, and they must consider, in a comprehensive manner, the research progress, the epidemic prevention and control situation, societal concerns, the consequences of publication, and various other issues. They must ensure the accuracy of the published content and guide societal expectations in a reasonable manner. During the period of epidemic prevention and control, all universities, research institutions, medical institutions, enterprises and their staff shall not publish information on scientific research related to epidemic prevention and control without approval. Papers exchanged on the Chinese Medical Association

#### 四、加强科研攻关成果信息发布工作统筹

疫情防控期间，各地各单位要认真贯彻落实习近平总书记关于疫情防控工作的一系列重要指示精神，进一步强化大局意识、责任意识，加强审核把关，主动沟通协调，形成新冠肺炎科研成果信息发布全国“一盘棋”格局。重要敏感科研成果信息要反复核实，把握不准的要及时按程序向科研攻关组及相关部门请示。

#### 五、强化监督问责

对未按规定程序报批，发布未经证实的虚假科研成果信息，造成严重不良社会影响的，要追究责任。

联系人：赵婧， [REDACTED] [REDACTED]  
 吴运高， [REDACTED] [REDACTED]  
 传真： [REDACTED]， 联系邮箱： [REDACTED]

NOT NIH REDACTIONS

国务院应对新型冠状病毒肺炎  
 疫情联防联控机制科研攻关组  
 （代章）  
 2020年3月3日

（此件不公开）

抄送：国务院联防联控机制宣传组。

科学技术部办公厅

2020年3月3日印发

February 6, 2020, Email at 12:43am from Peter Daszak to Ralph Baric, Linfa Wang, and Others  
Inviting Them to Sign the Statement

A Statement in support of the  
scientists, public health and medical  
professionals of China

Feb 6, 2020 12:43:40 AM EST

**A Statement in support of the scientists, public health and medical  
professionals of China**

**Subject:** A Statement in support of the scientists, public health and medical professionals of China  
**From:** Peter Daszak [REDACTED]  
**To:** Ralph Baric [REDACTED]  
[REDACTED]  
**Cc:** [REDACTED]  
**Sent:** February 6, 2020 12:43:40 AM EST  
**Attachments:** Statement of support, 2019nCoV China Final.docx

NOT NIH  
REDACTIONS

A Statement in support of the  
scientists, public health and medical  
professionals of China

Feb 6, 2020 12:43:40 AM EST

Dear Ralph, Linda, Jim, Rita, Linfa and Hume,

I've been following the events around the novel coronavirus emergence in China very closely and have been dismayed by the recent spreading of rumors, misinformation and conspiracy theories on its origins. These are now specifically targeting scientists with whom we've collaborated for many years, and who have been working heroically to fight this outbreak and share data with unprecedented speed, openness and transparency. These conspiracy theories threaten to undermine the very global collaborations that we need to deal with a disease that has already spread across continents.

We have drafted a simple statement of solidarity and support for scientists, public health and medical professionals of China, and would like to invite you to join us as the first signatories. If you agree, we will send this letter to a group of around half-a-dozen other leaders in the field and then disseminate this widely with a sign-up webpage for others to show their support by signing up to its language. I will then personally present this at my plenary during the ICID 2020 conference in Malaysia in two weeks, with the goal of also getting widespread attention in SE Asia to our support for the work that our colleagues in China are undertaking.

I sincerely hope you can join us. Please review the letter, and let me know if you are willing to join Billy Karesh and myself as co-signatories. Also, please confirm your title and affiliation that will be shown in the letter. We plan to make circulate this widely to coincide with a letter from the Presidents of the US National Academies of Science, Engineering, and Medicine, which will likely be released tomorrow or Friday.

Thank you for your consideration and support of the scientific and public health community around the world!

Cheers,

Peter

**Peter Daszak**  
President

EcoHealth Alliance  
460 West 34<sup>th</sup> Street – 17<sup>th</sup> Floor  
New York, NY 10001

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

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

### **Statement in Support of the Scientists, Public Health, and Medical Professionals of China Combating the Novel Coronavirus Outbreak**

We, the undersigned, are scientists who have followed the emergence of 2019-nCoV, and are deeply concerned about its global impact on people's health and well-being. We have watched as the scientists, public health and medical professionals of China have worked heroically to rapidly identify the pathogen behind this outbreak, put in place significant measures to reduce its impact, and share their results transparently with the global health community. We sign this statement in solidarity with all scientists, public health, and medical professionals in China who continue to save lives and protect global health during the challenge of this novel coronavirus outbreak. We want you to know that we are all in this together, with you in front of us on the battlefield against the novel coronavirus.

The rapid, open and transparent sharing of data on 2019-nCoV is now being threatened by rumors and misinformation around the origins of this outbreak. We stand together to strongly condemn conspiracy theories suggesting that 2019-nCoV does not have a natural origin. Scientific evidence overwhelmingly suggests that this virus originated in wildlife, as have so many other emerging diseases (1-4). This is further supported by a letter from the Presidents of the US National Academies of Science, Engineering, and Medicine, and by the scientific communities they represent (INSERT REF). Conspiracy theories will do nothing but create fear, rumors, and prejudice that jeopardize our global collaboration in the fight against this virus. We need to prioritize scientific evidence and unity over misinformation and conjecture now. We want you all to know that we stand with you, the science and health professionals of China, in your fight against this virus.

We invite others to join us in supporting the scientists, public health, and medical professionals of Wuhan and across China. Stand with our colleagues on the front-line!

*Please add your name in an act of support by going to [INSERT LINK HERE].*

**Signatories**

Dr. Peter Daszak, President, EcoHealth Alliance  
Dr. Jim Hughes, Professor Emeritus, Emory University  
Dr. Rita Colwell, former Director of National Science Foundation  
Dr. Ralph Baric, Professor, The University of North Carolina, Chapel Hill  
Dr. Linda Saif, Distinguished University Professor, The Ohio State University  
Dr. Billy Karesch, Executive Vice President, EcoHealth Alliance  
Dr. Linfa Wang, Professor, Duke-NUS Medical School  
Dr. Hume Field, Honorary Professor, The University of Queensland

**References**

1. P. Zhou *et al.*, A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature*, (2020).
2. R. Lu *et al.*, Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. *The Lancet*, (2020).
3. N. Zhu *et al.*, A Novel Coronavirus from Patients with Pneumonia in China, 2019. *New England Journal of Medicine*, (2020).
4. L. Ren *et al.*, Identification of a novel coronavirus causing severe pneumonia in human: a descriptive study. *Chin Med J. Epub ahead of print*, (2020).

February 6, 2020, Email at 3:16pm from Peter Daszak to Ralph Baric Relaying Wang's Request  
Not to Sign the Statement

To: Peter Daszak [REDACTED]  
Cc: [REDACTED]  
From: Baric, Ralph [REDACTED]  
Sent: Thur 2/6/2020 4:01:22 PM (UTC-05:00)  
Subject: RE: No need for you to sign the "Statement" Ralph!!

NOT NIH REDACTIONS

I also think this is a good decision. Otherwise it looks self-serving and we lose impact. ralph

From: Peter Daszak [REDACTED]  
Sent: Thursday, February 6, 2020 3:16 PM  
To: Baric, Ralph S [REDACTED]  
Cc: [REDACTED]  
Subject: No need for you to sign the "Statement" Ralph!!  
Importance: High

I spoke with Linfa last night about the statement we sent round. He thinks, and I agree with him, that you, me and him should not sign this statement, so it has some distance from us and therefore doesn't work in a counterproductive way.

Jim Hughes, Linda Saif, Hume Field, and I believe Rita Colwell will sign it, then I'll send it round some other key people tonight. We'll then put it out in a way that doesn't link it back to our collaboration so we maximize an independent voice.

Cheers,

Peter

**Peter Daszak**  
President

EcoHealth Alliance  
460 West 34<sup>th</sup> Street – 17<sup>th</sup> Floor  
New York, NY 10001

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

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



February 8, 2020, Email at 8:52pm from Peter Daszak to Rita Colwell Alleging WIV Researchers  
Requested the Statement

NOT NIH REDACTIONS

From: Peter Daszak [REDACTED]

Sent: Saturday, February 08, 2020 8:52 PM

To: Rita Colwell [REDACTED]

Cc: Rita Colwell [REDACTED]  
[REDACTED]

Subject: RE: coronavirus statement

Importance: High

Hi Rita,

I appreciate your comments and I think at this point, that work has already been done, with >50 genomes published from 12 countries, and phylogenetic analyses published by authors from multiple countries. I've tried to make this a bit more clear, and have edited the letter as follows, so it hopefully addresses your comments:

- 1) I've inserted a reference to the GISAID webpage where 57 [to date] full genome sequences of 2019-nCoV from 12 countries are published and analyzed
- 2) I've inserted a reference to the CDC webpage on 2019-nCoV which makes the following statement, completely in concurrence with our letter:  
*"2019-nCoV is a betacoronavirus, like MERS and SARS, both of which have their origins in bats. The sequences from U.S. patients are similar to the one that China initially posted, suggesting a likely single, recent emergence of this virus from an animal reservoir."*

In addition, please note that we will not be referring to this as a 'petition' but as a 'statement in support of' – This is in the title and will be in all materials we send out. This is to avoid the appearance of a political statement – this is simply a letter from leading scientists in support of other scientists and health professionals who are under serious pressure right now.

I hope you are willing to sign on to this - your voice will be very influential, particularly in keeping these critical bridges open between the USA and China. You should know that the conspiracy theorists have been very active, targeting our collaborators with some extremely unpleasant web pages in China, and some have now received death threats to themselves and their families. They have asked for any show of support we can give them.

As soon as we hear back from you we'll get ready to send this to our larger list (attached), but of course if you don't feel comfortable, I'll make sure your name is not associated with this.

Cheers,

Peter

**Peter Daszak**  
President

EcoHealth Alliance  
460 West 34<sup>th</sup> Street – 17<sup>th</sup> Floor  
New York, NY 10001

**From:** Morens, David (NIH/NIAID) [E]  
**Sent:** Tue, 19 Oct 2021 19:24:03 +0000  
**To:** Peter Daszak ((b)(6)); Keusch, Jerry ((b)(6));  
Kessler, Robert ((b)(6)); Taubenberger, Jeffery (NIH/NIAID) [E]  
((b)(6))  
**Subject:** FW: Sen. Marshall Introduces Legislation to Halt Viral Gain of Function Research  
**Attachments:** Viral GoF-Research Moratorium Act.pdf

*David*

**David M. Morens, M.D.**

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

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

📠 301 496 4409

💻 ((b)(6))

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**From:** Folkers, Greg (NIH/NIAID) [E] ((b)(6))  
**Sent:** Tuesday, October 19, 2021 1:19 PM  
**To:** NIAID COGCORE <COGCORE@mail.nih.gov>; NIAID OCGR Leg <NIAIDOCGRLeg@mail.nih.gov>; NIAID

OD AM <NIAIDODAM@niaid.nih.gov>

**Subject:** Sen. Marshall Introduces Legislation to Halt Viral Gain of Function Research

# Sen. Marshall Introduces Legislation to Halt Viral Gain of Function Research

• October 19, 2021

(Washington, D.C., October 19, 2021) – U.S. Senator Roger Marshall, M.D. led a group of colleagues in introducing the [VIRAL GAIN OF FUNCTION RESEARCH MORATORIUM ACT](#) to place a moratorium on all federal research grants to universities and other organizations conducting gain-of-function research and risky research on potential pandemic pathogens. This legislation is in response to the congressional inquiries and various [MEDIA INVESTIGATIONS](#) revealing national security issues including federal agencies authorizing dangerous research with certain foreign entities that may have contributed to the COVID-19 pandemic.

Original cosigners of this legislation are Senators Rand Paul, M.D. (R-KY), Joni Ernst (R-IA), Tommy Tuberville (R-AL), Marsha Blackburn (R-TN), Bill Hagerty (R-TN), Mike Braun (R-IN), James Lankford (R-OK), Marco Rubio (R-FL), and Tom Cotton (R-AR).

“It’s outrageous that a comprehensive global investigation on the origins of COVID-19 has still not been carried out, and with mounting evidence pointing towards the labs in Wuhan, additional guardrails on gain-of-function research must be established to make sure nothing like this ever happens again,” **said Senator Marshall.** “For the last decade, Dr. Fauci has funded gain-of-function research on SARS viruses, and until we get to the bottom of the origins of COVID-19, the federal government should not provide another dime in funding for viral gain-of-function research in the name of global health.”

“While Communist China continues to keep the American people and the world in the dark about the origins of the COVID-19 pandemic, Wuhan lab-linked organizations like EcoHealth Alliance are failing to tell the truth about U.S.

taxpayer money being doled out to fund their dangerous studies on coronaviruses,” **said Senator Ernst.** “This important effort will block lowans’ hard-earned tax dollars from funding viral gain-of-function research—and help prevent another pandemic from ever happening again.”

“Even as Dr. Fauci denies it, there is strong evidence COVID-19 started in a lab in Wuhan,” **said Dr. Paul.** “However, if we have learned anything from this pandemic, it’s that risky virus enhancing research – like the type conducted at the Wuhan Institute of Virology, also funded by the U.S. government – is an unnecessary form of science that could lead to the death of millions of people. The Viral Gain of Function Research Moratorium Act puts a stop to federal research grants to universities and organizations that participate in this type of research, ensuring that taxpayer money will no longer be used to fund deadly manmade viruses.”

“Communist China has worked hard to suppress information about COVID-19, including its origins and the role of gain-of-function research in its development,” **said Senator Lankford.** “This potentially dangerous research and any US involvement in it needs to be fully exposed. I will continue to advocate for defunding China’s Wuhan Institute of Virology and ending US support for any high-risk gain-of-function research. As we put Americans’ safety and health first, we must continue to keep a watchful eye on the plans and tasks of the communist Chinese government.”

“The Biden administration dropped the ball in determining the origins of COVID-19. Biden’s Chief Medical Advisor, Anthony Fauci, has been a leading advocate for deadly gain-of-function (GoF) research, and the Wuhan Institute of Virology received American taxpayer dollars to fund GoF research on his watch. We must halt GoF research until we can determine the necessary safety guardrails,” **said Senator Blackburn.**

“I’ve long said that identifying the origin of the COVID-19 pandemic is vital for preventing future pandemics. The moratorium on gain-of-function research will allow more time to understand how gain-of-function research may have played a role in catalyzing the pandemic, while ensuring that no additional gain-of-function research is being conducted or posing risk of future pandemic. Additionally, this moratorium will ensure that American taxpayers will not be funding foreign

research projects, like those conducted in the Wuhan Institute of Virology,” **said Senator Braun.**

“More than a year and half after the initial outbreak of COVID-19 in Wuhan, serious questions remain regarding the origins of this deadly virus and its possible connection to federally-funded gain of function research in China,” **said Senator Rubio.** “The American people deserve to know the truth, and until a full and transparent investigation is guaranteed and real oversight is imposed on this risky line of research, no taxpayer dollars should be squandered by unelected bureaucrats operating in the dark.”

“American lives and livelihoods have been lost due to COVID-19, and we need answers about any link between gain-of-function research and the origins of the pandemic,” **said Senator Tuberville.** “The Chinese government won’t tell the full story, and Dr. Fauci takes every opportunity to tout the importance of gain-of-function research. Until the truth has been brought to light, Alabamians’ hard-earned tax-payer dollars should not be used to fund any research that seeks to threaten the health and safety of our nation.”

“Significant evidence suggests that COVID-19 originated in the Wuhan Institute of Virology, which received gain-of-function research grants and funding. Until the origin of this virus can be confirmed, funding for similar research programs should be halted to help prevent another global crisis,” **said Senator Cotton.**

### **Background:**

The U.S. National Institutes of Health (NIH) has historically applied a broad and inconsistent definition of gain-of-function (GoF) research – a process that aims to genetically alter a virus or organism to gain (or lose) function on its transmissibility or pathogenicity. However, viral GoF on infectious diseases places great risk to global health as it directly aims to alter viruses deadly to people. Recognizing the threat of GoF research and biosecurity issues in lab facilities, White House officials **PLACED A MORATORIUM** on this work in 2014. Unfortunately, the National Institute of Allergy and Infectious Diseases, led by Dr. Anthony Fauci, continued funding GoF research **UNDER EXCEPTIONS TO THE MORATORIUM.** In 2017 – with key cabinet appointments vacant or pending Senate confirmation – NIH successfully advocated for the **LIFTING OF THE MORATORIUM.**

The majority of the funded research in question involves EcoHealth Alliance. A non-profit organization based in New York, their GoF projects involved researchers at the Wuhan Institute of Virology, Wuhan University, and the China's CDC and Prevention of Guangdong Province. In addition to the NIH, other federal agencies involved in this type of risky research include the U.S. Agency for International Development and the U.S. Department of Defense (DoD). In fact, the DoD PROVIDED OVER \$40 MILLION in funding to the EcoHealth Alliance to conduct risky research at China's Wuhan Institute of Virology with no transparency and no accountability.

Senator Marshall has been actively involved in uncovering the origin of COVID-19, but certain agencies have refused to cooperate fully. Last month, Senator Marshall – along with Senators Chuck Grassley (IA) and Marsha Blackburn (TN) – SENT A FOLLOW-UP LETTER demanding answers to questions that may shed light on the origins of COVID-19. Specifically, the Senators requested answers regarding NIH's data retention policies for the Sequence Read Archive, the largest public database for DNA sequencing data. NIH had deleted coronavirus gene sequences data from the database at the request of researchers from Wuhan University. NIH INADEQUATELY ADDRESSED previous congressional oversight inquiries dating back to June. The exchange between the Senators and NIH was REPORTED ON BY THE WALL STREET JOURNAL.

In May, Senator Marshall – along with Senators Rand Paul (KY), Ron Johnson (WI), James Lankford (OK), Rick Scott (FL), Tom Cotton (AR), and Rep. Mike Gallagher (WI) LED A LETTER highlighting a response to the World Health Organization's study of SARS-CoV-2's origins from a group of eighteen scientists stating that the leak of the virus from a lab is a "viable" theory and should be thoroughly investigated. The letter touched on several high profile biosafety incidents at the labs and GoF research studies that led to a 2014 HHS and NIH pause on funding research for gain of function experiments "*involving influenza, SARS, and MERS viruses.*" This pause did not halt ongoing research being conducted or research that received an exception from the head of the USG funding agency.

###

117TH CONGRESS  
1ST SESSION

**S.** \_\_\_\_\_

To provide a moratorium on all Federal research grants provided to any institution of higher education or other research institute that is conducting gain-of-function research.

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IN THE SENATE OF THE UNITED STATES

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Mr. MARSHALL introduced the following bill; which was read twice and referred to the Committee on \_\_\_\_\_

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**A BILL**

To provide a moratorium on all Federal research grants provided to any institution of higher education or other research institute that is conducting gain-of-function research.

1 *Be it enacted by the Senate and House of Representa-*  
2 *tives of the United States of America in Congress assembled,*

3 **SECTION 1. SHORT TITLE.**

4 This Act may be cited as the “\_\_\_\_\_ Act of  
5 \_\_\_\_\_”.

1 **SEC. 2. PROHIBITION ON FEDERAL RESEARCH GRANTS**  
2 **FOR INSTITUTIONS AND RESEARCH INSTI-**  
3 **TUTES CONDUCTING GAIN-OF-FUNCTION RE-**  
4 **SEARCH.**

5 (a) DEFINITION OF GAIN-OF-FUNCTION RE-  
6 SEARCH.—In this section, the term “gain-of-function re-  
7 search” means any research that—

8 (1) may be reasonably anticipated to confer at-  
9 tributes to influenza, MERS, or SARS viruses such  
10 that the virus would have enhanced pathogenicity or  
11 transmissibility in any organism; or

12 (2) involves the enhancement of potential pan-  
13 demic pathogens or related risky research with po-  
14 tentially dangerous pathogens.

15 (b) PROHIBITION.—Notwithstanding any other provi-  
16 sion of law, no research grants supported by Federal funds  
17 may be awarded to institutions of higher education, or  
18 other research institutes, that are conducting gain-of-func-  
19 tion research.