NATIONAL REVIEW

NIH Admits to Funding Gain-of-Function Research in Wuhan, Says EcoHealth Violated Reporting Requirements

Caroline Downey

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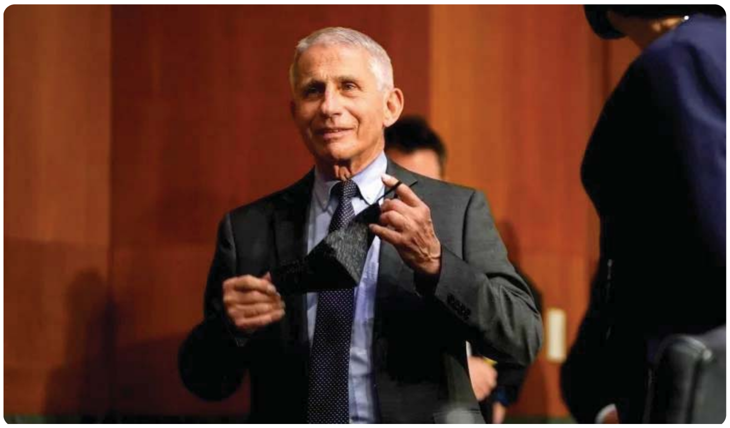

A top NIH official admitted in a Wednesday letter that U.S. taxpayers funded gain-of-function research on bat coronaviruses in Wuhan and revealed that EcoHealth Alliance, the U.S. non-profit that funneled NIH money to the Wuhan Institute of Virology, was not transparent about the work it was doing.

In the letter to Representative James Comer (R., Ky.), Lawrence A. Tabak of the NIH cites a “limited experiment” that was conducted to test if “spike proteins from naturally occurring bat coronaviruses circulating in China were capable of binding to the human ACE2 receptor in a mouse model.” The laboratory mice infected with the modified bat virus

TRENDING

1. Sheriff: Baldwin fired shot on movie set that killed woman
2. Sheriff says family on California hike died of extreme heat
3. Photo shows Alec Baldwin in tears outside sheriff's office after the prop-firearm shooting that left 'Rust' cinematographer dead
4. Laundrie family lawyer said Brian was 'visibly upset' when he left for the reserve, and his father 'wished he hadn't left but he couldn't stop him'
5. A student who listed his Black classmate on Craigslist as a 'slave for sale' has been given a probationary sentence

got into heated exchanges with National Institute of Allergy and Infectious Disease director Anthony Fauci during his May and July testimonials before Congress over the gain-of-function question. At the second hearing, Paul accused Fauci of misleading Congress by denying that the U.S. had funded gain-of-function projects at the Wuhan Institute of Virology.

Gain-of-function research involves extracting viruses from animals and artificially engineering them in a laboratory to make them more transmissible or deadly to humans.

In keeping with Fauci's refusal to use "gain-of-function," Tabak avoids the term, though the work he described matches its commonplace definition precisely.

A previously unpublished EcoHealth grant proposal filed with NIAID, obtained by *The Intercept,* had already exposed that $599,000 of the total grant to the Wuhan Institute of Virology was for research designed to make viruses more dangerous and/or infectious.

Dr. Richard Ebright, biosafety expert and professor of chemistry and chemical biology at Rutgers University, had previously rebutted Fauci's claim that the NIH "has not ever and does not now fund gain of function research in the Wuhan Institute of Virology [WIV]" as "demonstrably false."

Ebright told National Review that the NIH-financed work at the WIV "epitomizes" the definition of gain-of-function research, which deals with "enhanced potential pandemic pathogen (PPP)" or those pathogens "resulting from the enhancement of the transmissibility and/or virulence of a pathogen."

In addition to his admission that gain-of-function research was being conducted with NIH money, Tabak also revealed that EcoHealth failed to comply with its reporting responsibilities under the grant. EcoHealth was required to submit to a "secondary review" in the event of certain developments that might increase the danger associated with the research. So, when Wuhan researchers successfully to NIH “any and all unpublished data” relating to this award’s project for compliance purposes.

The remainder of the document attempts to prove that the naturally occurring bat coronaviruses used in the 2014-2018 NIH grant experiments “are decades removed from SARS-CoV-2 evolutionarily,” only sharing 96-97 percent of the genome.

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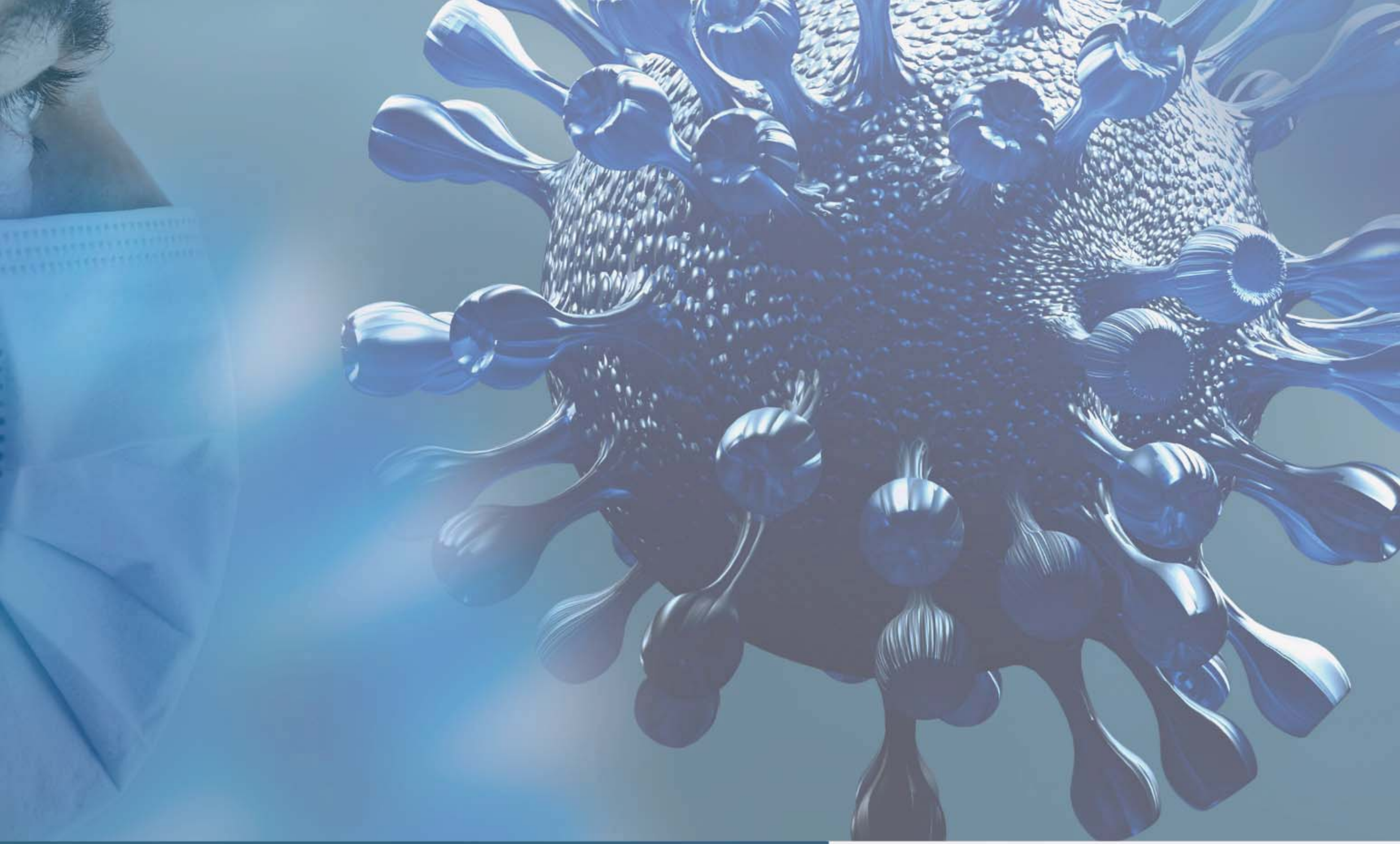

AUGUST 2021

THE ORIGINS OF COVID-19:

AN INVESTIGATION OF THE WUHAN INSTITUTE OF VIROLOGY

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

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." [1]

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[1] "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/.

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 identified 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 modify 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 Daszak, 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.

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 lab bench or table.

GLOSSARY OF TERMS

Biosafety Level 2 (BSL2)	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.
Bio Safety Level 3 (BSL3)	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.
Biosafety Level 4 (BSL4)	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.
Wuhan Institute of Virology (WIV)	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."

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 know 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 as 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. [2] 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.[3] 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.[4] 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.[5]

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.

[4] Van de Bovenkamp, Judith and Yuan Fei. "Economic Overview of Hubei Province." *Neatherlands 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

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.[6] 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."[7] Construction was completed in 2015, but due to delays the BSL-4 space did not become operational until early 2018.[8]

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.[9]

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[6] "History." *Wuhan Institute of Virology*, http://english.whiov.cas.cn/About_Us2016/History2016/.

[7] 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

[8] 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

[9] 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.[10] Shi is also the Director of the Chinese Academy of Sciences (CAS) Key Laboratory of Special Pathogens and Biosafety,[11] 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[12]
Liu Qiaojiue	Key Laboratory of Special Pathogens and Biosafety[13]	Party Branch of Research Center for Emerging Infectious Diseases
Zhang Xiaowei	Key Laboratory of Special Pathogens and Biosafety and Key Laboratory of Virology[14]	Party Branch of the Research Center for Microbiology and Nanobiology

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[10] "Shi Zhingli." Wuhan Institute of Virology, http://www.whiov.cas.cn/sourcedb_whiov_cas/zw/rck/200907/t20090718_2100074.html

[11] "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

[12] "Party Branch." Wuhan Institute of Virology, http://www.whiov.cas.cn/djkxwh/dqzz/dzb/

[13] 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/

[14] 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 [15]	Graduate Party Branch of the Research Center for Emerging Infectious Diseases
Tang Shuang	State Key Laboratory of Virology [16]	Party Branch of the Research Center for Microbial Resources and Bioinformatics
Wu Yan	State Key Laboratory of Virology [17]	Party Branch of Molecular Virus and Pathology Research Center
He Lihong	State Key Laboratory of Virology [18]	Party Branch of the Research Center for Microbial Resources and Bioinformatics
Wang Qingxing	State Key Laboratory of Virology [19]	Graduate Party Branch of the Research Center for Molecular Viruses and Pathology
Yang Mengsi	State Key Laboratory of Virology [20]	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.”[21]

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.

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[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/djkxwh/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.[22]

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."[23] 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."[24] 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."[25] 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.[26] 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."[27] 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.[28]

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]."[29] **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.[30]

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[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.

[23] "New Year's Speech by the Director in 2021." *Wuhan Institute of Virology,* http://www.whiov.cas.cn/gkjj/szzc_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/szzc_160220/

[25] *Ibid.*

[26] "About WIV." *Wuhan Institute of Virology,* 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.

[28] *Ibid.*

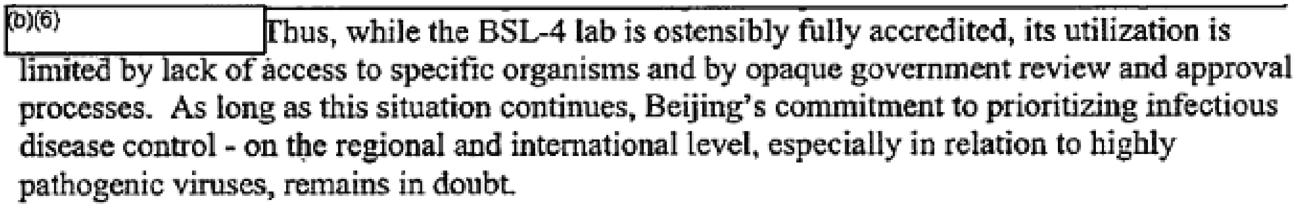
[29] *Ibid.*

[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."[31] 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.**[32]

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.*

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[31] 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/.

[32] 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/

Entitled, "Current status and future challenges of high-level biosafety laboratories in China,"[33] 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."[34] 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.**[35]

Yuan also raised concerns about a lack of specialized biosafety managers and engineers to run the labs.[36] **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[37]	WNBL	March 1, 2019	$401,284.10
Procurement of Positive Pressure Protective Clothing[38]	WNBL	March 21, 2019	$177,161.40
Hazardous Waste Treatment System Renovation Project[39]	WNBL	July 31, 2019	$1,521,279.28

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[33] 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

[34] *Ibid.*

[35] *Ibid.*

[36] *Ibid.*

[37] "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

[38] "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

[39] "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 [40]	Unclear	August 14, 2019	$132,200,025.47
Security Service Procurement Project [41]	WNBL	September 12, 2019	$1,281,022.33
Central Air Conditioning Renovation Project [42]	Unclear	September 16, 2019	$606,382,986.11
Procurement of Air Incinerator and Testing Service [43]	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.[44] 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.

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[40] "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/1nXLD#selection-229.0-229.228

[41] "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

[42] "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

[43] "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

[44] "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	*Rousettus leschenaultii*
Species molecular identification	*Rousettus* 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. *Virol Sin*. 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 [45]

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." [46]

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."[47] She also claimed that researchers had "only entered a limit[ed] data in this database" despite it having more than 22,000 entries.

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[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.

[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.

In an apparent contradiction of her *BBC* interview, Shi admitted that “access to the visitors is limited,”[48] 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.**[49]

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**”[50] (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.[51] 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.[54] The post’s survival on a heavily CCP censored site confirms its legitimacy.

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[48] Sudworth.

[49] *Ibid.*

[50] *Ibid.*

[51] “Yuan Zhiming.” *Wuhan Institute of Virology*, http://www.whiov.cas.cn/sourcedb_whiov_cas/zw/rck/200907/t20090718_2100080.html

[52] 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/.

[53] 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

[54] 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.[55] 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."[56]

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.[57] 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.[58]

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.[59] This website was scrubbed on May 28, 2020, and the lists of committee members removed. However, archived copies of the website are available online.

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[55] "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

[56] 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

[57] 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

[58] 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.

[59] "Committees." *Wuhan Institute of Virology,* https://web.archive.org/web/20200527045823/http://english.whiov.cas.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.

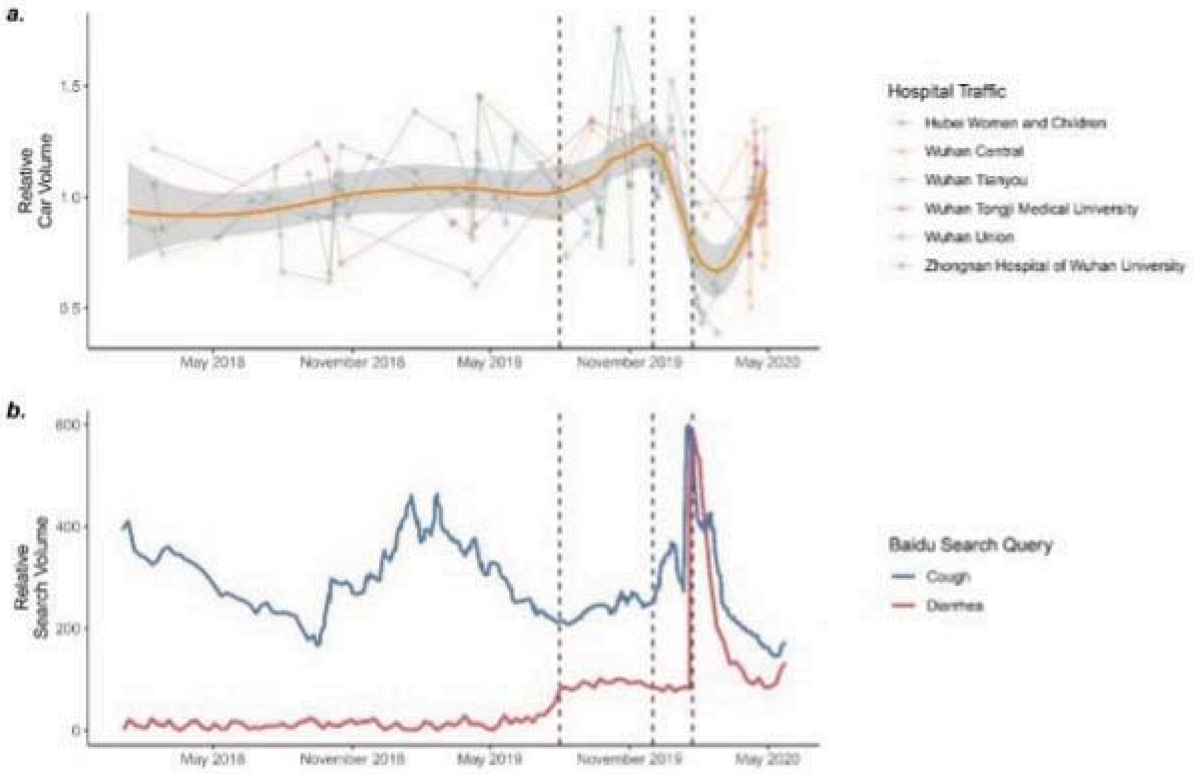

Fig. 7: Time-series of Different Influenza-like Illnesses, Symptoms and Surveillance signals[62]

This peak corresponded with an increase in searches for "cough" and "diarrhea" in Wuhan on Baidu, a Chinese search engine.[60] According to the CDC, both cough and diarrhea are symptoms of COVID-19.[61] 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.[63]

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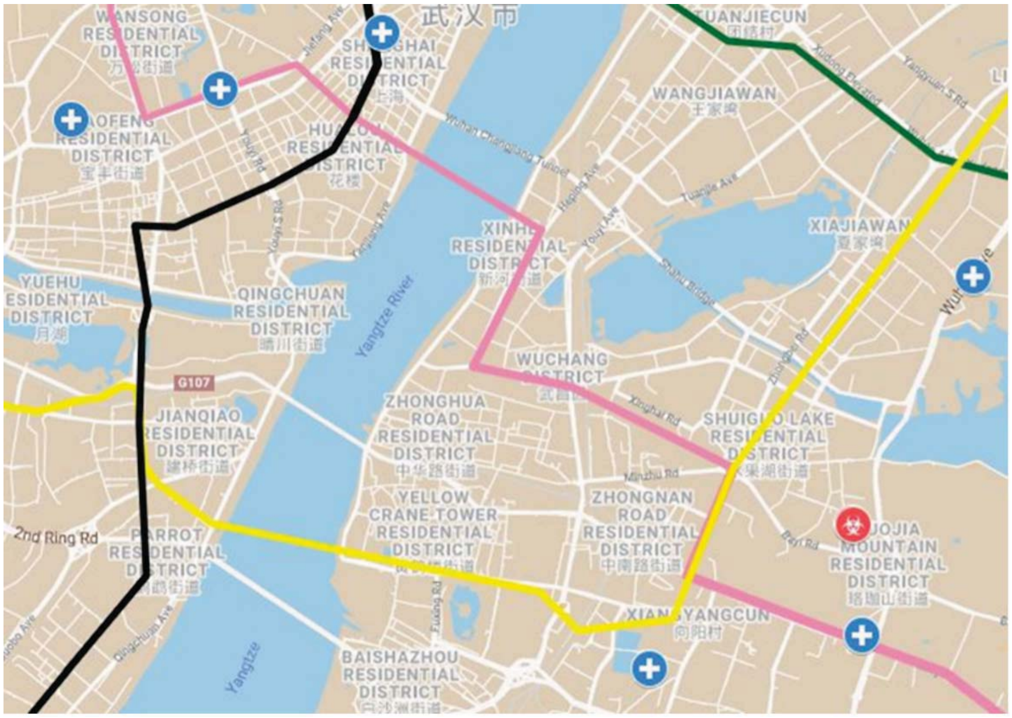
[60] Nsoesie, Elaine Okanyene, et. al. "Analysis of hospital traffic and search engine data in Wuhan China indicates early disease activity in the Fall of 2019 (2020)." *Digital Access to Scholarship at Harvard,* 2020. http://nrs.harvard.edu/urn-3:HUL.InstRepos:42669767

[61] "Symptoms of COVID-19." *Centers for Disease Control and Prevention*. https://www.cdc.gov/coronavirus/2019-ncov/symptoms-testing/symptoms.html

[62] Nsoesie

[63] "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.[64] 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.[65]

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[64] 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.

[65] "Military Games to Open Friday in China." *China Daily,* 17 Oct. 2019, 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.[66] 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.[67] 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,"[68] 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.**[69]

The service member also revealed his family members became ill as his symptoms increased,[70] 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,[71] and Sweden.[72]

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"**

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[66] "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.

[67] "Competition Venues." *Wuhan 2019 Military World Games*, https://web.archive.org/web/20191020154108/en.wuhan2019mwg.cn/html/Competition_venues/.

[68] 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

[69] 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.

[70] *Ibid.*

[71] Houston.

[72] 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.

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.[73]

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.[74]

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.[75]

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[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/.

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.[76]

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 – it 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 the cover-up conducted 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."**
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> **– Dr. Ralph Baric**

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[76] 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

[77] 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/.

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.[78] 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."[79] 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.[80] 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 Daszag; 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.

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[78] Zaugg, Julie. "In Wuhan with Bat Woman, at the origins of the Covid-19." *L'Illustre*, 22 Jan. 2021, https://www.illustre.ch/magazine/a-wuhan-avec-bat-woman-aux-origines-du-covid-19

[79] *Ibid.*

[80] *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.”[81]

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.[82] 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.[83]

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,

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[81] *Ibid.*

[82] 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

[83] 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

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."[84] 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."[85]

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*.[86]

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.[87]

Purpose: This work marked "the first recorded isolation of a live SL-CoV"[88] [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."[89]

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."[90]

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.

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[84] *S*riram, 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.

[85] Ren.

[86] 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/

[87] *Ibid.*

[88] *Ibid.*

[89] *Ibid.*

[90] *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.[91]

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 SCH014, 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."[92] **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"[93] 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."[94] 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.[95]

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).[96]

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.

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[91] 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/

[92] 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

[93] Menachery

[94] *Ibid.*

[95] *Ibid.*

[96] 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." [97]

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.[98] In addition to standard BALB/c mice (a strain of albino, lab-breed house mice used in experimentation[99]), 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).[100]

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.[101]

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."[102]

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.[103]

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[97] 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%2Fpnas.1517719113

[98] *Ibid.*

[99] "Inbred Strains: BALB." MGI, www.informatics.jax.org/inbred_strains/mouse/docs/BALB.shtml.

[100] Menachery 2016.

[101] 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%2FJVI.03079-15

[102] 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%2Fjournal.ppat.1006698

[103] 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."[104] 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.[105] 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."[106] This project focused on, among other things, evaluating new vaccines and establishing "humanized small animal models"[107] for in vitro pathogen testing.[108]

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), investigating "genetic evolution and transmission mechanism of important bat-borne viruses."[109] 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."[110] The project was funded at a value of roughly $850,000 USD (grant no. 31770175) and is slated to run until December 2021.[111] 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.[112]

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[104] "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

[105] *Ibid.*

[106] *Ibid.*

[107] *Ibid.*

[108] *Ibid.*

[109] Shi, Zheng-li. "Curriculum Vitae." https://www.ws-virology.org/wp-content/uploads/2017/11/Zhengli-Shi.pdf

[110] "Study on the evolutionary mechanism of bat SARS-like coronavirus adapted to host receptor molecules and the risk of cross-species infection." *MedSci*, https://archive.is/g35C6#selection-1425.0-1425.139

[111] *Ibid.*

[112] "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."[113] 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.[114] The YSFP "supports the young researchers to independently select topics within the scope of the scientific funding and carry out basic research."[115] This project, selected by Ben Hu, was titled, "Pathogenicity of two new bat SARS-related coronaviruses to transgenic mice expressing human ACE2."[116] 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.[117] 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." [118]

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.**

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[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." F*aculty 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

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."[120] 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.[121]

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[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.[122]

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.[123] **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.[124] 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.[125]

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."[126] 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.

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[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.[127]

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."[128] 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.[129] 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**

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[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.

[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

[129] *Ibid.*

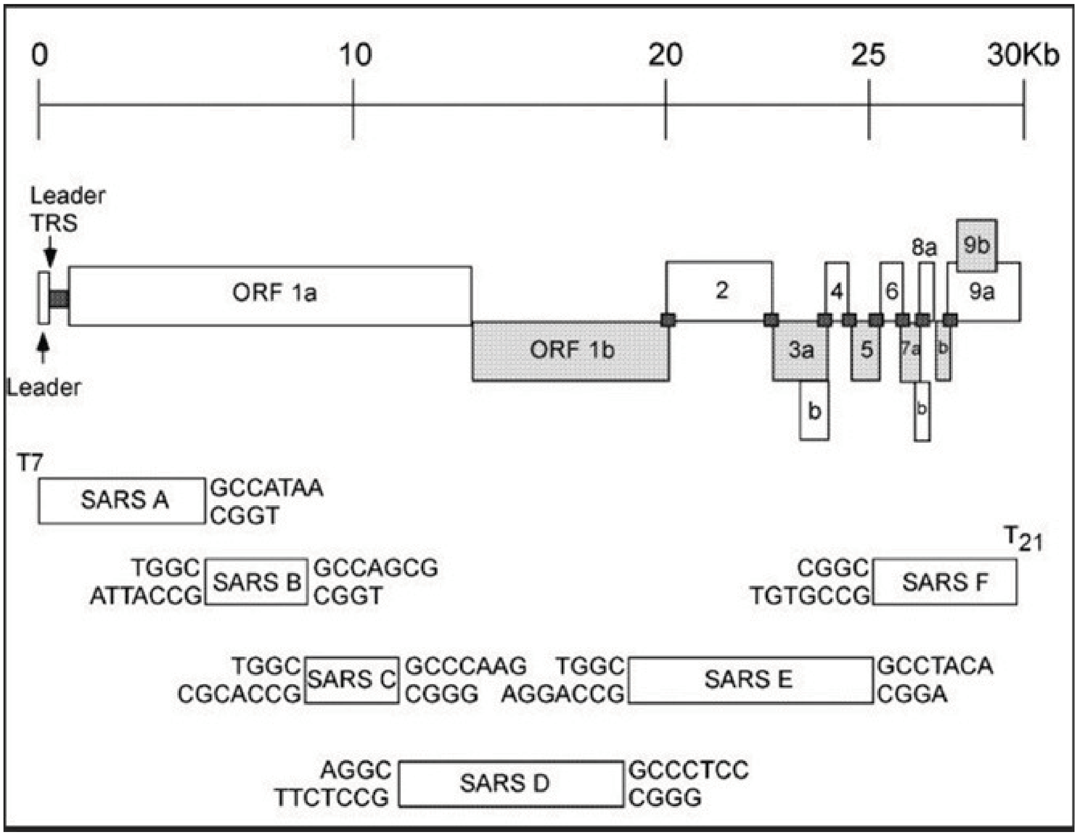

Fig. 5: Baric's "No-See-Um" System

The paper stated these viruses were "indistinguishable from wild type,"[130] 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."[131] 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."[132]

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."[133] **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.**[134]

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[130] *Ibid.*

[131] 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.

[132] *Ibid.*

[133] Jiang, Ren-Di et al. "Pathogenesis of SARS-CoV-2 in Transgenic Mice Expressing Human Angiotensin-Converting Enzyme 2." *Cell*, 21 May 202, 182(1): 50-58.e8. https://dx.doi.org/10.1016%2Fj.cell.2020.05.027

[134] 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."[135] 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 the 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."[139] 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.[140]

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[135] 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

[136] *Ibid.*

[137] *Ibid.*

[138] "Leiping Zeng." *Stanford*, https://profiles.stanford.edu/leiping-zeng

[139] 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-mojiang-mine-its-role-origins-covid-19-2021-06-09/.

[140] 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-coronavirus1/

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."[141] 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."[142] 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,"[143] 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.[144] 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%.[145] 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."[146] 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

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[141] 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

[142] Ibid.

[143] 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

[144] Wang, Yanan. "Human-to-Human Transmission Confirmed in China Coronavirus." *AP NEWS*, 20 Jan. 2020. https://apnews.com/14d7dcffa205d9022fa9ea593bb2a8c5

[145] 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.

[146] 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.**[147]

A close examination of the paper, and the corrections published months later, reveal inconsistences 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.**[148]

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.[149] 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.[150] 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.[151]

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*.[152] 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."[153] "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.**

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[147] *Ibid.*

[148] 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

[149] Shi, Zheng-li. "Reply to Science Magazine." *Science Magazine,* https://www.sciencemag.org/sites/default/files/Shi%20Zhengli%20Q%26A.pdf

[150] 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.

[151] 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/franciscodeasis/status/1370183826731888641?s=20.

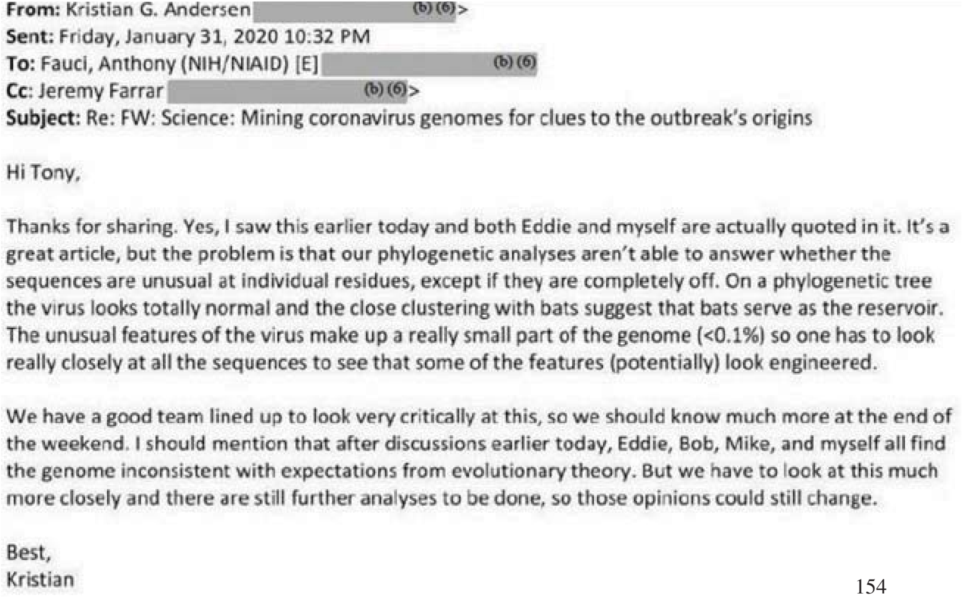
[152] Andersen, Kristian G et al. "The proximal origin of SARS-CoV-2." *Nature Medicine,* 17 March 2002, 26(4):450-452. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7095063/

[153] *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 [redacted] (b)(6)>
Sent: Friday, January 31, 2020 10:32 PM
To: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b)(6)
Cc: Jeremy Farrar [redacted] (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[155]. 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.[156] It is unclear what was said on this call that led to Anderson doing so.

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[154] Andersen, Kristian G. Email to Anthony Facui and Jeremy Farrar. 31 Jan. 2020. https://s3.documentcloud.org/documents/20793561/leopold-nih-foia-anthony-fauci-emails.pdf

[155] 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

[156] 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/covid-19-fauci-lab-leaks-wuhan-china-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 [157]

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."[158] 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 on the website for the Wuhan Branch of the Chinese Academy of Sciences has also been removed.[159] 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?

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[157] 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

[158] "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

[159] 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

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.[160]

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.'"[161]

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.[162]

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."[163]

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."[164] 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.[165]

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[160] 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.

[161] Guli.

[162] Xin.

[163] 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.

[164] 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

[165] 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.

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:

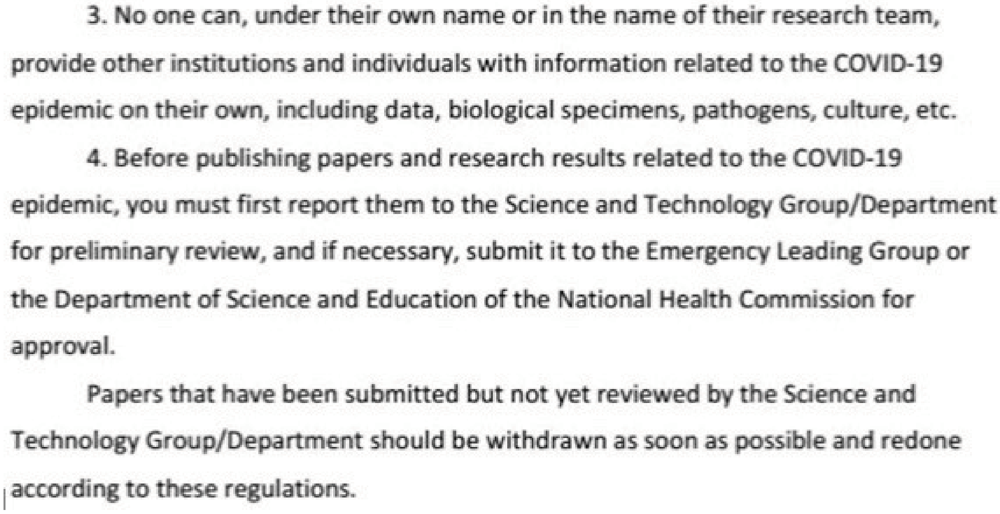
> Following extensive discussions with and presentation from Chinese counterparts, it appears that little had been done in terms of epidemiological investigations around Wuhan since January 2020. The data presented orally gave a few more details than what was presented at the emergency committee meetings in January 2020. No PowerPoint presentations were made and no documents were shared.[166]

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.[167]

Experts interviewed in February 2020 by *The Global Times* stated that PRC labs paid "insufficient attention to biological disposal."[168] This included disposing of lab materials into sewage systems.[169] 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[170]

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[166] 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

[167] 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.

[168] *Ibid.*

[169] *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.[171]

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.[172] 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.”[173] The notice announced the research group was taking control of all publication work related to the pandemic for “coordinated deployment.”[174] 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.”[175]

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[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

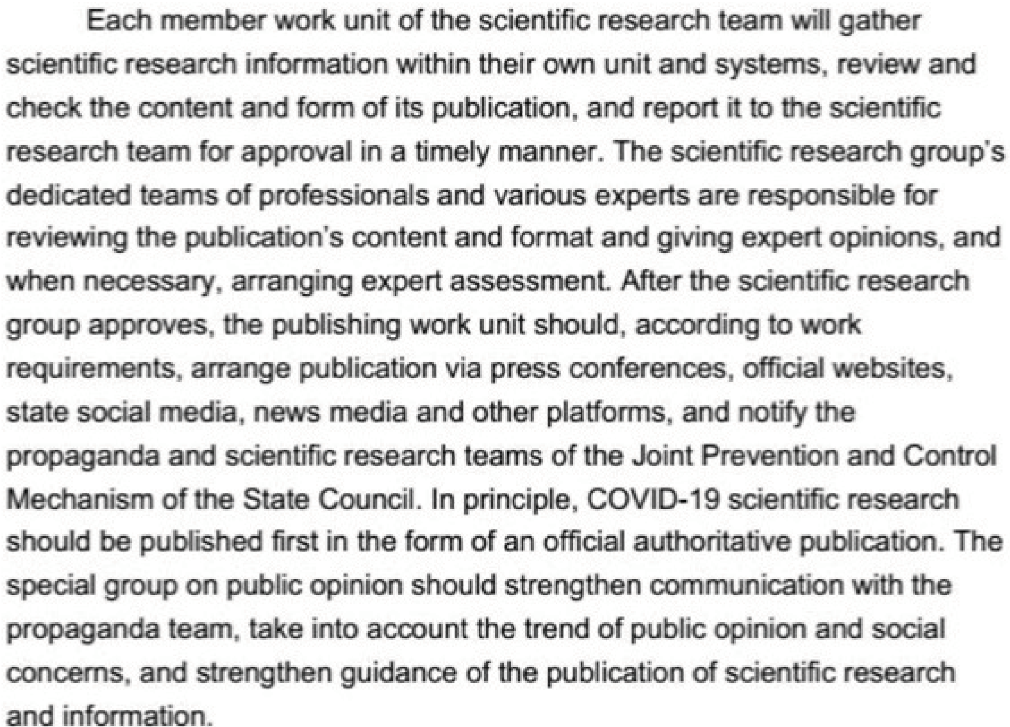
[171] Wang, Zhenya. “Experts Judge the Source of the New Crown: December 8 Last Year May Not Be the Earliest Time of Onset.” *Health Times,* 27 Feb. 2020, www.jksb.com.cn/index.php?m=wap&a=show&catid=629&id=160018.

[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."[176] 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."[177] It also discusses what they call the "tired old theory that the virus could have leaked from a lab"[178] 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.[180] 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.

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[176] *Ibid.*

[177] "The Point: Clearing up Confusion in the McCaul Report On Covid-19." *CCTV News*, 25 July 2020, www.youtube.com/watch?v=n5qYogMTZOw.

[178] *Ibid.*

[179] *Ibid.*

[180] *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."[181] 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.**[182]

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.[183] The article was from the *Global Times* research.ca, a website that pushes pro-Putin propaganda and has reported ties to Russian state media.[184] His tweet was amplified by the Chinese Embassy in South Africa.[185]

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[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

[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/.

[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/8cRxkSZB3z." *Twitter*, 16 Mar. 2020, www.twitter.com/ChineseEmbSA/status/1239453193689587712

Lijian Zhao 赵立坚 @zlj517 · Mar 12, 2020

China government official

2/2 CDC was caught on the spot. When did patient zero begin in US? How many people are infected? What are the names of the hospitals? It might be US army who brought the epidemic to Wuhan. Be transparent! Make public your data! US owe us an explanation!

1:03 3.9M views

From Global Times

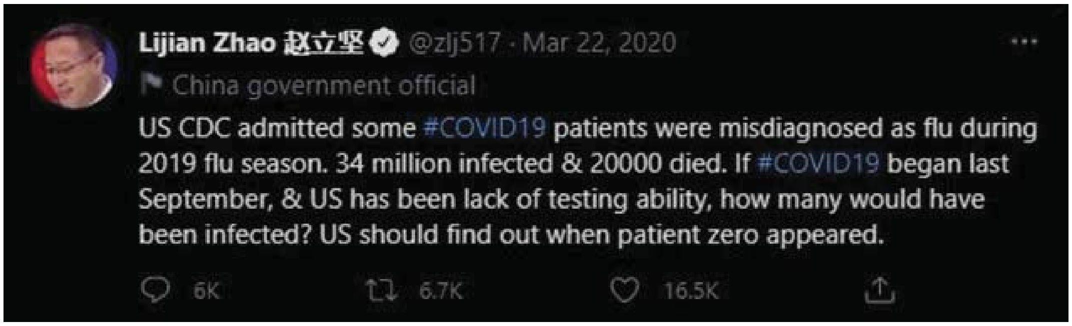
Get the facts about COVID-19

7.6K 11K 14.1K

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. [186]

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.[187]



Lijian Zhao 赵立坚 @zlj517 · Mar 22, 2020

China government official

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.

6K 6.7K 16.5K

Fig. 13: PRC Spokesman Tweet Suggesting the COVID-19 Pandemic Started in September 2019.

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[186] 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.

[187] 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."[188] The statement continued, "Conspiracy theories do nothing but create fear, rumours, and prejudice that jeopardise our global collaboration in the fight against this virus."[189] 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."[190]

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.**[191]

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[192] before completing a Ph.D. in molecular biology at the University of California, Davis in the United States.

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[188] 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/

[189] *Ibid.*

[190] 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

[191] 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

[192] Wang, Linfa. "Curicullum Vitae." 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 vsiit with Hu and Shi, with whom he has authored dozens of papers. He departed the city on January 18th,[192] less than three weeks before Daszak externally circulated his draft *Lancet* statement. Wang is included on the email soliciting cosigners.[193]

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.**[194]

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.[195]

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[196]) 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."[197] **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**.[198]

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.

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[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.

[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

[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

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." [199] 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.**[200]

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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[200] *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 inform our understanding and be the basis for interpretation of the available information.[201]

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."[202] 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.[203]

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.[204] 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,"[205] which include the lab leak hypothesis and questions regarding the possible genetically modified nature of SARS-CoV-2. It also refers to the WIV's sequence database that was taken offline as a "rumour about missing data."[206] This is similar language to that which Daszak used during his Chatham House interview – despite the database remaining offline.[207] Committee Minority Staff was unable to determine whether Daszak assisted in the drafting or editing of the WHO report.

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[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."[208] This is despite the fact that four days later Nature Communications published "Origin and cross-species transmission of bat coronaviruses in China."[209] 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 phylogenetic analysis "suggesting a likely origin for SARS-CoV-2 in Rhinolophus spp. bats."[210] 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.[211]

April 24th was the day the NIH terminated the project Understanding the Risk of Bat Coronavirus Emergence, which was funded under grant R01AI110964,[212] which is cited in the paper as funding this work.[213] 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."[214] 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"[215] 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?

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[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"[216] 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.**[217]

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.[218]

This is, of course, untrue. Researchers at the WIV fully sequenced RaTG13's genome in 2018.[219] 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.

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[216] Subbaraman.

[217] "Sustaining the Response: Inside the WHO-China Mission." *Chatham House,* 10 March 2021, https://www.youtube.com/watch?v=GMIlEF58944&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.

[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.[220]

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.[221]
- 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 asymptotic 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,[222] issues a notice for laboratory inspections in late September.[223] 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.[224] 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."[225] The budget provided was in excess of $1.2 million.[226]

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,[227] 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 Januarty 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.

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[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

[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/jzxcs/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.

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 inconsistences 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 closet 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 toBaric'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-on-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 accidently 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 stead 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.

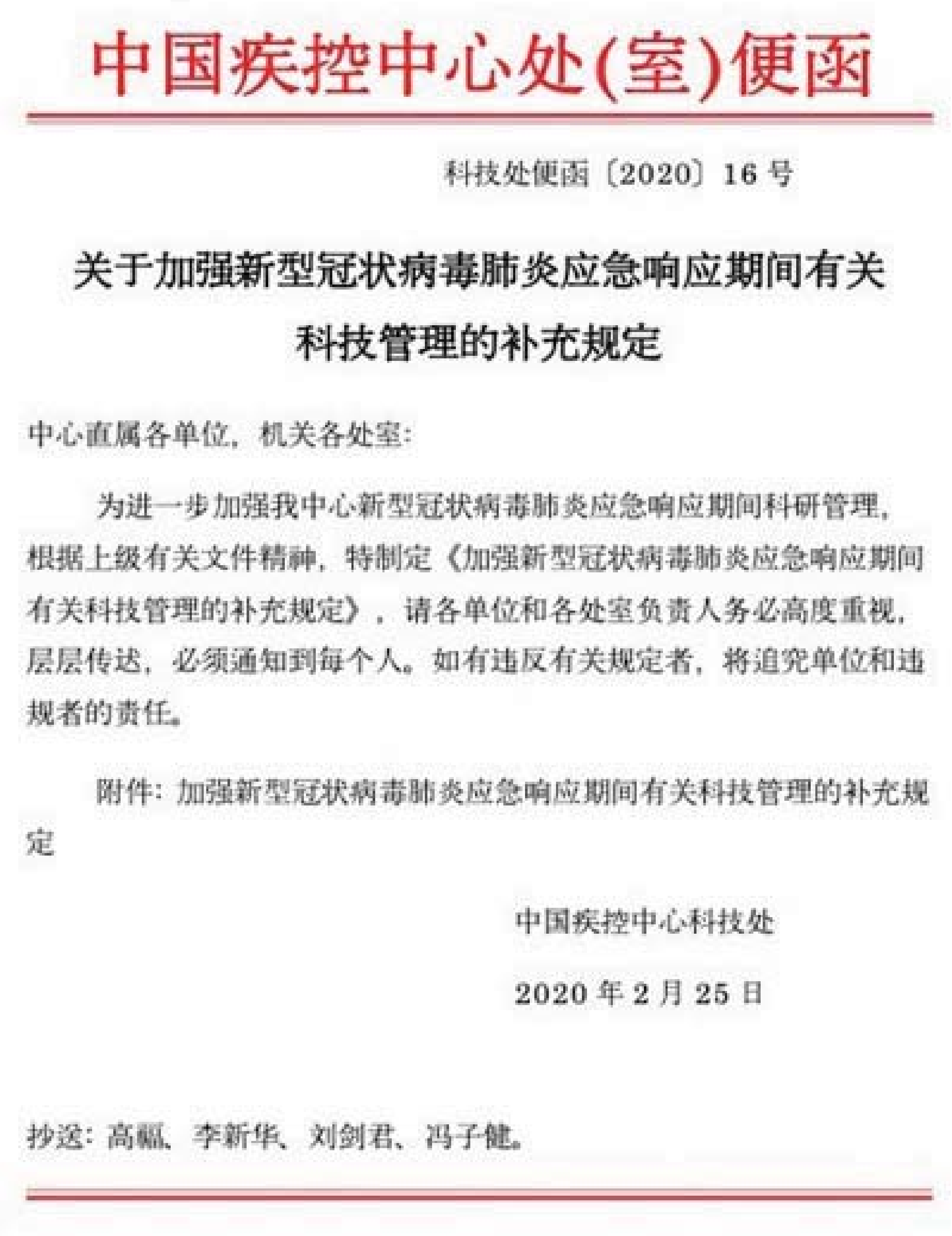
Nov. 17, 2020: As a result of public pressure, Shi, Hu, and other WIV researchers publish an addendum to their February 3rd paper, confirming that RaTG13 was ID4991 collected from the cave in Yunnan, and revealing they collected 293 coronaviruses from the cave between 2012 and 2015.

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

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：

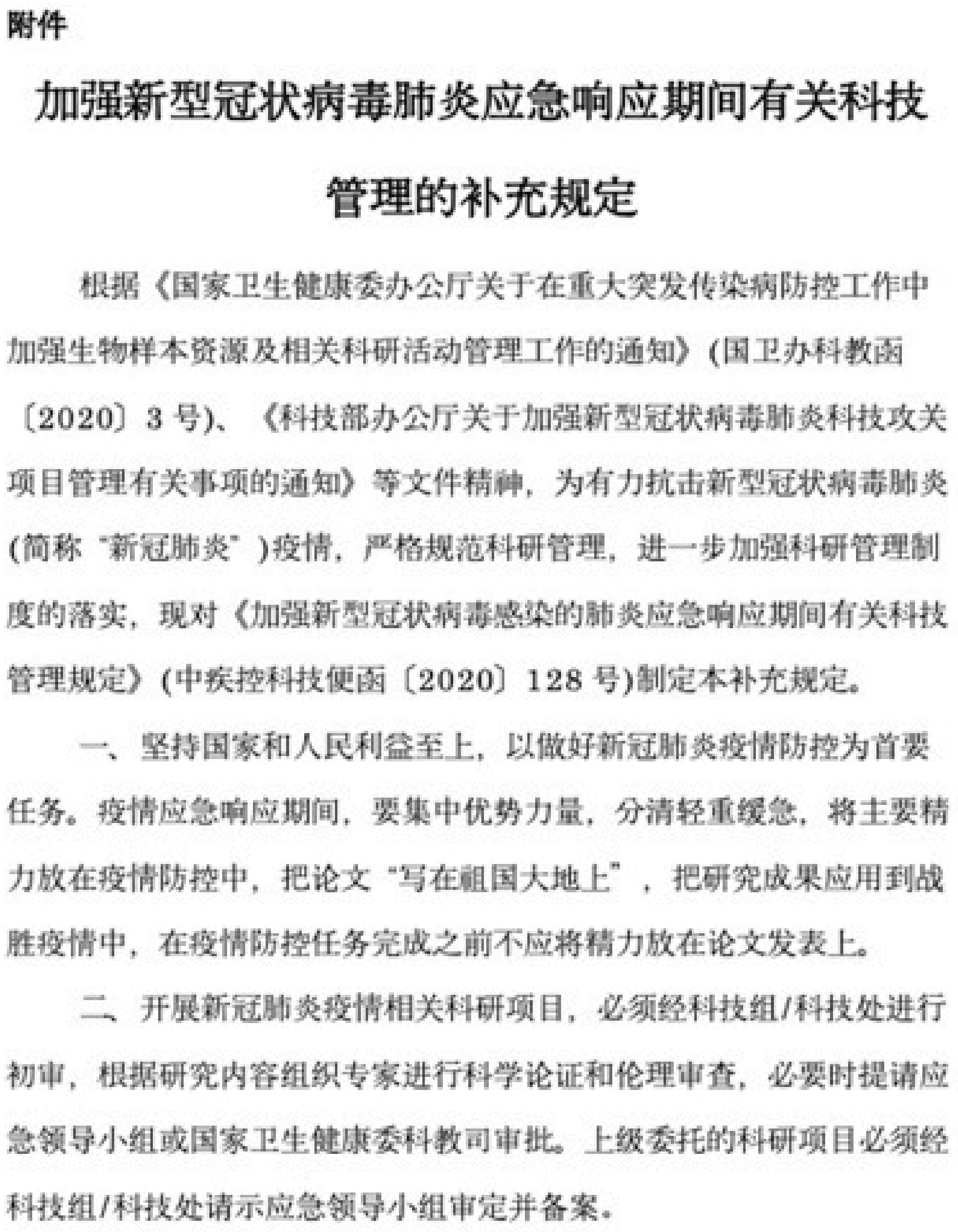
为进一步加强我中心新型冠状病毒肺炎应急响应期间科研管理，根据上级有关文件精神，特制定《加强新型冠状病毒肺炎应急响应期间有关科技管理的补充规定》，请各单位和各处室负责人务必高度重视，层层传达，必须通知到每个人。如有违反有关规定者，将追究单位和违规者的责任。

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。



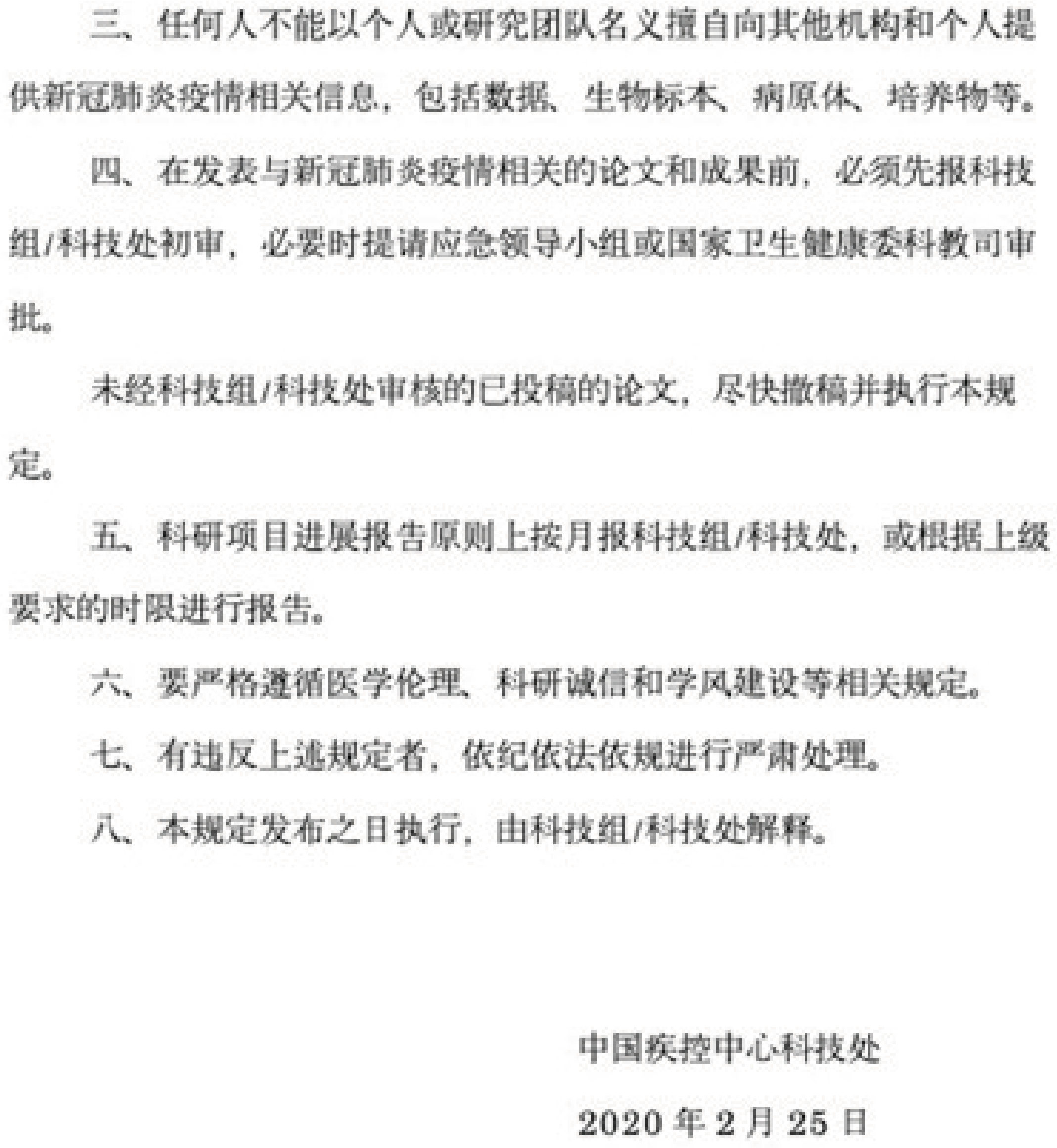
附件

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

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.

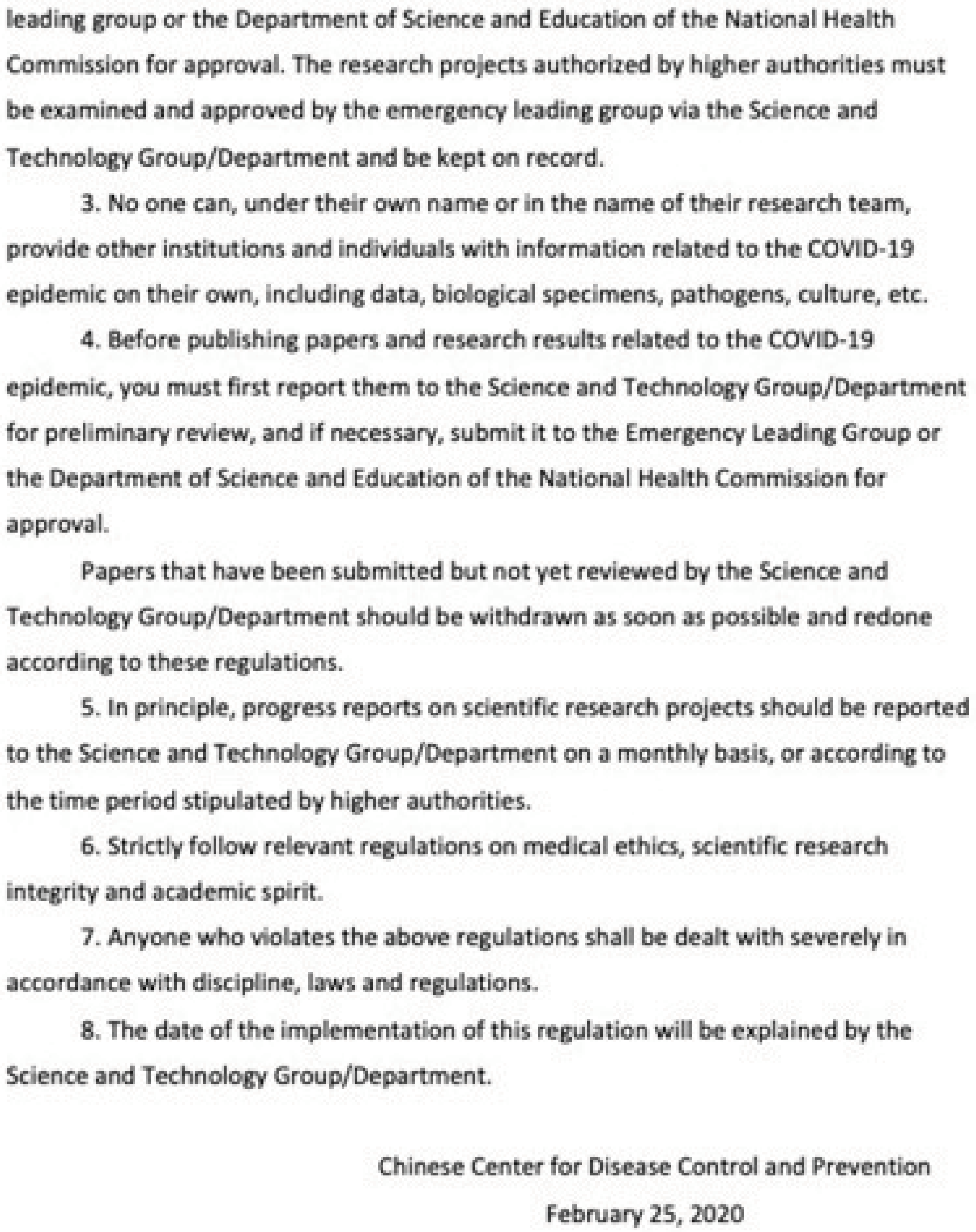
Annex

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

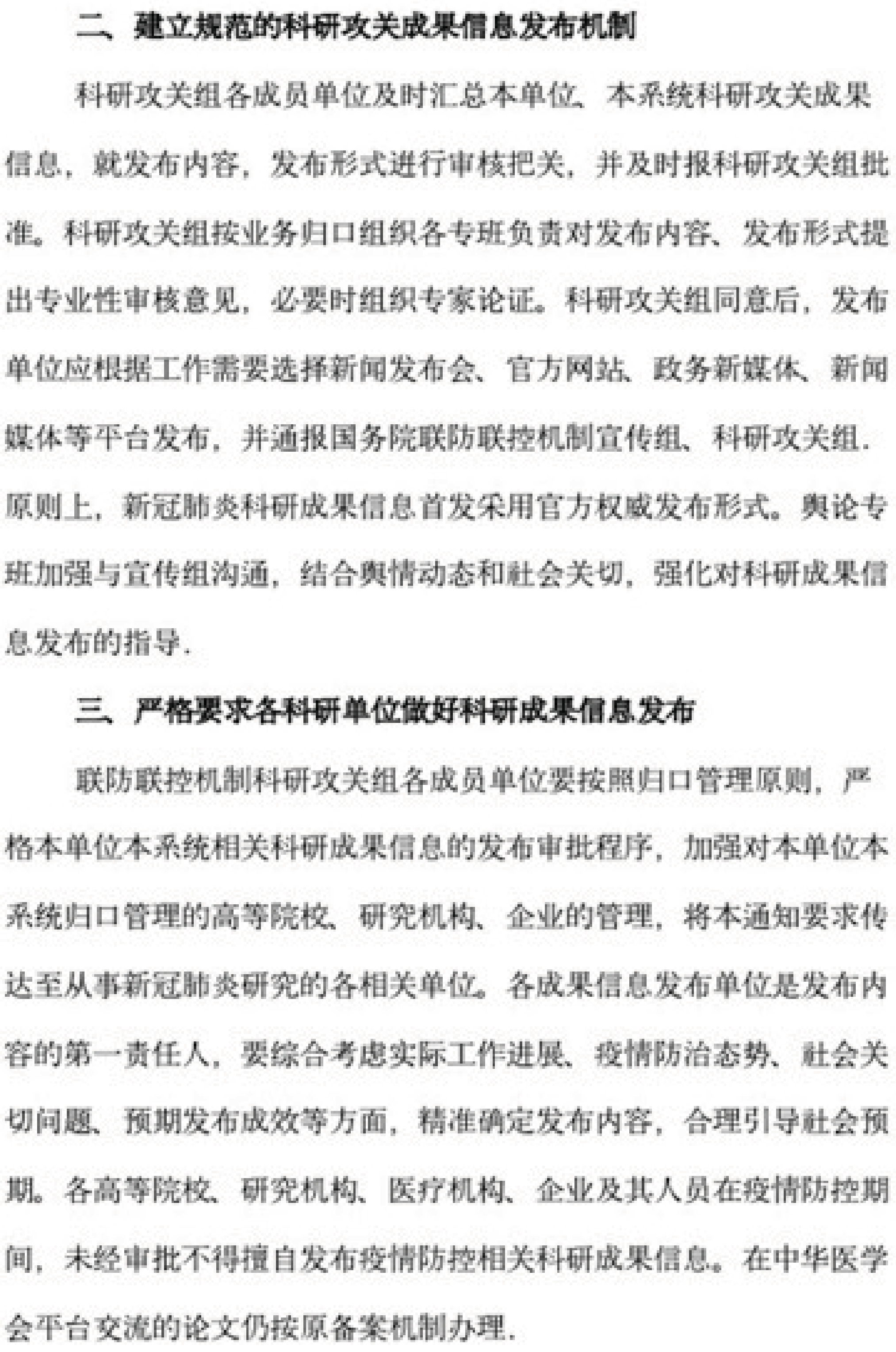
关于规范新冠肺炎科研攻关成果信息发布管理的通知

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。

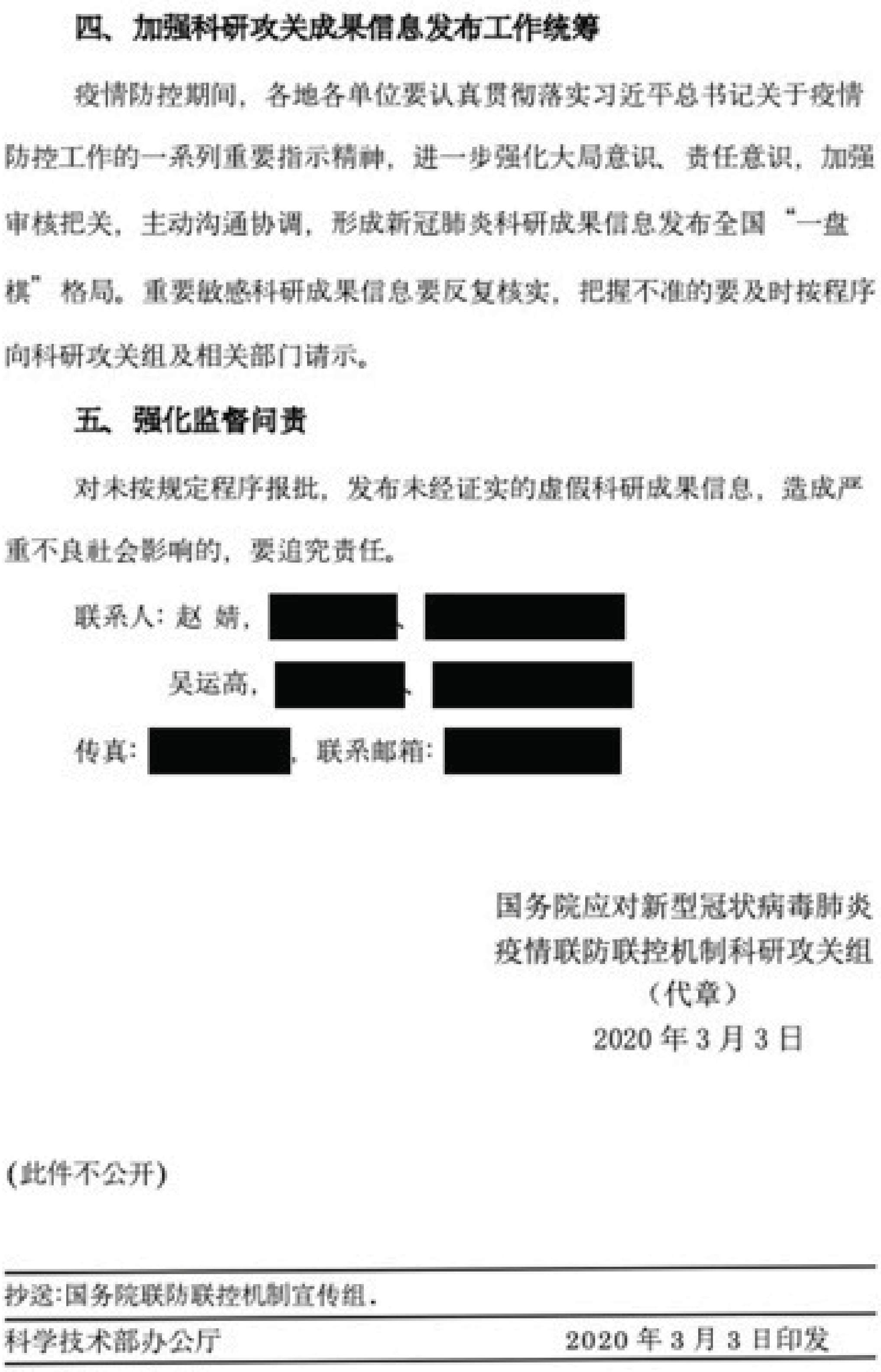


二、建立规范的科研攻关成果信息发布机制

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。

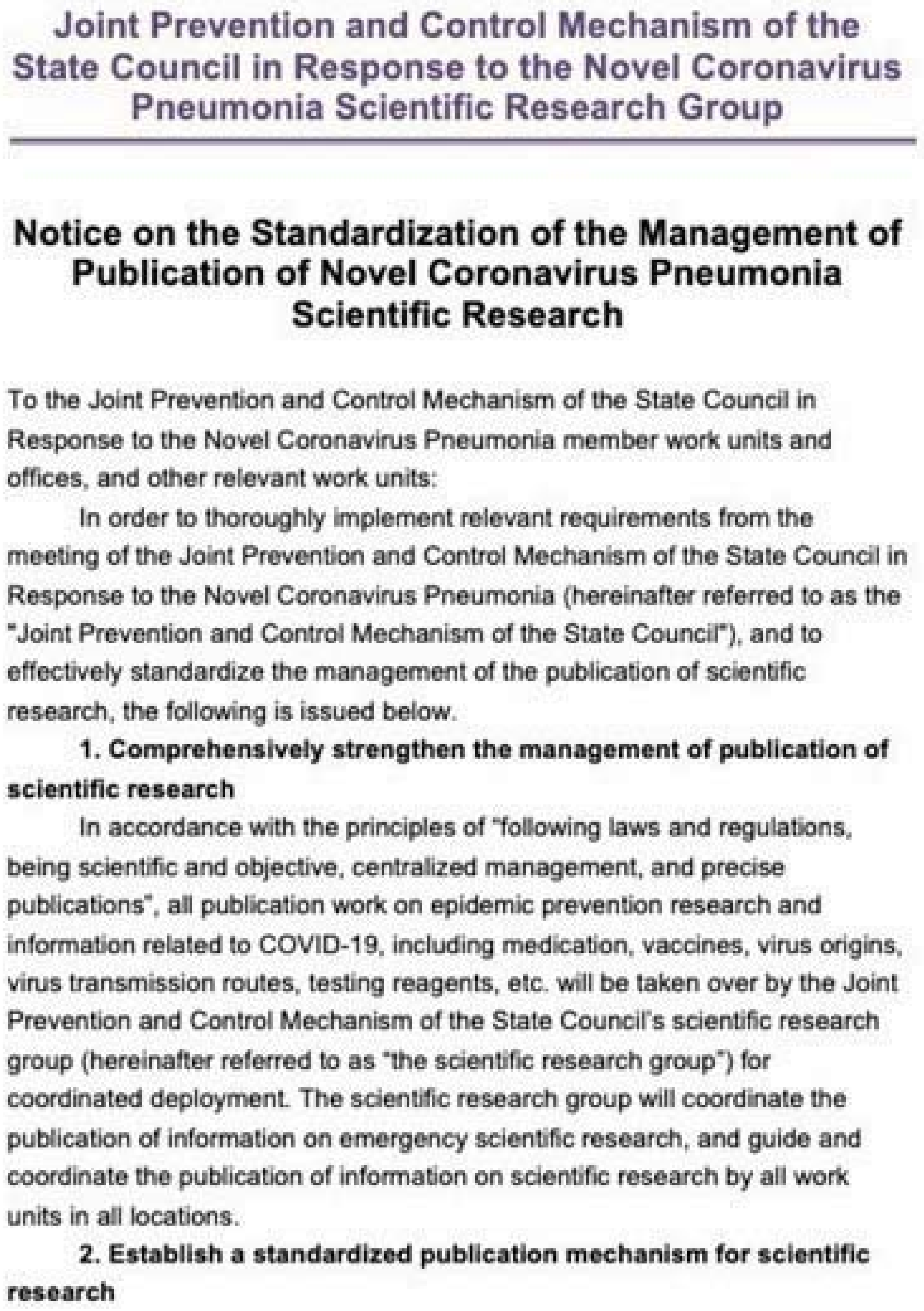
联系人：赵 婧，[redacted]、[redacted]
吴运高，[redacted]、[redacted]
传真：[redacted]，联系邮箱：[redacted]

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

Notice on the Standardization of the Management of Publication of Novel Coronavirus Pneumonia Scientific Research

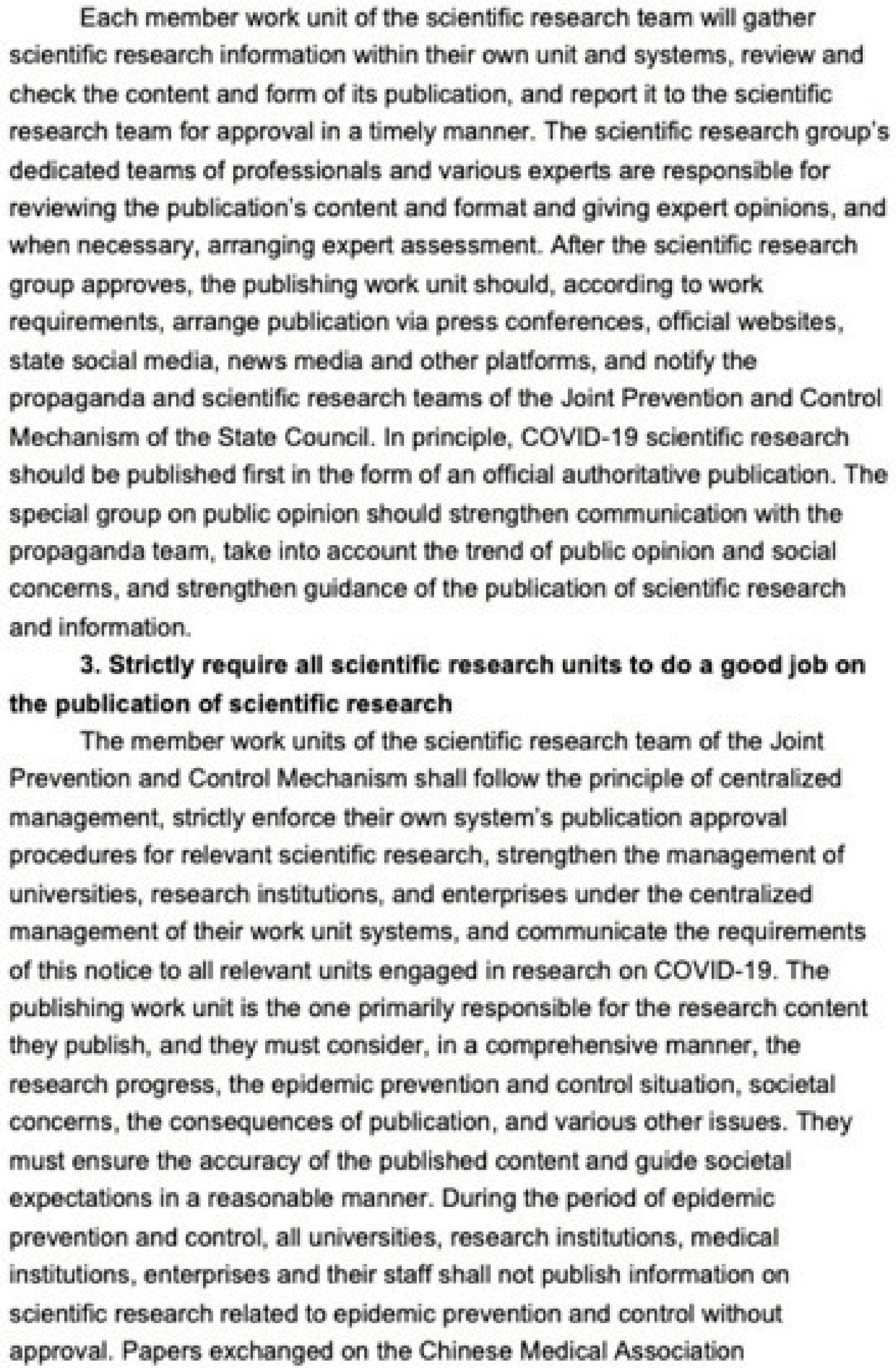
To the Joint Prevention and Control Mechanism of the State Council in Response to the Novel Coronavirus Pneumonia member work units and offices, and other relevant work units:

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.

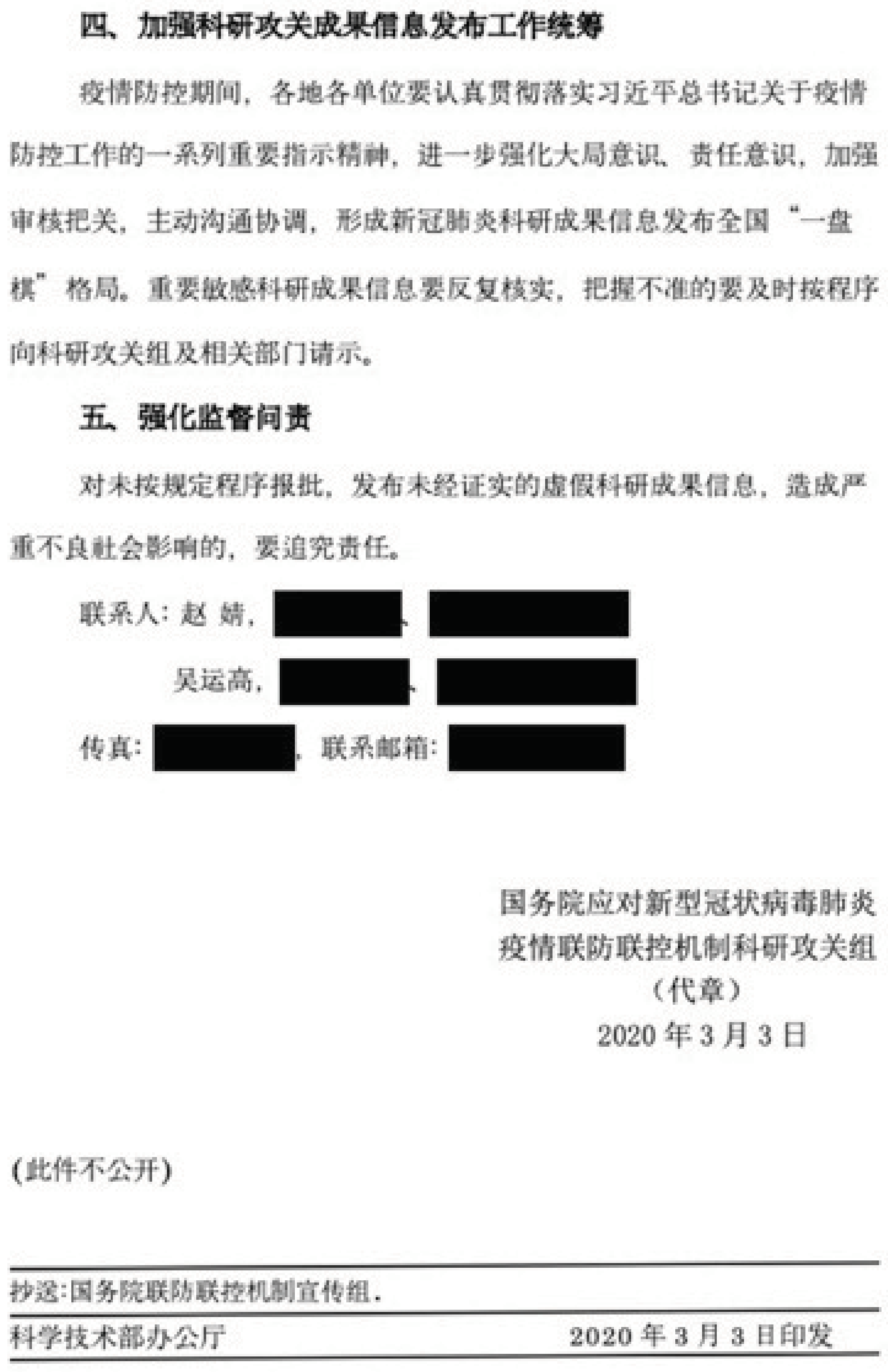
2. Establish a standardized publication mechanism for scientific research



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]

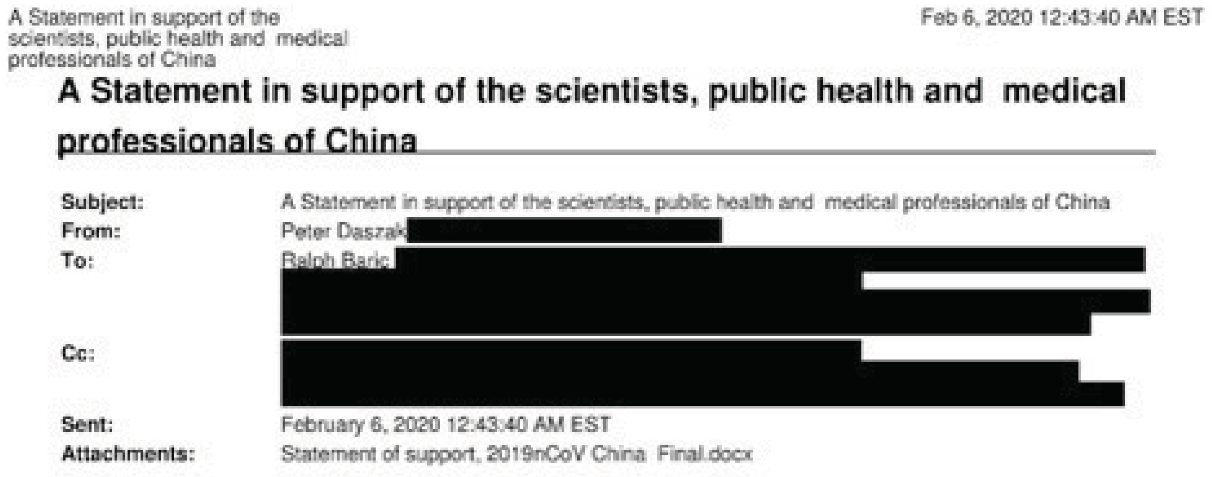
国务院应对新型冠状病毒肺炎
疫情联防联控机制科研攻关组
（代章）
2020 年 3 月 3 日

(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]
Cc: [redacted]
Sent: February 6, 2020 12:43:40 AM EST
Attachments: Statement of support, 2019nCoV China Final.docx

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 34th Street – 17th Floor
New York, NY 10001

Tel. +1 212-380-4474
Website: www.ecohealthalliance.org
Twitter: @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.

A Statement in support of the
scientists, public health and medical
professionals of China

Feb 6, 2020 12:43:40 AM EST

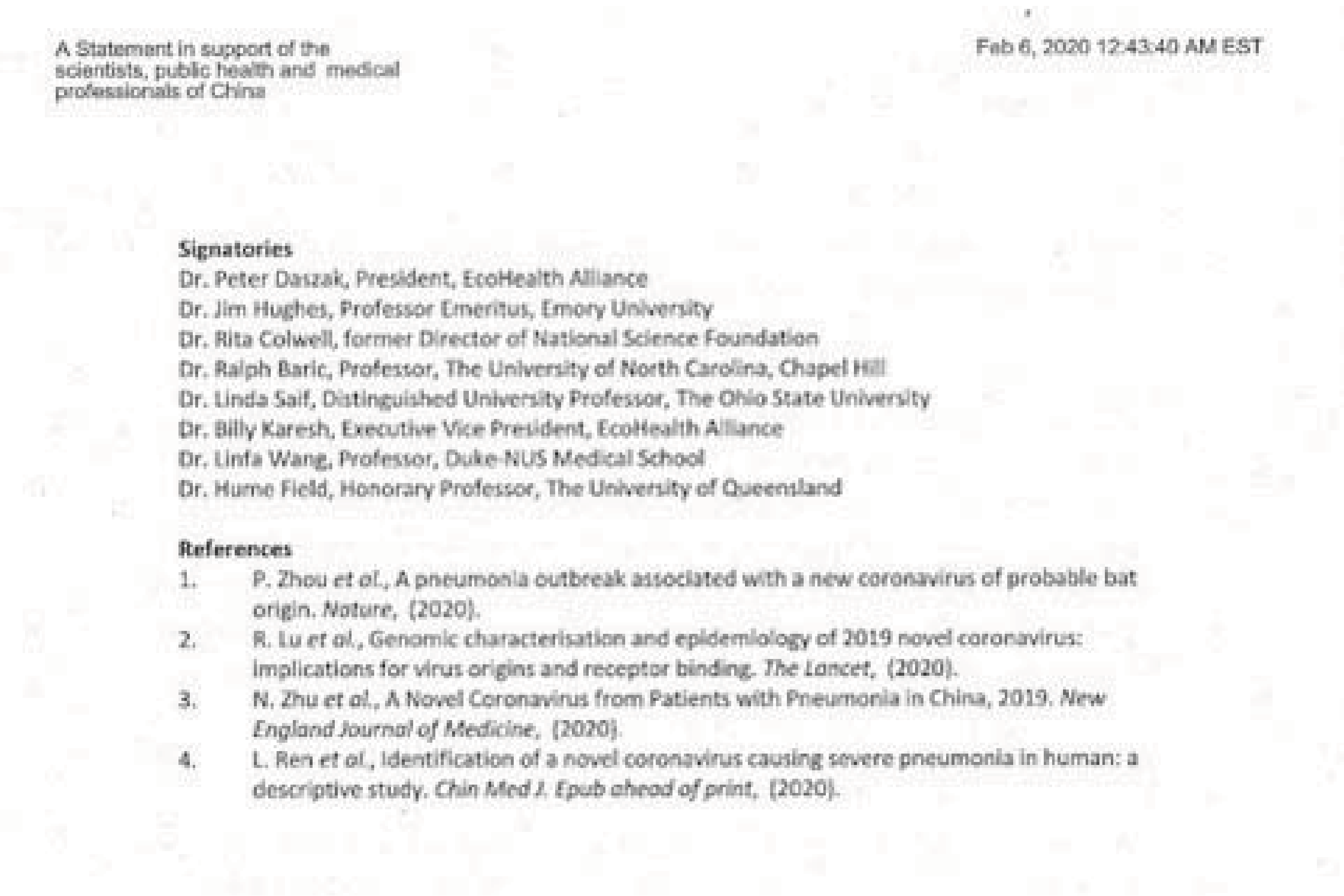
Statement in Support of the Scientists, Public Health, and Medical Professionals of China Combating the Novel Coronavirus Outbreak

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].



A Statement in support of the
scientists, public health and medical
professionals of China

Feb 6, 2020 12:43:40 AM EST

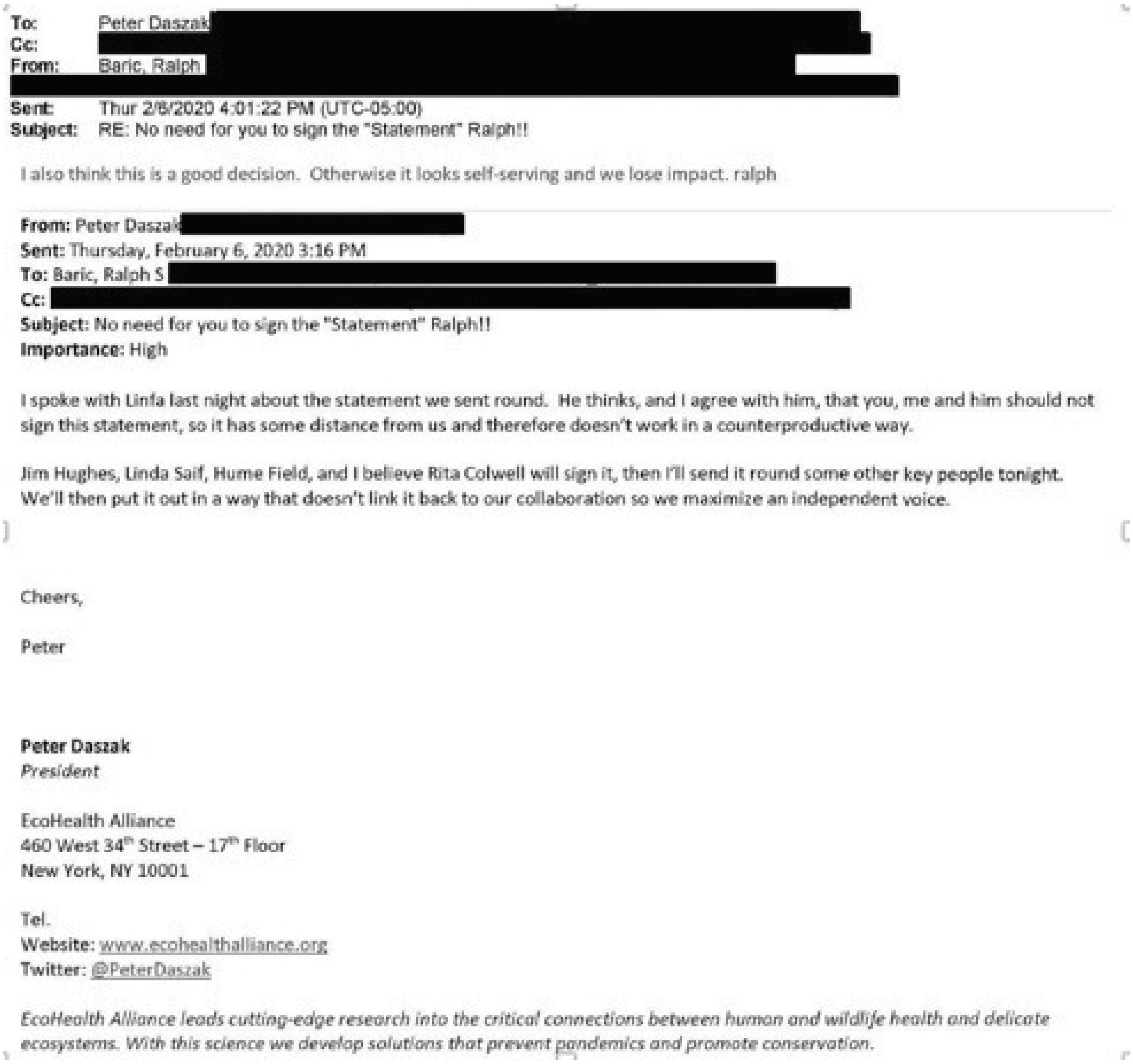
Signatories

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 Karesh, 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!!

I also think this is a good decision. Otherwise it looks self-serving and we lose impact. ralph

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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 34th Street – 17th Floor
New York, NY 10001

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

From: Peter Daszak [redacted]
Sent: Saturday, February 08, 2020 8:52 PM
To: Rita Colwell [redacted]
Cc: Rita Colwell [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.

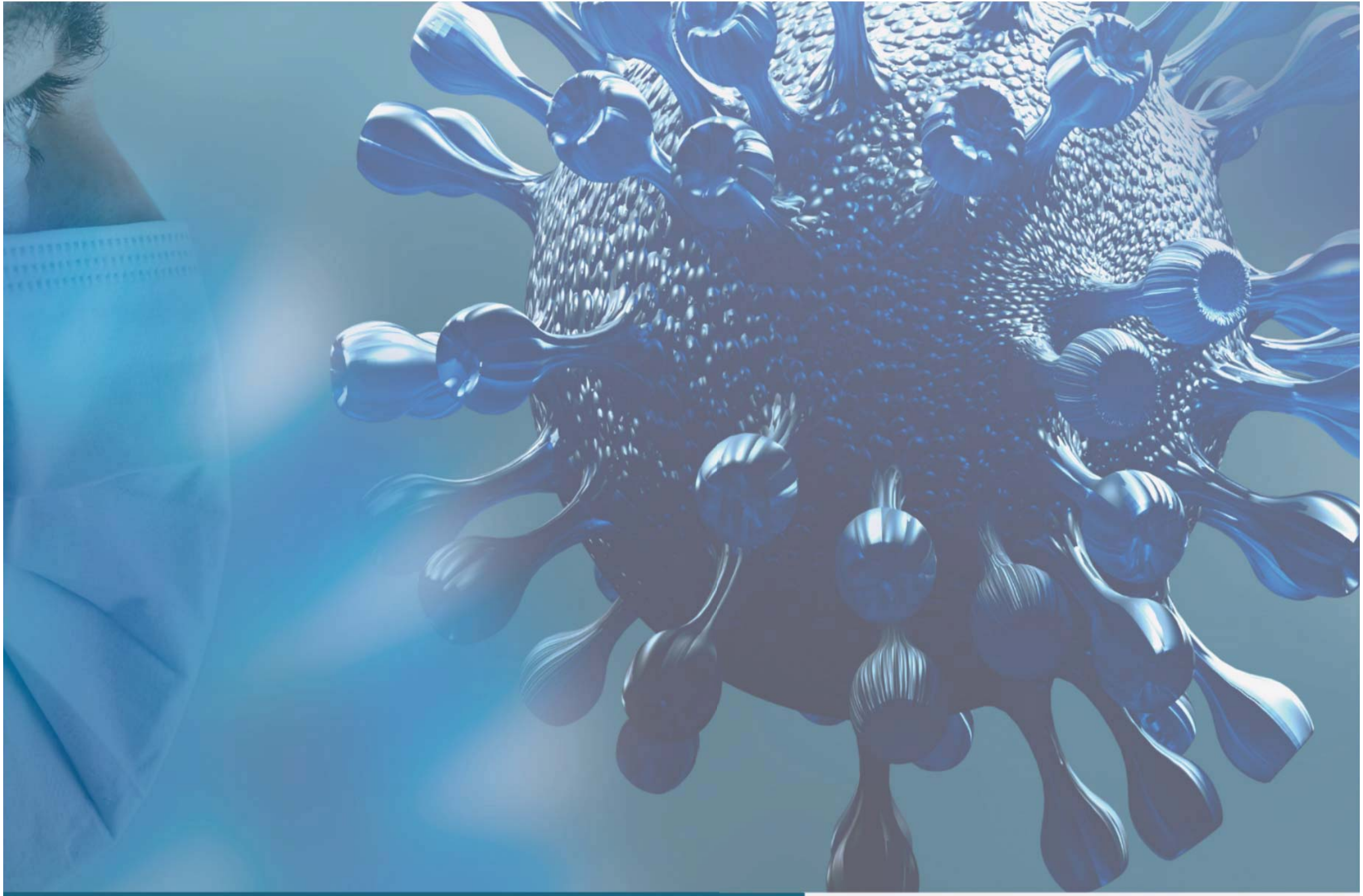
As soon as we hear back from you we'll get ready to send this to our larger list (attached), but of course if you don't feel comfortable, I'll make sure your name is not associated with this.

Cheers,

Peter

Peter Daszak
President

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



2021 年 8 月

COVID-19 起源：

有关武汉病毒研究所的调查

众议院外交委员会少数党幕僚报告

首席共和党成员迈克尔·T·麦考尔

第 117 届国会

目 录

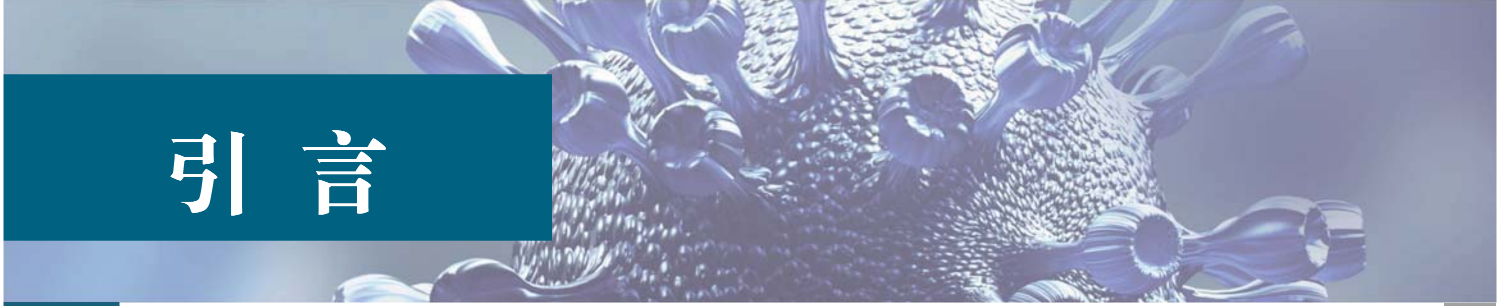
关于最终报告补充的引言

执行摘要

词汇表

关键人物

最终报告补充



引言

504 天前，在 2020 年 3 月 6 日，众议院外交委员会少数党幕僚在资深成员迈克尔 · T · 麦考尔（Michael T. McCaul）的指示下开始对 SARS-CoV-2 与 COVID-19 全球大流行病起源进行调查。众议院外交委员会少数党幕僚有关《COVID-19 全球大流行病起源，包括中国共产党和世界卫生组织的角色》的最终报告在 2020 年 9 月末发表。在该报告发表之际，全世界据估计有 3080 万 COVID-19 病例，大约有 958,000 人死亡。今天，累计数字超过 1.964 亿起病例并有 4,194,061 人死亡。

众议院外交委员会少数党幕僚继续调查 COVID-19 全球大流行病的起源，随时审议最新可以获得的信息，包括通过专家证词。我们之所以这样做是因为我们的人口中有大约 4800 万年龄在 12 岁以下的人不能接种疫苗，而其他人因有基础疾病而仍未接种疫苗，使相当大比例的美国公民面临感染风险。在我们准备这份补充报告之际，有关全球各地出现各种毒株的报道增加了，而中华人民共和国（PRC）当局继续隐瞒有关大流行病初期数月的关键信息。我们一直而且将继续敦促我们的多数党同事重视这项调查并对 COVID-19 起源展开全面的两党调查。拜登总统已表示他希望发现这场大流行病是如何开始的，我们在美国人民面前也有职责来使用我们手中的一切工具来追寻这一目标。我们一如既往地做好了以两党方式应对这项以及其它外交政策挑战的准备。我们绝不能放松让习总书记和 PRC 当局交代答案的压力。

我们在此通过对我们 2020 年最终报告作出补充来分享这些努力的结果。这项更新尤其专注于病毒是否可能从 PRC 湖北省武汉市的一家医学研究实验室泄露以及试图掩盖这一泄露的做法。撰写本报告内容时所采用的证据是基于开源信息并包括已发表的学术研究、PRC 官方出版物（既有公开也有内部的）、访谈、电子邮件和社交媒体帖文。

自从最终报告于 2020 年 9 月 21 日发表以来，人们对 COVID-19 起源提出了新的问题。由于 PRC 继续缺乏透明，小约瑟夫 · R · 拜登（Joseph R. Biden, Jr.）总统 2021 年 5 月 26 日下令美国情报界在 90 天后就 COVID-19 起源准备一份报告，“包括它是源自人类与受感染动物的接触还是来自实验室事故。[1]”

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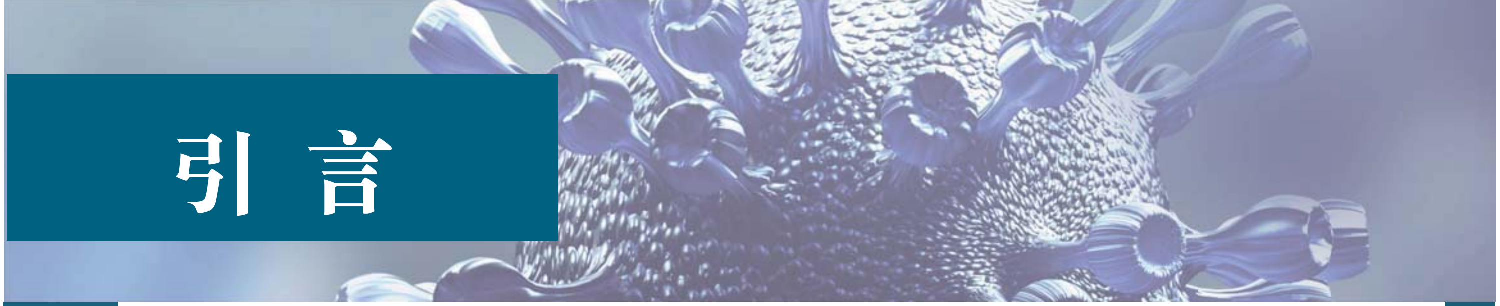
[1] “Statement by President Joe Biden on the Investigation into the Origins of COVID-19.” *The White House*, 26 May 2021, www.whitehouse.gov/briefing-room/statements-releases/2021/05/26/statement-by-president-joe-biden-on-the-investigation-into-the-origins-of-covid-19/.



引 言

基于委员会少数党幕僚收集和分析的材料，优势证据显示，SARS-CoV-2 是武汉病毒研究所的一家实验室在 2019 年 9 月 12 日之前的某个时候意外释放的。该病毒、或者经过基因操作的该病毒序列有可能是在 2012 年和 2015 年之间在云南省的一个洞穴里收集的。武汉病毒所的研究人员、中共内部官员、而且可能还有美国公民直接从事了混淆病毒起源相关信息并压制有关实验室泄露可能性的公开辩论的努力。这些相关方有义务对本报告中提出的问题作出回应并尽快加以澄清并提供任何免责证据。在那之前，必须假定习总书记和中国共产党把维护党的地位置于本国人民和全球各地遭受 COVID-19 大流行病后果之苦的人的生命之上。

执行摘要

在世界卫生组织宣布大流行病的一年多之后，世界仍然饱受 SARS-CoV-2 的出现及其造成的疾病 COVID-19 之苦。世界范围已有 4 百多万人丧失了生命，包括 61 万 2 千多美国人。世界各地经济体遭受疫情重创。

武汉病毒研究所

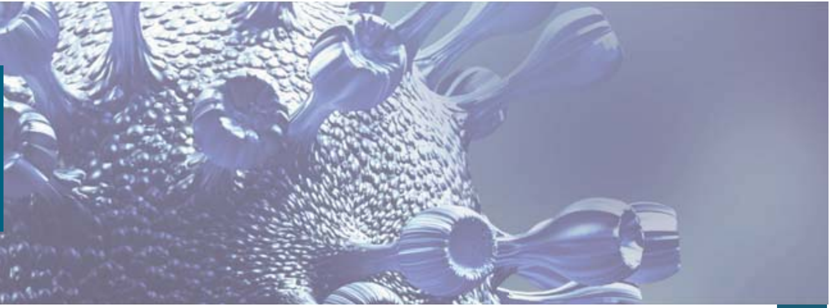
去年 9 月，众议院外交委员会少数党幕僚在资深成员迈克尔 ·T ·麦考尔指示下就 COVID-19 起源公布了一份报告。那份报告凸显了病毒有可能从武汉病毒研究所泄露的可能性。然而，随着我们继续调查并发现更多信息，我们如今相信，现在是彻底否认湿货市场是疫情源头的时候了。我们还相信，优势证据证明，病毒的确是从武汉病毒所泄露的，而且这发生在 2019 年 9 月 12 日之前的某一时候。

这是基于本报告列举的大量事实，包括：

- 武汉病毒所的病毒与样本数据库的在线访问在 2019 年 9 月 12 日被突然移除；
- PRC 的顶级科学家 2019 年对安全表达了关注，随后武汉病毒所不同寻常地安排了维修；
- 参加 2019 年 10 月在武汉举行的世界军人运动会的运动员患病并出现类似 COVID-19 症状；
- 2019 年 9 月和 10 月的武汉卫星图像显示武汉病毒所总部周围的当地医院的人数增加，同时有异常多的患者出现了类似 COVID-19 的症状；
- 一名中国人民解放军的生物武器专家可能在 2019 年末被任命为武汉病毒所生物安全四级实验室负责人；以及
- 中国共产党和在武汉病毒所工作或与该所有关的科学家所采取的掩藏或掩盖该所从事的研究种类的行动。

基因改造

本报告还列举了充足的证据表明，武汉病毒所的研究人员与美国科学家合作并在 PRC 政府与美国政府双方的资助下，在武汉病毒所对冠状病毒进行了功能增益研究，有时是在二级生物安全水平的条件下进行的。这项研究的主要侧重点是改造无法感染人类的冠状病毒的刺突蛋



白，使其可以与人类免疫系统相结合。这种研究的公开目的是找出具有大流行病潜力的冠状病毒并制造出一种广谱冠状病毒疫苗。在很多例子中，科学家成功地制造了“嵌合病毒”——也就是用其它病毒碎片制造的病毒——并且有可能感染人类的免疫系统。在类似于牙医诊所的安全水平下展开如此危险的研究，一个天然或经基因改造的病毒有可能轻易地从实验室逃逸并感染社区。

委员会少数党幕僚还确认了一些科学家，他们直接与武汉病毒所有关，并在当前大流行病开始之前的数年间从事过功能增益研究，而且有能力不留任何证据而对冠状病毒做出基因改造。早在 2005 年，美国科学家拉尔夫 · 巴里克博士（Dr. Ralph Baric）协助建立了一种不留任何基因改造痕迹的方式。而早在 2017 年，在武汉病毒所工作的科学家们能够做到同样的事情。这清楚表明，科学界提出的 SARS-CoV-2 没有基因改造标记因而不可能是人造的主张是不坦诚的。

我们的结论是，有充足的证明显示，该病毒有可能被基因操作，而且至关重要的是，我们必须全面调查这一假说，以确定此间是否发生了这一情况。

掩盖

在最初的报告中，我们列举了中国共产党和世界卫生组织不遗余力掩盖初期流行病的多种方式以及他们的掩盖行为如何使原本可能是一场当地疫情变成了一场全球大流行病。中国拘捕医生以压制他们的声音。记者被失踪。他们毁坏了实验室样本。他们隐瞒了有明显人传人证据的事实。他们拒绝允许真正的溯源调查。与此同时，世卫组织——在总干事谭德塞（Tedros Adhanom Ghebreyesus）的领导下——未能就即将到来的大流行病向世界发出警告。相反，他学舌中共的谈话口径，行事如同习总书记的傀儡。

在这份补充报告中，我们发现了进一步的证据，证明了武汉病毒所的顶级科学家和美国科学家彼得·达萨克博士（Dr. Peter Daszak）是如何进一步掩盖真相的。他们的行为包括霸凌就病毒是否可能从实验室泄露提出问题的其他科学家；在如何能够不留痕迹地改造病毒的问题上误导世界；而且在很多情况下在他们所从事的研究性质以及他们为该项研究所采用的低等级安全标准的问题上直接说谎。

这些行为不仅延误了对实验室泄露可能性进行的初始调查，损失了宝贵时间，而且进一步证明病毒有可能从武汉病毒所泄露。这些行为还让人们对美国政府的拨款在海外实验室的使用方式提出质疑并让人们呼吁对这些拨款进行更多的监督。

接下来的步骤

经过这次深入的调查，我们相信，现在是要求彼得·达萨克前来国会作证的时候了。在有关武汉病毒所从事的研究类型方面，仍然有很多只有他才能回答的悬而未解的问题。此外，我们相信，国会可以通过立法，不仅追究那些负有责任者的责任，而且也帮助防止未来的大流行病，立法措施包括但不限于：

- 制定禁令，不得从事和资助任何包括功能增益研究在内的工作，直到制定出国际性并且具有法律约束力的标准之后，而且必须是在该标准以可证实的方式得到遵守的条件下，该禁令方可取消。
- 制裁中国科学院及相关实体。
- 将武汉病毒研究所及其领导层列入“特别被指定国民和被封锁人员名单”，并实施额外和恰当的次级制裁。
- 授权对未能确保恰当安全水平和信息分享的学术、政府与军事生物研究设施实施新的制裁。

词汇表

功能增益研究	“增强病原体致病能力的研究”——美国卫生与公共服务部
刺突蛋白	包膜病毒表面的一种蛋白结构，负责将病毒与宿主细胞表面相结合，使病毒的基因材料能够输入宿主细胞。
RBD	受体结合域（Receptor-binding Domain）。与宿主细胞的某个具体受体相结合的某个病毒刺突蛋白的具体短片段。
第一作者	一篇学术论文署名排在第一位的作者，通常是对该论文做出最多贡献的人。
通讯作者	编辑和外部读者若对某学术论文有问题时的联系人。
美国国际发展署“预测”项目（USAID PREDICT）	一个由美国国际发展署（USAID）出资的流行病学研究拨款项目。该“预测”项目为生物取样提供资金，目的在于识别和收集病毒。该项目向生态健康联盟（EcoHealth Alliance）提供过拨款资助。
SARS	严重急性呼吸综合症（Severe Acute Respiratory Syndrome）。由 SARS-CoV 冠状病毒引起的病毒性的呼吸疾病。最早被鉴定为 2002 年—2003 年的一次流行病的原因。
MERS	中东呼吸综合症（Middle East Respiratory Syndrome）。由 MERS-CoV 冠状病毒引起的病毒性的呼吸疾病。最早被鉴定为 2012 年一次疫情的原因。
SARS-CoV-2	引起 COVID-19 的乙型冠状病毒。
冠状病毒	在哺乳动物和鸟类造成疾病的一种核糖核酸（RNA）病毒。病情严重程度从普通感冒到 SARS-CoV-2 各有不同。
乙型冠状病毒	冠状病毒的四个属之一。见于蝙蝠和啮齿动物体内。该属病毒包括 SARS、MERS 和 SARS-CoV-2。

词汇表

一级生物安全水平	被设计用来研究已知没有造成健康成年人患病并且对实验室人员及环境仅构成最低潜在危害的微生物。可在一张开放式的实验台或实验桌上展开工作。
二级生物安全水平	用于研究对实验室人员及环境构成中度危害的微生物。微生物一般为本地型，并与严重程度各有不同的疾病有关联。个人防护装备包括实验室外套和手套。可以开放式工作或在生物安全柜内工作。常被比作在牙医诊所看到的安全水平。
三级生物安全水平	用来研究本地或外来并且可通过呼吸传播造成严重甚至潜在致命疾病的微生物。呼吸传播是以吸入为方式的接触渠道。研究人员应当接受医学监控，并可能接种针对其所研究的微生物的疫苗。除了标准个人防护装备外，可能必须佩戴防毒面具。必须在生物安全柜内展开工作。废气不得再循环，实验室必须保持定向空气流动，空气从洁净区域被引入实验室，并流向潜在受污染区域。
四级生物安全水平	这是最高级别的生物安全水平。四级生物安全水平（BSL-4）研究的微生物是危险和外来的，构成高度的空气传播感染风险。这些微生物造成的感染经常是致命性的，而且没有治疗方法和疫苗。研究人员在进入实验室之前必须更换衣服，离开时必须淋浴。所有微生物研究工作都必须在三级生物安全柜内进行，或者穿上全身式、供气式和正压防护服。实验室必须位于另外的建筑内，或者位于管制地段，而且必须有专门的供气和排气以及真空管路和除污系统。
武汉病毒研究所（WIV）	中华人民共和国武汉的一家研究机构，研究重点是病毒学。由中国科学院管理。

词汇表

武汉国家生物安全实验室	武汉病毒所的新园区，位于武汉江夏区郑店科研园区。武汉病毒所四级生物安全水平实验室所在位置。
武汉病毒研究所总部	较旧的武汉病毒所设施，位于武汉市武昌区，靠近中国科学院武汉分院。
中国科学院	负责自然科学的中华人民共和国国家级学院，直属中华人民共和国国务院。
WIV1	第一个被分离出来的新型冠状病毒。由武汉病毒所研究人员在 2013 年从蝙蝠粪便样品中分离出来。是一种与 SARS 相似的冠状病毒。
WIV16	第二个被武汉病毒所研究人员分离出来的冠状病毒。2016 年从单一蝙蝠粪便样本中分离出来。是一种与 SARS 相似的冠状病毒。
Rs4874	第三个被武汉病毒所研究人员分离出来的冠状病毒。2017 年从单一蝙蝠粪便样本中分离出来。是一种与 SARS 相似的冠状病毒。
ID4491/RaTG13	2013 年在一处矿洞收集的与 SARS 相似的冠状病毒，与 SARS-CoV-2 有 96.1%的相似度。
ACE2	血管紧张素转化酶 2（Angiotensin converting enzyme-2），见于不同动物的某些细胞表面，包括人类、小鼠和果子狸。
hACE2	人类版本的血管紧张素转化酶 2。主要见于鼻、口和肺等人体全身各处的细胞和组织的表面。在肺部，hACE2 有大量的第二型肺泡细胞，这是存在于被称为肺泡的肺内囊泡的一种重要细胞类型，肺泡吸入氧气，排出二氧化碳废气。这是 SARS-CoV-2 侵入人体细胞的主要进入点。
嵌合病毒	一种人工制造的病毒。通过把两个或更多的病毒碎片结合在一起而制成。

词汇表

天然病毒	在自然界发生的病毒，“野生型”。
反向遗传学系统	一种分子遗传学的方法，用来帮助了解某个基因的功能，方式是分析在基因内部进行特定核酸序列基因改造而造成的表型效应。可用来制造与天然病毒区分不出来的嵌合病毒。
弗林蛋白酶切割位点	SARS-CoV-2 刺突蛋白的一种酶，增加病毒对人类的传染性。SARS-CoV-2 是唯一具有该结构的乙型冠状病毒。
系统发育分析	对某一物种或一组有机物或某一有机物的某一特性的进化发展所进行的研究。用来鉴别同一科内不同病毒之间的关系。
CGG 双重编码组	“CGG-CGG”。这个有六个核苷酸（三个核苷酸为一组，亦称一个编码组）的组是产生弗林蛋白酶切割位点的 12 个核苷酸的一半。CGG 双重编码组在冠状病毒中相对罕见，而在同一科的冠状病毒中，唯有 SARS-CoV-2 有这样的双重编码组。
生态健康联盟 （EcoHealth Alliance）	一个总部位于纽约的非政府组织，工作重点是新发传染病。将美国政府的资金拨给武汉病毒所。生态健康联盟的研究人员经常与武汉病毒所的研究人员共同撰写研究论文。领导人为彼得 · 达萨克。

关键人物

王延轶博士 （Dr. Wang Yanyi）	武汉病毒研究所所长
袁志明博士 （Dr. Yuan Zhiming）	武汉国家生物安全（四级）实验室主任。中国共产党中国科学院武汉分院党委书记。武汉病毒所隶属中国科学院武汉分院。
石正丽博士 （Dr. Shi Zheng-li）	武汉病毒研究所资深科学家。担任新发传染病研究中心主任、中国科学院高致病性病原及生物安全重点实验室主任、武汉国家生物安全实验室生物安全四级实验室副主任。
胡犇博士 （Dr. Ben Hu）	武汉病毒所研究人员，曾是石正丽的博士生。深度参与武汉病毒所的冠状病毒研究。
王林发博士 （Dr. Linfa Wang）	中华人民共和国公民，杜克-新加坡国立大学医学院新发传染病项目主任兼教授、武汉病毒所新发传染病中心科学顾问委员会主任。
彼得 · 达萨克博士 （Dr. Peter Daszak）	生态健康联盟首席执行官。石正丽及武汉病毒所其他人员的长期合作者。把科研基金分包给武汉病毒所，以帮助资助冠状病毒研究。
拉尔夫 · 巴里克博士 （Dr. Ralph Baric）	北卡罗莱纳大学教堂山分校的研究人员，与石正丽及其他武汉病毒所研究人员在冠状病毒研究上进行过合作。

最终报告补充

I. 武汉市：大流行病的震中

武汉是冠状病毒大流行病的震中。位于中华人民共和国（PRC）中部的武汉是中国最长的河流长江与汉江的交汇处，是湖北省的省会城市，号称有约 1110 万人口，面积约 3280 平方英里[2]。这里有一些中国最高的摩天大楼、包括著名的武汉大学在内的多所高校、重要的历史文化遗址以及一个有影响力的研究实验室——武汉病毒研究所（WIV）。武汉的面积是休斯顿的五倍，人口比纽约和芝加哥的加起来还要多，由此可见该市的规模。

武汉有 PRC 中部最大的欧式火车站汉口火车站以及另外两个主要火车站。汉口站与天河国际机场直接相连，这个机场是 PRC 中部最繁忙的机场，地理位置上处在 PRC 机场网络的中心。从天河机场，旅客可以直飞纽约、旧金山、巴黎、米兰、罗马、汉堡、曼谷、东京、首尔、迪拜等世界各地的许多目的地。

PRC 称武汉为九个“国家中心城市”之一，这是官方的国家标签，意味着它与首都北京、上海和其它主要城市一起，在文化、政治和经济发展方面起主导作用[3]。由于它的四通八达，隶属于经济事务和气候政策部的政府机构荷兰企业局在 2016 年 8 月的一份报告中把武汉确定为不仅是 PRC 境内的一个主要枢纽，而且是中国“一带一路”倡议中的全球主要枢纽[4]。该市还是重要的铁路贸易所在地。新华社 2018 年的一份报告曾预计，从武汉到欧洲用于出口货物的货运列车约有 500 列[5]。法国、美国、韩国和英国在该市设有领事馆。武汉被选为在 2019 年 10 月举办的第七届国际军事体育理事会（CISM）世界军人运动会的城市。军运会期间，来自 100 多个国家的 9000 多名军事人员入住武汉专门为这次运动会修建的运动员村。

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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.

[4] Van de Bovenkamp, Judith and Yuan Fei. “Economic Overview of Hubei Province.” *Neatherlands 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

II. 实验室泄漏的证据

正如在之前发布的报告里所讨论的，武汉病毒研究所仍然是关于SARS-CoV-2和COVID-19大流行病起源的辩论焦点。近几个月来，有关武汉病毒所的新信息曝光，使我们能够更好地了解该所、在那里工作的科学家所进行的研究以及它与中国共产党及其军队——人民解放军（PLA）的关系。我们现在认为，优势证据表明病毒是从武汉病毒所的一处设施泄露出来的。

武汉病毒研究所

武汉病毒所成立于 1956 年，当时名为中国科学院武汉微生物研究室。研究所 1978 年以来归中国科学院管辖[6]。该研究所目前拥有至少两个园区——位于郑店科研园区（见图 1）被讨论得很多的武汉国家生物安全实验室（WNBL）以及位于武汉武昌区小洪山园区（见图 2）的较旧设施（以下称为武汉病毒所总部）。武汉国家生物安全实验室是一个含有多栋建筑物的大型设施，包括 20 个生物安全二级（BSL-2）实验室、两个生物安全三级（BSL-3）实验室和 3000 平方米的生物安全四级（BSL-4）空间，"包括四个独立的实验室区域和两个动物套房。[7]"建造工作于 2015 年完成，但由于延迟，生物安全四级的空间直到 2018 年初才投入运行[8]。

图 1：武汉国家生物安全实验室（WNBL）

关于武汉病毒所的公开讨论所没有涉及到的是在位于武汉武昌区那个较旧设施武汉病毒所总部进行的研究。该设施位于武昌区，在武汉国家生物安全实验室东北 12 英里处，仍然是

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[6] "History." *Wuhan Institute of Virology*, http://english.whiov.cas.cn/About_Us2016/History2016/.

[7] 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

[8] 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

武汉病毒所的行政总部。除了这里的生物安全二级实验室外，武汉病毒所 2003 年还在该设施建造了一个生物安全三级实验室[9]。正是在这里，也就是在武汉的中心，石正丽博士和她的团队在 COVID-19 大流行病之前的几年里对冠状病毒进行了功能增益研究。

图 2：武汉病毒研究所位于武昌的总部

根据武汉病毒所的网站，石正丽现任武汉病毒所新发传染病研究中心主任、武汉国家生物安全实验室生物安全四级实验室副主任、生物安全三级实验室主任、生物安全工作委员会主任[10]。石还是中国科学院高致病性病原及生物安全重点实验室主任[11]，该实验室包括了大多数在武汉病毒所从事冠状病毒功能增益研究的科学家。

需要指出的是，武汉病毒所内有一个中国共产党的委员会以及一个纪律检查委员会。党委分为四个党总支部，这些党总支部按照武汉病毒所的各个部门、研究中心和办公室再分为党支部。每个支部都有自己的宣传委员。众议院外交委员会少数党幕僚在这些宣传委员中确认了八名武汉病毒所的研究人员，其中几名与石正丽领导的重点实验室有关联。

武汉病毒所的研究人员	**相关实验室**	**宣传委员**[12]
刘巧洁	中国科学院高致病性病原及生	新发传染病研究中心党支部

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[9] 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

[10] “Shi Zhingli.” *Wuhan Institute of Virology*, http://www.whiov.cas.cn/sourcedb_whiov_cas/zw/rck/200907/t20090718_2100074.html

[11] “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

[12] “Party Branch.” Wuhan Institute of Virology, http://www.whiov.cas.cn/djkxwh/dqzz/dzb/

	物安全重点实验室主任[13]	
张晓玮	中国科学院高致病性病原及生物安全重点实验室主任[14]	分析微生物与纳米生物学研究中心党支部
沈旭瑞	中国科学院高致病性病原及生物安全重点实验室主任[15]	新发传染病研究中心党支部
唐霜	病毒学国家重点实验室[16]	微生物资源与生物信息研究中心党支部
吴妍	病毒学国家重点实验室[17]	分子病毒与病理研究中心党支部
贺丽红	病毒学国家重点实验室[18]	微生物资源与生物信息研究中心党支部
王清星	病毒学国家重点实验室[19]	分子病毒与病理研究中心研究生党支部
杨梦思	病毒学国家重点实验室[20]	分析微生物与纳米生物学研究中心研究生党支部

表 1： 在武汉病毒所担任中共宣传委员的研究人员

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[13] 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/

[14] 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/

[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/

纪律检查委员会负责“保证党的路线方针政策、党的纪律、相关法规和研究所规章制度的贯彻落实。[21]”

除了担任宣传委员的研究人员外，武汉病毒所的其他关键人物也担任中共官员。王延轶博士担任武汉病毒所所长，并于 2010 年加入由中国共产党控制的少数党中国致公党。2018 年，也就是她成为武汉病毒研究所所长的那一年，她还当选为致公党武汉市副主任委员。直到 2019 年底，该所的生物安全四级实验室一直由袁志明博士管理。他是武汉病毒研究所所属机构中国科学院武汉分院的中共党委书记。当地中共领导人不仅管理武汉病毒所本身，还直接管理它的生物安全四级实验室[22]。

王所长在 2021 年新春致辞中提到武汉病毒研究所的党委，承诺党委将“切实发挥基层党组织的战斗堡垒作用和党员的先锋模范作用”[23]。武汉国家生物安全实验室还拥有自己的党支部——郑店实验室党支部，“荣获湖北省直机关工委‘红旗党支部’荣誉称号，以实际行动展现了党员的先锋模范带头作用。[24]”值得注意的是，在讨论 COVID-19 大流行病时，王所长在 2021 年的致辞中竭力解决实验室的安全问题——“研究所高等级生物安全实验室全年安全运行 300 余天。[25]”她 2020 年 4 月之后的某一时候张贴出来的 2020 年致辞中没有提到这一点。

武汉国家生物安全实验室的生物安全四级（BSL-4）实验室是根据 2003 年 SARS 大流行病后 PRC 与法国签署的一项协议而建立的[26]。当时，PRC 所有生物安全三级实验室都是由中国人民解放军控制。尽管法国国防部和情报部门表示担忧，但是时任法国总统雅克 · 希拉克（Jacques Chirac）及其总理让-皮埃尔 · 拉法兰（Jean-Pierre Raffarin）批准了这个项目——拉法兰本人将其描述为“一项政治协议”[27]。当时 PRC 被怀疑有生物战项目，因此军方和情报机构担心，建设生物安全四级实验室所需的军民两用技术可能会被 PRC 政府滥用。法国政府内部达成的忐忑不安的妥协是，协议将要求必须在实验室中开展有法国研究人员在场的 PRC-法国联合研究[28]。

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[21] “Commission for Discipline Inspection.” *Wuhan Institute of Virology,* http://www.whiov.cas.cn/djkxwh/dqzz/jw/

[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.

[23] “New Year's Speech by the Director in 2021.” *Wuhan Institute of Virology, http://www.whiov.cas.cn/gkjj/szzc_160220/*

[24] “New Year's Speech by the Director in 2021.” *Wuhan Institute of Virology, http://www.whiov.cas.cn/gkjj/szzc_160220/*

[25] *Ibid.*

[26] “About WIV.” *Wuhan Institute of Virology*, 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.

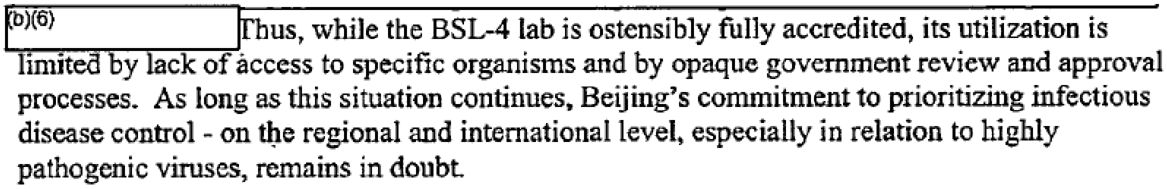
[28] *Ibid.*

2016 年，PRC 申请了数十套实验室工作必备的防护服。法国负责批准敏感设备出口的两用项目委员会拒绝了这项请求。根据法国方面的报道，这项请求“远超出武汉（实验室）所需”[29]。**这使得法国国防部内部的担忧继续增加，他们担心中国正试图进行军事研究或是建立用于军事目的的第二个生物安全四级实验室。**尽管协议规定生物安全四级实验室是联合研究的场所，而且时任法国总理贝尔纳 · 卡泽纳夫（Bernard Cazeneuve）在 2017 年的开幕仪式上宣布投入五百万欧元用于联合研究，但是时至今日只有一位法国科学家被派到这个实验室。他的任期在 2020 年结束[30]。

安全担忧和不寻常的维修

早在 2004 年，当北京的一个实验室发现 SARS 泄漏时，就有几份关于 PRC 实验室的安全问题的报告。此后的几年里还发生了其他几起意外泄漏事件。这些报告包括多起 PRC 一些顶级科学家对武汉病毒所的安全性表示担忧的例子。

正如我们去年发布的 COVID-19 的起源报告所讨论的那样，2018 年，美国国务院官员向华盛顿特区发回的电报，突出强调了对武汉病毒所安全问题的担忧。电报报告说，武汉病毒所的科学家提到“严重缺少经过妥善培训的技术人员和研究人员来安全操作这个高等级生物安全实验室”[31]。电文还质疑 PRC 是否会信守承诺优先考虑按照实验室设计应该进行的重要研究。



(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.

图 4：2018 年 1 月 19 日美国驻北京大使馆致美国国务院华盛顿总部的电报节选

一年后的 2019 年 6 月，中国疾病控制与预防中心主任高福（George Gao）表达了对武汉病毒所安全操作程序的担忧。在《生物安全与健康》（*Biosafety and Health*）杂志上发表的一篇几乎是预言家式的声明中，高福写道（强调为报告作者所加）：

> 生物医学技术的进步，如基因组编辑和合成生物技术，有可能为人类疾病的生物干预提供新的途径。这些进展也可能产生积极影响，使我们能够用新的方法来应

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[29] *Ibid.*

[30] Izambard.

[31] 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/.

> 对风险。**然而，这些技术的扩散意味着，雄心勃勃、粗心大意、笨拙无能甚至完全心怀不满的人也可以使用它们，他们可能会以危及我们安全的方式滥用它们。**例如，虽然 CRISPR 相关技术为靶向细胞基因组编辑提供了革命性的解决方案，但它也可能导致基因组内的意外脱靶突变，或在人类、动物、昆虫和植物中引发基因驱动启动的可能性。同样，病原体的基因改造可能扩大宿主范围，并增加传染性和毒性，可能导致流行病的新风险。例如，2013 年，几个研究小组表明，具有少量核苷酸突变的 H5N1 流感病毒和重新插入 2009 年 H1N1 大流行病毒的 H7N9 分离物可能具有在雪貂之间通过空气传播的能力。**同样，合成的蝙蝠源类 SARS 冠状病毒感染人类细胞的能力也增强了。因此，改造动物（包括人类）、植物和微生物（包括病原体）的基因组必须受到高度监管[32]。**

三个月后，2019 年 9 月，武汉国家生物安全实验室的生物安全四级实验室主任、石正丽的上司袁志明在《生物安全与生物安保杂志》（ Journal of Biosafety and Biosecurity）上发表了一篇文章。这篇以《中国高等级生物安全实验室的现状和未来挑战》[33]为标题的文章详细讨论了国家生物安全实验室的建设。袁指出了多个关键问题，包括生物安全管理体系不足、实验室高效运作资源不足以及专业能力不足。袁承认，病原体、废物和实验动物管理规定的执行“需要加强”[34]，其透明度之高令人吃惊。在谈论中国政府提供的资源水平不足时，他说:

> **维修成本通常被忽略；几个高生物安全水平的机构没有足够的运营资金用于日常但至关重要的程序。由于资源有限，一些生物安全三级实验室以极低的运营成本维持运作，甚至在某些情况下根本没有运营成本[35]。**

袁还对实验室缺乏专业的生物安全管理人员和工程师表示担忧[36]。**必须要指出的是，武汉病毒所的研究人员此前曾在生物安全二级和生物安全三级的水平上对冠状病毒进行了功能增益研究。这一点很重要，因为中国疾控中心的负责人和武汉病毒所的生物安全四级实验室的负责人都对这项研究及其进行这项研究的实验室的安全性表示了担忧。**

耐人寻味的是，在袁发表了提出这些担忧的文章之前，2019 年，武汉病毒所似乎一直在进行维护和修理项目。必须要指出的是，在进行危废处理系统改造项目时，武汉国家生物安全实

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[32] 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] 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

[34] *Ibid.*

[35] *Ibid.*

[36] *Ibid.*

验室只运行了不到两年的时间。在设施开始运营后这么短时间内进行如此重大的翻修看起来有些不寻常。PRC 政府采购网站上发布的采购公告提供了武汉病毒所两处地点看起来在持续进行维修工作的证据。

项目名称	**地点**	**日期**	**预算金额（美元）**
郑店园区 P3 实验室及实验动物中心维保项目[37]	武汉国家生物安全实验室	2019 年 3 月 1 日	$401,284.10
正压防护服采购[38]	武汉国家生物安全实验室	2019 年 3 月 21 日	$177,161.40
危废处理系统改造工程[39]	武汉国家生物安全实验室	2019 年 7 月 31 日	$1,521,279.28
环境空气消毒处理系统、可拓展型自动化样品存储管理系统采购项目[40]	不明	2019 年 8 月 14 日	$132,200,025.47
保安服务采购项目[41]	武汉国家生物安全实验室	2019 年 9 月 12 日	$1,281,022.33

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[37] “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

[38] “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

[39] “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

[40] “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/1nXLD#selection-229.0-229.228

[41] “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

中央空调改造工程[42]	不明	2019 年 9 月 16 日	$606,382,986.11
采购空气焚烧装置以及测试服务项目[43]	不明	2019 年 12 月 3 日	$49,388.81

表 2：武汉病毒所 2019 年的采购项目

对武汉国家生物安全实验室郑店园区 P3 实验室及实验动物中心的维修保护、采购环境空气消毒处理系统、对危废处理系统以及中央空调系统进行改造的提及，都对这些系统在 COVID-9 爆发之前几个月的运作情况提出了问题。

消失的数据库

2019 年 9 月 12 日，武汉病毒所的在线公共样本和病毒序列数据库“蝙蝠源和鼠源病毒病原数据库”下线[44]。该数据库包含了采集自蝙蝠和小鼠的样本和病原体数据的 2.2 万多个条目。数据库包含了每个样本的关键信息，包括收集的动物种类、收集地点、病毒是否成功分离、收集的病毒种类以及与其它已知病毒的相似性。

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[42] “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

[43] “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

[44] “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	*Rousettus leschenaultii*
Species molecular identification	*Rousettus* 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. *Virol Sin*. 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

图 6：数据库条目示例[45]

迄今为止，对于这个数据库为何被移除、何时或是否将恢复在线，还没有给出一致的答案。

石正丽被列为该项目的数据通讯作者。当被问及数据库被下线的问题时，石给出了几个相互矛盾的答复。在 2020 年 12 月接受英国广播公司（BBC）采访时，她表示，在武汉病毒所员工的工作和私人邮箱遭到网络攻击后，数据库因“安全原因”被迫关闭。她还坚称，武汉病毒所的病毒序列信息保存在由美国国家生物技术信息中心（National Center for Biotechnology Information）运营的 GenBank 数据库中。石宣称：“这是完全透明的，没有什么隐藏的。[46]”

然而，在 2021 年 1 月 26 日发给询问该数据库的某人的一封电子邮件中，石正丽表示，该数据库因“在 COVID-19 大流行病期间”的网络攻击而被关闭[47]。她还声称，研究人员“在这个数据库中只输入了有限的数据”，尽管它有超过 2.2 万个条目。与她的英国广播公司的采访明显

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[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.

[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.

矛盾的是，石承认“访问权限是有限的”[48]，但她仍然坚称：

> **……我们关于不同种类的蝙蝠冠状病毒（部分序列或全长基因组序列）的所有工作已经公布，序列和样本信息已提交到 GenBank[49]。**

石正丽在邮件结尾写道：“如果你的好奇心是基于‘人为或实验室泄漏 SARS-CoV-2’的阴谋论，或者是基于你的怀疑提出的一些无聊问题，我不会回答你的任何问题。**没信任，就免谈。**[50]”（强调为报告作者所加。）

新的领导层和人民解放军的参与

武汉病毒所的网站显示，袁志明是中国科学院武汉分院院长、武汉国家生物安全（生物安全四级）实验室主任[51]。然而，PRC 的网站微博豆瓣 2020 年 2 月 7 日发布的消息称，解放军官员已被派往武汉控制疫情应对行动。**2020 年 1 月，中国人民解放军的生化武器防御专家陈薇少将被派往武汉[52]，接管武汉国家生物安全四级实验室[53]。**鉴于该网站审查批评中共的帖子的历史，包括审查与天安门屠杀相关的词汇，将这些信息发布到豆瓣上具有重要意义[54]。这篇文章在受到中国共产党严格审查的网站上存活下来，证实了它的合法性。

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[48] Sudworth.

[49] *Ibid.*

[50] *Ibid.*

[51] “Yuan Zhiming.” *Wuhan Institute of Virology,* http://www.whiov.cas.cn/sourcedb_whiov_cas/zw/rck/200907/t20090718_2100080.html

[52] 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/.

[53] 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

[54] Honorof, Marshall. “China Marks Tiananmen Massacre with 'Internet Maintenance Day.'” *NBC News*, 4 June 2013, https://www.nbcnews.com/id/wbna52096871

委员会少数党幕僚还从一位前美国高级官员那里得到证词，陈薇将军实际上是在 2019 年末，而不是像公开报道的 2020 年 1 月，接管了武汉国家生物安全四级实验室。陈将军接管武汉病毒所的一部分显示，随着有关该病毒的消息的传播，中共对那里发生的活动感到担忧。如果她在 2019 年就接管了实验室，这就意味着中共更早就知道了这个病毒，而且疫情爆发开始得更早——这个话题本节有进一步的讨论。

陈将军是位于北京的军事医学科学院的研究人员，也是第十二届全国人民代表大会的代表[55]。2018 年 1 月，陈将军被挑选为第十三届中国人民政治协商会议（CPPCC）全国委员会的委员。据美中经济与安全审查委员会（U.S.-China Economic Security Review Commission）说，政协是一个“关键的协调机构，汇集了中国其他利益集团的代表，并由中国最高决策机构中共中央政治局常务委员会的一名成员领导。[56]”

据美国国务院 2021 年 1 月 15 日发布的事实清单，在疫情爆发前的几年里，武汉病毒所的研究人员代表解放军从事了包括动物实验在内的机密研究[57]。石正丽博士多次否认解放军参与了武汉病毒研究所的工作。在一场仅由罗格斯医学院主办的演讲中，石说:

> 我们——我们的工作，我们的研究是开放的，而且我们有很多国际合作。据我所知，我们所有的研究工作都是公开的，透明的。所以，在 COVID-19 刚开始的时候，我们听到称我们与军方在我们的实验室有一些项目，等等诸如此类的这些谣言。但这是不正确的，因为我是实验室的主任，负责研究活动。我不知道这个实验室做过任何这种研究工作。这是错误的信息[58]。

这种说法是明显错误的。在 COVID-19 大流行病之前，武汉病毒所与解放军的研究人员有多种联系；武汉病毒所的英文网站上列出了好几人。武汉病毒所病毒学国家重点实验室学术委员会中的一名副主任委员来自第二军医大学，一名委员来自中国 302 军医院。新发传染病中心科学咨询委员会的成员中有军事医学科学院军事兽医研究所的一名研究员。这个网站于 2020 年 5 月 28 日被删除，委员会的成员名单也被删除[59]。不过，该网站的存档副本可以在网上找

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[55] “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

[56] 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

[57] 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

[58] 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.

[59] “Committees.” *Wuhan Institute of Virology*, https://web.archive.org/web/20200527045823/http://english.whiov.cas.cn/About_Us2016/Committees/

到。

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.

图 3： 武汉病毒所病毒学国家重点实验室学术委员会页面的存档版本

这就提出了一个明显的问题，那就是：为什么曾在其中一个委员会任职的石正丽会对军方研究人员与武汉病毒所合作的事情撒谎。**她的否认和网站被清理看来显然是试图混淆解放军与武汉病毒所的关系。**

武汉的医院交通模式地理空间分析

在武汉病毒所的病毒数据库被关闭前后，武汉市中心的各医院的车辆流量开始增加。波士顿大学公共卫生学院、波士顿儿童医院和哈佛医学院的研究人员使用卫星图像研究了 2019 年 12 月前两年半武汉医院的停车场的容量。他们发现，在被分析的六家医院中，有五家在 2019 年 9 月和 10 月，即首次报告 COVID-19 病例之前，停车场的相对日汽车量最高。这个高峰与中文搜索引擎百度上武汉对“咳嗽”和“腹泻”的搜索量的增加相对应[60]。美国疾病控制与预防中

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[60] 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

心（CDC）表示，咳嗽和腹泻都是 COVID-19 的症状[61]。这项研究表明，一种与 COVID-19 症状相似的病毒曾于 9 月和 10 月在武汉传播。

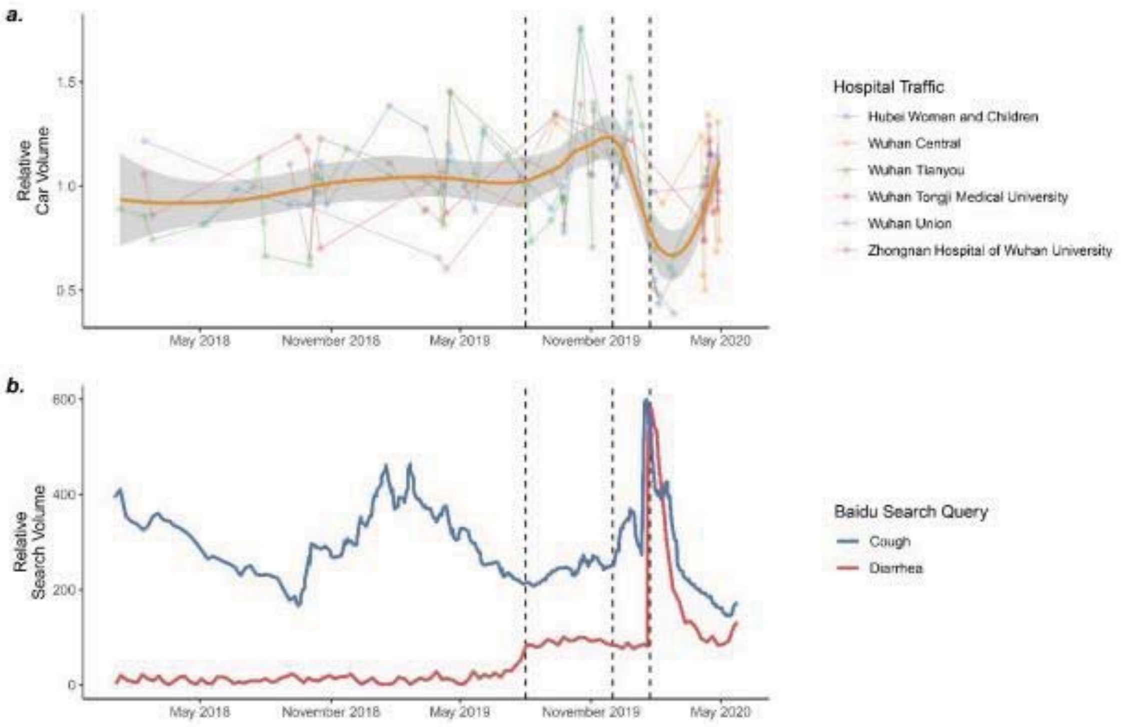

图 7：不同的类似流感的疾病、症状和监测信号的时间序列[62]

最初疫情爆发地点接近武汉病毒所

当人们生病时，他们可能会在家里或工作地点附近寻求医治。每一家因抱怨有 COVID-19 症状的患者而出现客流量增加的医院都位于武汉病毒所总部附近，并通过公共交通线路连接起来。下列地图显示了武汉病毒所总部（红色）与 2019 年 9 月和 10 月车辆流量增加的六家医院（蓝色）的位置。当绘制在地图上时，这六家医院聚集在武汉武昌的武汉病毒所总部周围，并通过武汉地铁与该设施连接起来——在地图上，各种线路以黑色、黄色、粉色和绿色显示。粉色线代表的是 2 号线，2017 年该线的日客运量超过了 100 万人次[63]。

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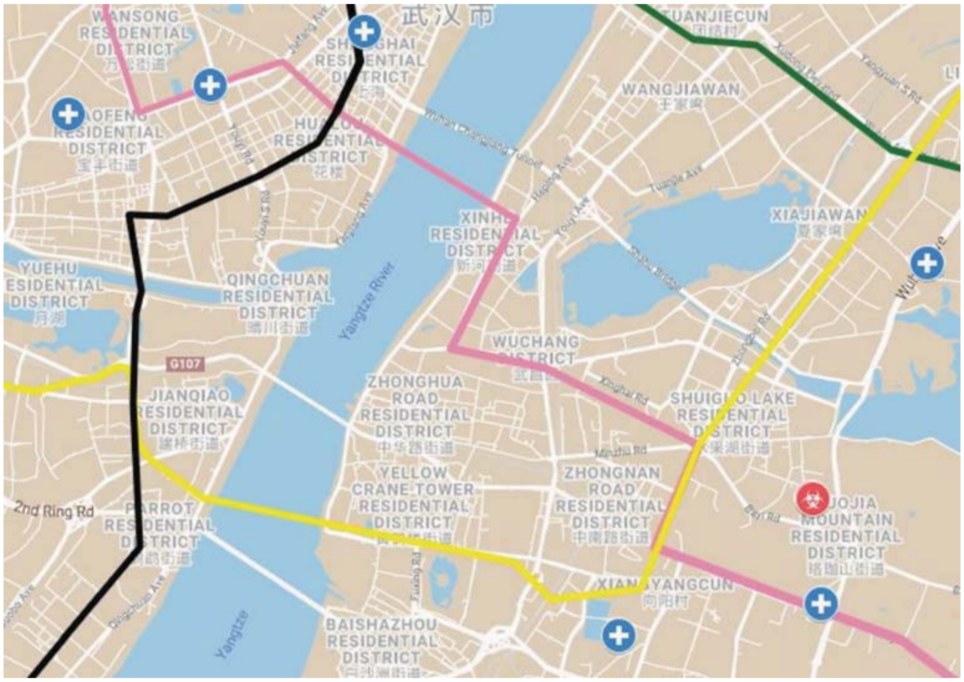
[61] "Symptoms of COVID-19." *Centers for Disease Control and Prevention*. https://www.cdc.gov/coronavirus/2019-ncov/symptoms-testing/symptoms.html

[62] Nsoesie

[63] "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



地图 1：哈佛研究各医院与武汉病毒研究所总部的关系

同样需要指出的是，据一位在生物安全四级实验室工作的澳大利亚科学家说，每天有班车把武汉病毒所研究人员从中国科学院武汉分院送到武汉国家生物安全四级实验室的设施然后再接回[64]。根据公开的地图数据，班车的上下车站点距离武汉病毒所总部不到 500 米。因此，来自武汉病毒所总部和武汉国家生物安全四级实验室的研究人员很可能使用武汉地铁和/或武汉国家生物安全四级实验室的班车作为他们日常工作通勤的一部分。

因此，基于武汉病毒所的大量样本库和对冠状病毒进行基因操作的历史，可以合理地得出结论认为，9 月初，一名或多名研究人员在实验室感染了 SARS-CoV-2，并将其带到城里。根据武汉病毒所的出版物，研究人员在用从野外收集的一种天然病毒进行实验时可能已经接触过这种病毒或被一种他们通过基因操作的病毒所感染。这些研究人员可能通过武汉地铁或班车往返武汉，为病毒的传播提供了媒介。这与武汉病人日益增多的最初迹象都以武汉病毒所位于武昌的设施为中心相吻合。

2019 年世界军人运动会和生病的运动员

2019 年 10 月 18 日，第七届国际军事体育理事会世界军人运动会在武汉开幕。这个运动会与奥运会类似，但由军人运动员组成，增加了一些军事项目。武汉世界军运会吸引了来自 109

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[64] 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.

个国家的 9308 名运动员，参加了 27 项运动的 329 项赛事。包括俄罗斯、巴西、法国、德国和波兰在内的 25 个国家派出了 100 多名运动员组成的代表团[65]。PRC 政府为世界军运会招募了 23.6 万名志愿者，动用了 90 家酒店、三个火车站和 2000 多名司机[66]。2019 年 10 月 20 日的比赛网站的存档版本列出了在武汉和湖北省举办活动的 30 多个场馆[67]。这个直播网站已经无法访问了——目前还不清楚它被删除的原因。

在比赛期间，许多国际运动员因现在看来是 COVID-19 的症状而生病。在一次采访中，一名卢森堡运动员将武汉描述为“鬼城”[68]，并回忆起他在抵达该市机场时被量体温。在接受加拿大报纸《金融邮报》（*The Financial Post*）采访时，一位参加过这次世界军运会的加拿大武装部队成员说（强调为报告作者所加）：

> **这是一座拥有 1500 万人口、处于封闭状态下的城市。这很奇怪，但我们被告知这是为了方便军运会参与者四处走动。我们到达 12 天后，(我) 就病得很重，发烧、发冷、呕吐、失眠。在我们回国的航班上，在 12 个小时的飞行过程中，60 名加拿大运动员被隔离（在飞机后部）。我们生病的症状从咳嗽到腹泻不一而足[69]。**

这名军人还透露，随着他的症状加重，他的家人也生病了[70]，这种情况与人传人的病毒感染和 COVID-19 相一致。德国、法国、意大利[71]和瑞典[72]的运动员也称他们有类似 COVID-19 的症状。

通过将列出的世界军运会场地与公开的地图数据进行交叉对照，可以把这些场地（黑色）与武汉病毒所总部（红）)和上述医院（蓝色）的所处位置视觉化。绿色标识代表公开表示相信自己在武汉期间感染了 COVID-19 的运动员，并被绘制在他们参加的赛事的主办场馆。这其中的一些运动员住在军人运动员村。

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[65] “Military Games to Open Friday in China.” *China Daily*, 17 Oct. 2019, www.china.org.cn/sports/2019-10/17/content_75311946.htm.

[66] “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.

[67] “Competition Venues.” *Wuhan 2019 Military World Games*, https://web.archive.org/web/20191020154108/en.wuhan2019mwg.cn/html/Competition_venues/.

[68] 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

[69] 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.

[70] *Ibid.*

[71] Houston.

[72] 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.

地图 2：武汉病毒研究所总部、医院、世界军运会与生病的运动员

至少有四个向军运会派遣体育代表团的国家现已确认，在 2019 年 11 月和 12 月，即在爆发疫情的消息首次公开之前，他们境内出现了 SARS-CoV-2 或 COVID-19 的病例。

1. **意大利。**2021 年 2 月，意大利的研究人员在美国疾病控制与预防中心的《新发传染病》（Emerging Infectious Diseases）杂志上发表了一个研究快报，描述了米兰一名 4 岁男孩的案例。对 2019 年采集的样本进行的回顾分析确定，这名在 2019 年 11 月 21 日出现咳嗽症状的男孩在意大利报告首例病例的三个月之前感染了 SARS-CoV-2。该男孩没有已报告的旅行记录[73]。

2. **巴西。**巴西研究人员于 2021 年 3 月发表的一篇文章研究了 2019 年 10 月至 12 月的废水样本。此前的研究已经证实，感染该病毒的人会有病毒通过胃肠道脱落的长时间经历。**11 月 27 日采集的一份样本检测出 SARS-CoV-2 RNA 呈阳性，**证实该病毒在 2020 年 1 月 21 日报告美洲第一例病例之前几个月就在巴西圣卡塔琳娜传播[74]。

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[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

3. **瑞典。**瑞典公共卫生局表示，该国有人可能早在 2019 年 11 月就感染了 SARS-CoV-2[75]。

4. **法国。**法国的研究人员还重新检测了 2019 年底的样本，以努力识别早期 COVID-19 病例。他们确认了一名 42 岁的男性，他于 12 月 27 日因类似流感的疾病就诊于急诊室。他与中国没有任何联系，也没有近期旅行史。**经重新检测，该患者的样本 SARS-CoV-2 呈阳性。**应当提出的是，在该男子发病前，他的一个孩子也出现了类似的症状，这表明法国的第一个病例可能早于 12 月 27 日[76]。

如上所述，来自法国、意大利和瑞典的运动员在武汉世界军运会期间也抱怨出现症状与 COVID-19 相似的疾病。**SARS-CoV-2 在不相接壤的两个大陆的四个国家的存在指向共同来源的可能性。如果像假定的那样，SARS-CoV-2 在传播到世界其他地方之前首先在武汉感染了人类，那么 2019 年武汉世界军人运动会似乎是全球传播的一个关键媒介——换句话说，它可能是首批“超级传播者”事件之一。**

结论

虽然很多公开辩论最初大多集中在大流行病是否起源于武汉华南海鲜市场，但是现在有优势证据显示，病毒是从武汉病毒研究所泄漏的。鉴于武汉病毒所有文献可查的对冠状病毒进行功能增益实验的历史，包括在生物安全二级实验室专门对病毒进行基因操作，使其更容易感染人类，以及他们拥有世界上最多的冠状病毒样本[77]，一名或多名研究人员偶然感染病毒并将病毒带出实验室是完全有可能的。上面列出的证据，加上中共当局的掩盖行为，强烈暗示武汉病毒研究所是当前大流行病的来源。

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[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/.

[76] 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

[77] 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/.

III. 基因改造的证据

另一个辩论话题是，这个病毒是否可能经过基因改造。在 SARS-CoV-2 出现前的几个月，武汉病毒所正在对冠状病毒进行功能增益研究，并且用这些病毒来对人类免疫系统进行实验。但是科学界声称这个病毒只可能是自然产生的。然而，正如本报告所展示的，我们相信，病毒可能经过改造，这是一个可能成立的假说。

2004 年到 2017 年间有关 SARS 样冠状病毒的研究

武汉病毒所对蝙蝠冠状病毒的研究工作可以追溯到 2000 年代初 SARS 疫情之后。2004 年，在开展 2002 年 SARS 大流行病溯源工作期间，石正丽与彼得 · 达萨克见了面。达萨克是生态健康联盟的首席执行官，这个总部在纽约的非政府组织为世界各地的科学研究提供经费[78]。过去一年半以来，外界对于生态健康联盟如何以及为什么将美国纳税人的钱提供给武汉病毒所提出疑问。那些资金是卫生与公众服务部（HHS）、国立卫生研究院（NIH）、国家科学基金会（NSF）和美国国际发展署（USAID）以项目资助的方式提供给生态健康联盟的。

从 2005 年开始，石正丽和达萨克开展冠状病毒合作研究，一直持续了 16 年。他们一起“领导了数十次前往布满蝙蝠的山洞的探险活动，搜集样本，并对它们进行分析。[79]”他们发现了 500 多种新型冠状病毒，包括大约 50 种与 SARS 或 MERS 相关的病毒。他们也再三参与可以让冠状病毒更易感染人类的功能增益研究[80]。正如下面所讨论的，武汉病毒所大多数与冠状病毒最为相关的科学出版物，都得到了达萨克通过生态健康联盟提供的研究经费。

文章和出版物：《蝙蝠是 SARS 样冠状病毒的自然储存库》，《科学》（Science）（2005）。

参与者：李文东，第一作者；石正丽，第二作者和三名通讯作者之一；彼得 · 达萨克；来自澳大利亚和中国的其他科学家。

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[78] Zaugg, Julie. “In Wuhan with Bat Woman, at the origins of the Covid-19.” *L'Illustre*, 22 Jan. 2021, https://www.illustre.ch/magazine/a-wuhan-avec-bat-woman-aux-origines-du-covid-19

[79] *Ibid.*

[80] *Ibid.*

经费：这篇论文的经费部分来自 PRC 政府国家重点基础研究发展计划（项目编号：2005CB523004）和科技部国家高技术发展计划（项目编号：2005AA219070）为 SARS-CoV 动物宿主专项研究提供的资助。论文也有美国政府的资助，NIH 和 NSF 通过“传染病生态学”项目资助（编号：R01-TW05869）的形式，从约翰 · F · 福格蒂国际中心和 V · 坎 · 拉斯姆森基金会提供资金。

目的：科研人员希望通过确定 SARS 样冠状病毒天然宿主蝙蝠的种类，来确定 SARS 的源头。

结论：“这些有关冠状病毒的发现，连同亨尼巴病毒属（23–25, 28）的相关数据似乎表明，蝙蝠中的人畜共患病毒存在基因多样性，这增加了病毒变体跨越物种屏障，在人类中引发疾病的可能性。因此，提高我们对储存宿主分布、动物与动物间和人与动物间互动（尤其是在湿货市场系统内），以及蝙蝠携带病毒基因多样性的认识和了解，以防止未来疫情爆发，是至关重要的。[81]”

相关性：这个结论将推动武汉病毒所与彼得 · 达萨克接下来 15 年的合作，由石正丽领导实验室工作。

2006 年，石正丽和达萨克与澳大利亚的一位研究人员合作，在美国疾病控制与预防中心刊发的同行评审月刊《新发传染病》上发表论文《蝙蝠与 SARS 综述》。石再次被列为第二作者，这项工作同样得到上述 PRC 和 NIH/NSF 的项目经费的支持[82]。在接下来的一年，这些经费还支持了《蝙蝠冠状病毒与它们宿主之间的进化关系》这篇论文在《新发传染病》上的发表。石被列为第六作者，排在另一位武汉病毒所研究人员之后。达萨克是两名通讯作者之一[83]。

2007 年，石和武汉病毒所另几名研究人员与其他科研人员一起发表了另一篇有关冠状病毒的研究。

文章与出版物：《严重急性呼吸综合症（SARS）冠状病毒与起源于蝙蝠的 SARS 样冠状病毒之间的受体使用差异》，《病毒学杂志》（Journal of Virology）。

参与者：武汉病毒所研究人员和王林发。石正丽被列为通讯作者。

经费：这项工作得到 PRC 政府以及澳大利亚和欧盟委员会的资助。

目的：这项研究专注于 SARS 样冠状病毒刺突蛋白所利用的受体。刺突蛋白是冠状病毒表面能够让病毒与细胞上的受体结合的主要结构。为了做这个实验，研究人员将 SARS-CoV

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[81] *Ibid.*

[82] 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

[83] 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

刺突蛋白的不同序列插入要研究的 SARS 样病毒的刺突蛋白，创造出多个嵌合病毒，并用它们针对蝙蝠、果子狸和人 ACE2 表达细胞进行实验。

结论：其中一个嵌合病毒能够通过人 ACE2 受体进入细胞。

相关性：ACE2 是血管紧张素转化酶 2（angiotensin converting enzyme-2）的缩写，这个转化酶是一种蛋白质，存在于人的口、鼻和肺部等细胞和组织的表面。“在肺部，ACE2 在 II 型肺泡细胞中极为丰富，II 型肺泡细胞是存在于肺泡的一种重要细胞类型，肺泡是吸收氧气排出废气二氧化碳这个过程发生的场所[84]。”ACE2 也是 SARS-CoV-2 刺突蛋白与人类细胞结合的位置。研究人员的结论是，“最小插入区域”是“足以将 SL-COV S （SARS 样冠状病毒刺突蛋白）从不能与 ACE2 结合转化为可以与人 ACE2 结合[85]。”

换句话说，一个不感染人类的 SARS 样冠状病毒能够通过人为改变，使其能够感染人类。这个研究工作是在二级生物安全条件下进行的。

石正丽和达萨克之后没有作为共同作者一同出现在论文当中，直到 2013 年。

文章与出版物：《一种利用 ACE2 受体的蝙蝠 SARS 样冠状病毒的分离与特征分析》[86]，《自然》（Nature）。

参与者：武汉病毒所和生态健康联盟研究人员，包括胡犇。石正丽、达萨克和王林发的贡献是设计了实验。石正丽和达萨克被列为通讯作者。

经费：这项研究的经费来自 PRC 政府的项目资助（包括项目编号：2013FY113500），以及美国国家过敏和传染病研究所（NIAID）的项目拨款（编号：R01AI079231），NIH/NSF“传染病生态与进化”项目拨款（编号：R01TW05869），由卫生与公众服务部部长办公室国际流感基金支持的来自 NIH 福格蒂国际中心的项目资助（编号：R56TW009502），还有来自 USAID 防范新发大流行病威胁的“预测”（PREDICT）项目的拨款[87]。

目的：这项工作标志着“第一次有记录地分离出一株活体 SL-CoV[88]”（SARS 样冠状病毒）。研究人员从蝙蝠的粪便样本中分离出了这个病毒，并将其命名为 WIV1。此外，他们还确认了两个新型蝙蝠冠状病毒（SHC014 和 Rs3367），并且报告说，这是“首次确认能够利用 ACE2 作为进入受体的野生型蝙蝠 SL-CoV。[89]”

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[84] 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.

[85] Ren.

[86] 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/

[87] *Ibid.*

[88] *Ibid.*

[89] *Ibid.*

> **结论：**“最后，这项研究表明针对野生动物的病原体发现项目在公共卫生方面的重要性。这些项目的目的是发现‘已知的未知’——此前未知的、与已知病原体密切相关的病毒毒株。这些项目聚焦特定高风险野生生物群落和疾病发生热点地区，也许是未来预测、准备和防范大流行病出现的全球战略的一个关键部分[90]。”
>
> **相关性：**通过分离出与 ACE2 结合的野生型（自然界中的常见毒株）SARS 样冠状病毒，并且将其在人类肺部组织中进行实验，论文作者证明，蝙蝠冠状病毒能够在不经过中间宿主的情况下，直接感染人类。

2014 年，石正丽和达萨克还联合撰写了另外两篇武汉病毒所与生态健康联盟合作的论文。其中一篇论文题为《在中国小型哺乳动物中发现不同的新型星状病毒》，第一作者是武汉病毒所研究人员胡犇，他也是此前石正丽/达萨克论文的共同作者之一。石正丽在这篇论文中是通讯作者，论文经费再次得到 PRC 政府（包括项目编号：2013FY113500）和 USAID“预测”项目的联合资助[91]。

接下来的 2015 年，石正丽向北卡罗来纳大学教堂山分校的拉尔夫 · 巴里克及其他研究人员提供了 SHC014 的刺突蛋白序列和质粒。SHC014 是石正丽、达萨克和武汉病毒所研究人员 2013 年在蝙蝠粪便样本中发现的病毒之一。美国研究人员利用那些样本创造了“一个在适应小鼠的 SARS-CoV 的骨架上表达蝙蝠刺突蛋白 SHC014 的嵌合病毒”[92]。**换句话说，他们从 SHC014 中移除刺突蛋白，将其插入到一个经由基因操作、使其更易感染小鼠的 SARS 冠状病毒之中。**这个研究是在三级生物安全的条件下进行的。新创造出的病毒后来显示与人 ACE2 结合，在人类主要的呼吸道细胞“有效率地”[93]复制，并抵抗住了抗体和疫苗。研究人员的结论认为，该研究“表明目前在蝙蝠种群中传播的病毒具有可能造成 SARS-CoV 再次出现的潜在风险”[94]。这个研究的经费来自 NIAID 和 NIH 的多个项目资助（编号：U19AI109761，U19AI107810，AI085524，F32AI102561，K99AG049092，DK065988），通过生态健康联盟获得的 USAID“预测”项目的资助，以及 PRC 政府的资助。巴里克是通讯作者[95]。

2015 年，石正丽、胡犇、王林发和达萨克还共同发表了另一篇论文。这篇题为《对一种与严重急性呼吸综合症直接祖先密切相关的新型蝙蝠冠状病毒的分离和特征分析》的论文发表在《病毒学杂志》上。论文的 12 位作者中，九位是武汉病毒所的研究人员，包括胡和石，他们

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[90] *Ibid.*

[91] 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/

[92] 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

[93] Menachery

[94] *Ibid.*

[95] *Ibid.*

是通讯作者。**在这篇论文中，武汉病毒所报告成功分离出了第二个新型冠状病毒 WIV16。**这个与 SARS 类似的冠状病毒是从 2013 年在 PRC 云南省昆明市收集来的一个蝙蝠粪便样本中分离出来的。与之前的研究一样，这个研究的经费也得到 NIAID 拨款（编号：R01AI110964）和 PRC 政府（包括项目编号：2013FY113500）的资助[96]。

除了前述与北卡大学教堂山分校研究人员的合作之外，石正丽还向他们提供了另外的蝙蝠冠状病毒序列和 WIV1 刺突蛋白的质粒。由此产生的论文《SARS 样病毒 WIV1-CoV 或将在人类中出现》2016 年 3 月发表在《美国国际科学院院刊》（Proceedings of the National Academy of Sciences of the United States of America）上。虽然石和达萨克（以及任何武汉病毒所的研究人员）都不在作者之列，但是巴里克是通讯作者。**这篇论文意义重大，因为作者讨论了从疾病监测推进到创造嵌合病毒来作为应对大流行病的一种方式**——“这份稿件描述了将监测拓展到序列分析以外领域的努力，通过构建嵌合和全长人畜共患冠状病毒来评估流行病出现的可能性。[97]”

在这项研究中，研究人员通过将 WIV1 的刺突蛋白插入适应感染小鼠的一个 SARS 毒株当中，制造出嵌合病毒。他们接着将这个嵌合病毒在人呼吸道上皮细胞和小鼠中进行实验[98]。除了标准的 BALB/c 鼠（一种白化品种，实验室培养的用于实验的小白鼠[99]），研究人员还对小鼠进行了基因操作，创造出一个表达人 ACE2（hACE2）受体的品种。虽然 hACE2 主要存在于小鼠肺部，但是也出现在大脑、肝脏、肾和肠胃组织中。这个 WIV1 嵌合病毒随后被用来在这些表达 hACE2 的小鼠身上进行实验，证明这种嵌合病毒可以感染人类。这项研究得到 NIAID 和 NIH 项目的资助（编号：U19AI109761，U19AI107810，AI1085524，F32AI102561，K99AG049092，DK065988，AI076159 和 AI079521）[100]。

2016 年，石正丽和达萨克还共同撰写了另外两篇专注于传染病的论文。一篇题为《蝙蝠严重急性呼吸综合症样冠状病毒 WIV1 编码一种参与调节宿主免疫反应的额外辅助蛋白 ORFX》的论文是与王林发共同撰写的。这篇论文代表武汉病毒所研究工作向前迈出重要一步。武汉病毒所研究人员在开展这个项目过程中，创建了一个反向遗传学系统，并使用这个系统对 WIV1 进行基因改造。WIV1 是 2013 年分离成功的那个活体病毒，北卡大学的研究人员在几个月前

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[96] 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

[97] 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%2Fpnas.1517719113

[98] *Ibid.*

[99] “Inbred Strains: BALB.” MGI, www.informatics.jax.org/inbred_strains/mouse/docs/BALB.shtml.

[100] Menachery 2016.

进行过操作。武汉病毒所研究人员通过删除或增加病毒 RNA 的基因信息，创造了这个病毒的多个版本。根据论文，使用这个活体病毒的所有实验都是在二级生物安全水平条件下进行的，这种条件不要求防毒面罩或生物安全柜。在论文的 11 位作者中，九位是武汉病毒所的研究人员，石是通讯作者。论文实验得到 NIAID 拨款资助（编号：R01AI110964）和 PRC 政府资金的支持[101]。

第二年，胡犇是论文《蝙蝠 SARS 样冠状病毒丰富基因库的发现为 SARS 冠状病毒起源提供新见解》的第一作者。与之前的论文一样，这篇论文的绝大多数作者（17 位中的 14 位）都在武汉病毒所工作。达萨克、石正丽和王林发也都被列为共同作者。石是两位通讯作者之一。达萨克的贡献是“获取经费[102]”。

此外，武汉病毒所研究人员还利用一年前他们首次推出的反向遗传学系统，将不同的与 SARS 类似的冠状病毒的刺突蛋白插入 WIV1，创造了八株不同的嵌合病毒。其中两株嵌合病毒（WIV1-Rs4231S 和 WIV1-Rs7327S）和一种天然病毒（Rs4874）都在表达 hACE2 的细胞中复制[103]。**再次要强调的是，武汉病毒所研究人员在武汉国家安全生物实验室生物安全四级实验室投入运转前的 2017 年，就创造了能够感染人类的嵌合冠状病毒。**这项研究得到 NIAID（编号：R01AI110964）、USAID“预测”项目和 PRC 政府（包括项目编号：2013FY113500）资金的联合支持。

2018 年到 2019 年武汉病毒所或与武汉病毒所科学家联合开展的 SARS 样冠状病毒研究

虽然石正丽和达萨克在 2018 年和 2019 年还共同撰写了其它几篇有关冠状病毒的论文，但是没有一篇包含使 SARS 样冠状病毒变得更易感染人类的功能增益研究。鉴于 2018 年中国科学院发起一个名为“病原体宿主与免疫干预”新专项课题[104]，这显得尤为奇怪。这个课题共设五个项目，其中一个是“研究病毒溯源、跨种传播及致病机制”——石是这个项目的两位负责科学家之一[105]。这个项目有三个重点方向：1）新病原的溯源、进化及传播机制；2）病毒跨种感染和致病的分子机制；3）病毒与宿主相互作用机制。武汉病毒所的另一名科学家崔宗强负责另

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[101] 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%2FJVI.03079-15

[102] 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%2Fjournal.ppat.1006698

[103] Hu, 2017.

[104] “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

[105] *Ibid*.

一个名为“感染与免疫研究的新方法、新技术”的项目[106]。该项目关注的重点包括评估新型疫苗和建立“人源化小动物模型”[107]用于体外病原体实验[108]。

2018 年 1 月，石被指派为一个新的中国科学院战略性先导科技专项的项目负责人（项目批准号：XDB29010101，金额 135 万美元），研究“蝙蝠携带重要病毒的基因进化和传播机制”[109]。这个项目，尤其是它所关注的传播机制，与前述的第一个重点研究方向契合。同月，石正丽开始了另一个项目，题为“蝙蝠 SARS 样冠状病毒适应宿主受体分子的进化机制及其跨种感染的风险的研究”[110]。 这个项目的经费为 85 万美元（项目批准号：31770175），项目周期持续到 2021 年 12 月[111]。这个拨款项目与前述第二个重点方向契合，它的简介特别提到了复制和改造冠状病毒（强调为报告作者所加）：

> 针对重要新发突发和烈性病毒（流感病毒、埃博拉病毒、**冠状病毒**、马尔堡病毒、沙粒病毒等），通过研究其**入侵不同宿主细胞的能力以及在不同宿主细胞的复制能力**，解析影响其跨种感染的关键分子及其致病机制。包括：病毒入侵，**病毒复制和组装**，以及感染模型[112]。

石正丽没有在大流行病开始前发表任何由这个项目资助的论文，因此不可能知道她在大流行病之前的几个月做了什么实验。

石正丽 2018 年和 2019 年的研究工作提供了进一步的证据，2019 年 1 月，石和其他几名科研人员参与的“中国蝙蝠携带重要病毒研究”被授予国家自然科学二等奖[113]。获奖的六名研究人员中，五人是前面讨论过的 2013 年那篇《一种利用 ACE2 受体的蝙蝠 SARS 样冠状病毒的分离与特征分析》论文的共同作者。

2019 年 1 月，胡犇获得青年科学基金项目 38.585 万美元的资助（项目批准号：31800142）[114]。青年科学基金项目“支持青年科学技术人员在科学基金资助范围内自主选题，开展基础研

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[106] *Ibid.*
[107] *Ibid.*
[108] *Ibid.*
[109] Shi, Zheng-li. “Curriculum Vitae.” https://www.ws-virology.org/wp-content/uploads/2017/11/Zhengli-Shi.pdf
[110] “Study on the evolutionary mechanism of bat SARS-like coronavirus adapted to host receptor molecules and the risk of cross-species infection.” *MedSci*, https://archive.is/g35C6#selection-1425.0-1425.139
[111] *Ibid.*
[112] “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
[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

究工作。[115]”胡犇所选项目的题目是《两株新型蝙蝠 SARS 相关冠状病毒对表达人 ACE2 的转基因小鼠的致病性研究》[116]。截至目前，这两株新型与 SARS 相关的冠状病毒还没有被确认，项目经费只在有关 SARS-CoV-2 的论文中被引述。

武汉病毒所研究人员向世卫组织调查团队证实，他们在 2018 年和 2019 年开展了测试嵌合冠状病毒的实验[117]。根据《科学》杂志发表的对石正丽的采访，所有冠状病毒实验，包括感染 hACE2 小鼠和果子狸的实验，都是在二级生物安全水平和三级生物安全水平的条件下进行的——“我们实验室的冠状病毒研究是在生物安全二级或生物安全三级实验室中展开的。[118]”

这项进行中的研究看起来与达萨克公开所称的研发广谱冠状病毒疫苗的目标相一致。2020 年 5 月 19 日，达萨克在接受《病毒学本周动态》（This Week in Virology）采访时，讨论了他资助的、与武汉病毒所对冠状病毒进行功能增益研究的目标（强调为报告作者所加）：

> 冠状病毒相当不错——我的意思是，你是一名病毒学家，你对所有这些都清楚——但是…你能够…呃很**容易地在实验室对它们进行操作**。刺突蛋白导致冠状病毒发生很多情况——人畜共患的风险。所以，你可以拿到序列，构建这个蛋白，我们和北卡大学的拉尔夫 · 巴里克合作做这个，然后把这个蛋白插入另一个病毒的骨架，在实验室做些研究。这样你发现一个序列后就可以做出更多预测——你有了这种多样性。现在，研发疫苗的逻辑进程是，如果要研发一个 SARS 疫苗，人们会用大流行病的 SARS 病毒，**但是让我们尝试插入一些其它相关的（病毒），获得一个更好的疫苗[119]。**

石正丽、胡犇和武汉病毒所的其他人就是在为达萨克收集、确认、基因改造这些新型病毒，并且用它们来对人体免疫系统进行测试。

总之，在 SARS-CoV-2 出现前的那些年，发生过这些事情：

- **石正丽和武汉病毒所其他人研究如何改变非感染性的 SARS 样冠状病毒的刺突蛋白，让这些病毒可以与人 ACE2 受体结合；**

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[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

- **石正丽、胡犇、达萨克、王林发和其他研究人员多次合作，对冠状病毒进行基因操作，以增强它们在人类中的感染性。**
- **石正丽负责的一项新的 PRC 战略优先研究项目，在二级生物安全水平和三级生物安全水平条件下，积极制造嵌合病毒和寻找新型病毒；**
- **证据显示石正丽与其他几位在 2013 年首次分离出活体冠状病毒的科研人员一直有合作；**
- **批准给胡犇的第二个项目在二级生物安全水平和三级生物安全水平条件下，用新型冠状病毒来测试人类免疫系统；**
- **研发一种广谱冠状病毒疫苗的公开努力。**

综上所述，显而易见的是，在大流行病开始前的 2018 年和 2019 年，石正丽及其同事，在达萨克的资助和支持下，积极对冠状病毒进行基因操作，并且用它们来测试人体免疫系统。

SARS-CoV-2 不同寻常的特点

委员会少数党幕僚对科学家、美国政府现任和前任官员的访谈，对 SARS-CoV-2 的自然起源提出了几点疑问，包括：

1. SARS-CoV-2 的高度传染性，他们认为与麻疹的传染性一样；
2. 缺乏确定的中间宿主（SARS 爆发四个月后以及 MERS 爆发九个月后都找到了中间宿主）；以及
3. 与人 ACE2 结合效率非常高。

自 SARS-CoV-2 开始在全球传播以来，这个病毒的高传染性一直是激烈讨论的话题。一些科学家和其他专家指出，感染病例数量惊人地多，这个证据表明，SARS-CoV-2 本质上与已知的天然乙型冠状病毒不同。例如，MERS 首次在 2012 年出现，感染人数不到 4000 人。SARS 首次在 2002 年出现，感染人数少于 10,000 人。在本报告撰写之际，SARS-CoV-2 在首次出现后的不到两年时间里，已经感染了超过 1.964 亿人。

SARS-CoV-2 在与人 ACE2 受体结合方面，也有相比其它宿主而言非常不寻常的特点。2020 年 2 月，美国研究人员仔细研究了这个问题。他们发现，SARS-CoV-2 的刺突蛋白“与它们常见宿主细胞受体的结合紧密程度是严重急性呼吸综合症（SARS）-CoV 上相应刺突蛋白的至少 10 倍[120]。”换句话说，相比引起 SARS 的病毒与人 ACE2 的结合，SARS-CoV-2 与人 ACE2

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[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/

的结合要紧密 10 倍多。研究人员认为，这很可能揭示了为什么这个病毒如此具有传染性[121]。

澳大利亚和英国的研究人员还考察了 SARS-CoV-2 如何与不同动物 ACE2 结合的情况，并在 2021 年 6 月 24 日将他们的研究发表在《科学报告》（Scientific Reports）上。这些科研人员发现，SARS-CoV-2 刺突蛋白与人 ACE2 的结合最强。他们报告说（强调为报告作者所加）：

> 这个发现令人吃惊，因为**人畜共患病毒通常在原始宿主物种中呈现最高的初始结合程度，**与新宿主物种受体的初始结合程度则较低，直到它适应了新宿主。随着病毒适应新宿主，病毒需要变异来提高其与新宿主受体的结合程度。由于**我们对结合程度的测算是基于疫情爆发之初 2019 年 12 月在中国分离出来的 SARS-CoV-2 样本，**S 蛋白与人 ACE2 极高的结合程度是出乎意料的[122]。

这篇论文的预印本的第一个版本提出的主张更进一步，在结论中写道，“数据表明 SARS-CoV-2 特别适应感染人类，**这就病毒究竟是因罕见概率事件发生于自然还是可能源于其它地方提出了重要问题”**（强调为报告作者所加）[123]。**这项研究提供证据显示，SARS-CoV-2 特别适应人类，似乎表明疫情始于非人畜共患来源。**

弗林蛋白酶切割位点

讨论最多的一个问题围绕 SARS-CoV-2 的弗林蛋白酶切割位点（FCS）展开。FCS 是让病毒能够与人类细胞结合并进入细胞的刺突蛋白的一部分。2020 年 2 月，法国和加拿大的科学家报告说，SARS-CoV-2 含有的一个 FCS，是相同演化支的其它冠状病毒所没有的。演化支就是被认为拥有类似共同祖先的病毒分支。这些科学家还报告说，当一个支气管炎病毒被插入一个类似的切割位点从而被改造后，这个病毒的致病性增加了[124]。虽然一些科学家指出，其它冠状病毒也含有弗林蛋白酶切割位点，但是系统发育分析显示，SARS-CoV-2 是唯一被确认带有这个特点的乙型冠状病毒支系 B（乙型冠状病毒的一个亚属）[125]。

2021 年 1 月，一组美国研究人员在《自然》杂志上发表论文《弗林蛋白酶切割位点缺失使 SARS-CoV-2 致病性减弱》。研究人员在文章中说，FCS“可能促进了 SARS-CoV-2 在人类中的

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[121] *Ibid.*

[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/

出现[126]。”他们利用反向遗传学系统，创造了一个缺少 FCS 的 SARS-CoV-2 变异株。结果显示，这个病毒在人类呼吸道细胞中变弱了，并且在表达 hACE2 小鼠中的发展也呈现出减弱状态。这显示了 FCS 在 COVID-19 快速传播中的重要性。

对于 SARS-CoV-2 的 FCS 是否自然产生于病毒，还是通过基因操作引入的问题，引发公开辩论。换句话说，FCS 究竟是天然发展形成的，还是通过基因操作加进去的？FCS 的部分基因序列包含一个 CGG 双重编码组（CGG-CGG）。这组六个核苷酸（三个核苷酸为一组，亦称一个编码组）是产生 FCS 的 12 个核苷酸的一半。SARS-CoV-2 是其所在的病毒家族中唯一被确认带有这种组合的冠状病毒。一些人士认为，这是基因操作的证据，并称这个双重编码组揭示出 FCS 是被人为插入病毒的[127]。

“无痕”方式

对病毒基因改造说或病毒人造说持批评意见的人士不断指出，SARS-CoV-2 基因组中缺乏基因操作的明显迹象。他们称，这是病毒不仅是自然形成的，而且是 COVID-19 大流行病只可能是人畜共患外溢结果的“证据”。这种论断忽视了与之恰恰相反的关键证据。

2005 年，北卡大学教堂山分校的一位研究人员拉尔夫 · 巴里克发表一篇题为《小鼠肝炎病毒发展与 SARS-CoV 感染性 cDNA 构建体》的论文[128]。巴里克之后在 2014 年到 2016 年与石正丽有合作。在那篇论文中，巴里克提到使用他与北卡大学同事研发的一种全新基因工程系统，通过“无痕”方式构造全长 SARS-CoV 基因组。这个方法能把不同部分的基因序列组合成全长基因组，创造一个新的具有传染性的冠状病毒[129]。论文包含以下这张图表，名为“SARS-CoV 感染克隆的系统组合战略”。这张图清楚展示出不同的 SARS 片段如何被用来生成一个全长的、定制的基因组序列。

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[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

[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.

[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

[129] *Ibid*.

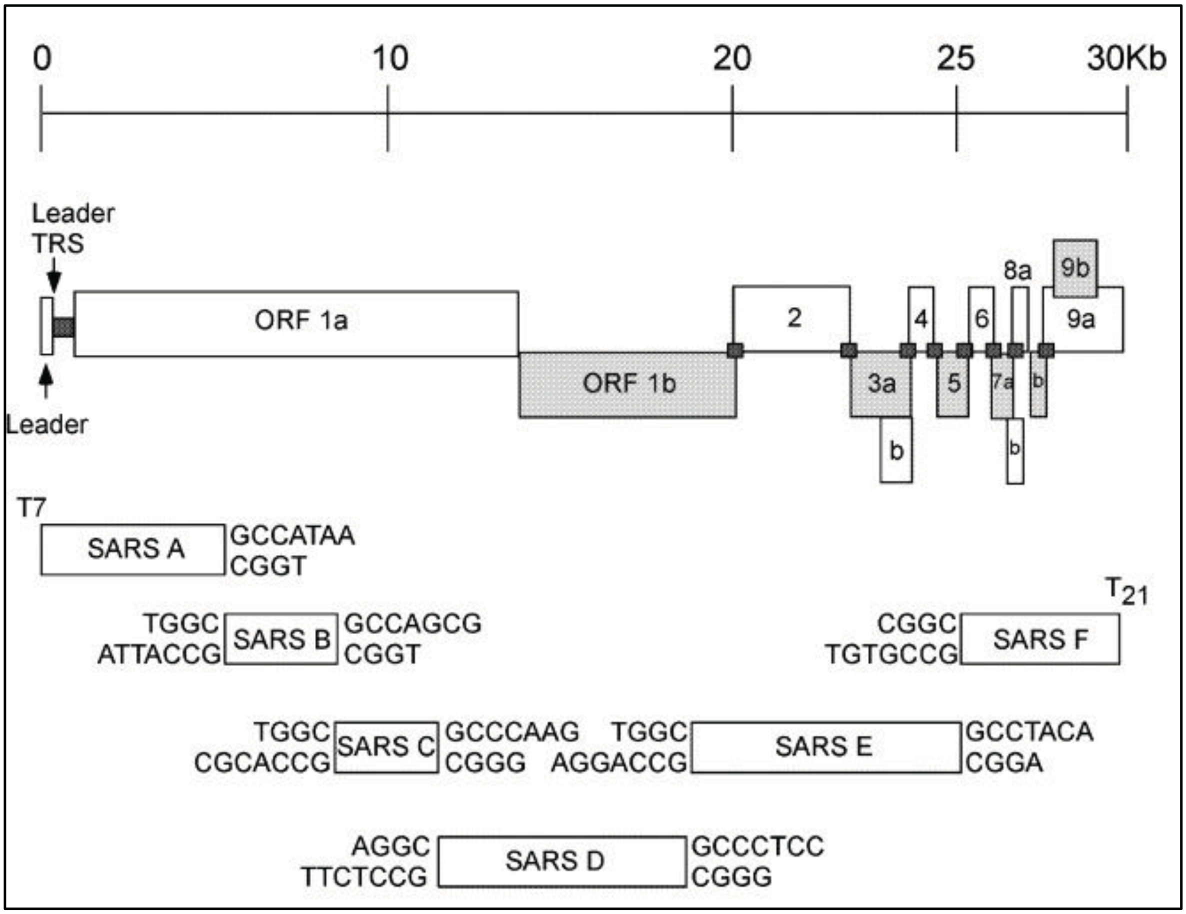

图 5：巴里克的“无痕”系统

论文说，这些病毒“难以与野生型区别[130]”，意思就是不可能分辨出它们是否是通过合成制造的。

巴里克在 2020 年 9 月的一次采访中证实了这种解释。他说：“你可以不留任何痕迹地改造一个病毒。但是你们寻找的答案只能从武汉实验室的档案中找到。[131]”他在提到 2015 年与武汉病毒所研究人员一起创造的嵌合病毒时说，他的团队会故意留下标志性的突变，以显示病毒是经过基因改造的。“否则就没有办法区分天然病毒和实验室制造的病毒了。[132]”

石正丽和巴里克合作过多篇有关冠状病毒的论文。最近一篇是在 2020 年 5 月，他们和其他研究人员一起发表了《SARS-CoV-2 在表达人类血管紧张素转化酶 2 的转基因小鼠中的致病

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[130] *Ibid.*

[131] 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.

[132] *Ibid.*

机制》[133]。**一年后，巴里克联署了2021年5月14日在《科学》杂志上的一封联名信。这封信认为，实验室泄漏说必须被认真对待，也应当予以充分评估[134]。**

2017年，在武汉病毒所工作的博士生曾磊平向中国科学院大学提交了题为《蝙蝠SARS样冠状病毒的反向遗传学系统的建立及ORFX功能研究》的博士论文[135]。其中提到的反向遗传学系统就是武汉病毒所2016年用来对病毒进行基因改造并在二级生物安全条件下对活体病毒进行实验的系统。曾磊平在博士论文中说，他和武汉病毒所其他研究人员利用这个系统“构建了以WIV1为骨架的S基因嵌合重组病毒BAC感染性克隆，在重组病毒基因组中**没有留下任何序列痕迹**（例如结合酶位点）。[136]”（强调为报告作者所加）

曾磊平在论文最后的讨论中重申了这种看不出证据的基因操作。他说：

> 我们建立了一个冠状病毒的反向遗传学系统，并且基于WIV1的基因组骨架，我们**构建了一个不留痕迹替代S基因的机制**，构建了12株S基因嵌合重组病毒的BAC感染性克隆，并进行成功拯救。测试了其中四株重组病毒（包括SL-CoV Rs4231，Rs4874，Rs7327和RsSHC014），查看这些毒株在人、果子狸、蝙蝠体内对ACE2的利用[137]。

曾磊平在提交论文之时受雇于武汉病毒所，石正丽是他的导师。**因此明确的是，石正丽和武汉病毒所其他人不仅拥有对冠状病毒进行“不留痕迹地”基因改造的能力，而且在目前这场大流行病发生前的那些年里就在积极地这么做。**曾磊平现在看起来是斯坦福大学生物工程的博士后研究员[138]。

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[133] Jiang, Ren-Di et al. “Pathogenesis of SARS-CoV-2 in Transgenic Mice Expressing Human Angiotensin-Converting Enzyme 2.” *Cell*, 21 May 202, 182(1): 50-58.e8. https://dx.doi.org/10.1016%2Fj.cell.2020.05.027

[134] 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

[135] 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

[136] *Ibid.*

[137] *Ibid.*

[138] “Leiping Zeng.” *Stanford*, https://profiles.stanford.edu/leiping-zeng

IV. 掩盖实验室泄漏的证据

除了前文讨论的事件（病毒数据库下线，世界军人运动会期间道路封闭，等等），还有其它几起事件似乎表明，PRC、武汉病毒所研究人员和其他人积极努力地压制和诋毁早期出现的一些议论，即病毒可能是人造的，或者它可能是从武汉病毒所的一处设施中泄漏的。

2012 年 4 月，有六名在 PRC 云南省一座铜矿工作的矿工患病。这些年龄在 30 岁到 63 岁之间不等的工人在昆明一家医院就诊时“持续咳嗽、发烧、头疼、胸痛、呼吸困难”[139]。六人中有三人最终死亡。武汉病毒所的研究人员被要求调查和测试患病矿工身上的病毒样本。他们也开始从矿井所在洞穴中的蝙蝠身上收集样本，并由此发现了几种新的冠状病毒。结果，武汉病毒所就此开始了对该矿的长期研究，每年都会收集样本。尽管如此，石正丽坚持认为这几名矿工是因一种生长在蝙蝠粪便上的真菌致死的[140]。

RαTG13 与 ID4991：SARS-CoV-2“最接近的近亲”

PRC 研究人员（当中大多数人隶属于武汉病毒所）2016 年发表的一篇论文把上述努力描述为研究人员“从 2012 年到 2013 年对云南省墨江县一处废弃矿井中的蝙蝠进行冠状病毒监测”[141]。石正丽和胡犇被列为该文的共同作者。武汉病毒所的研究人员发现了两种新的乙型冠状病毒——HiBtCoV/3740-2 和 RaBtCoV/4991。该研究做出结论说：“RaBtCoV/4991 与人类 SARS-CoV 的差异比它与其它的蝙蝠 SL-CoV 差异更大，可以被认为是该病毒谱系的一个新毒株。[142]” 石正丽设计并协调了这项研究，起草了论文原稿，并被列为通讯作者。

四年后，在武汉首次报道一种未知的类似 SARS 的冠状病毒后，石正丽和其他 28 名 PRC 科学家于 2020 年 1 月 20 日向《自然》杂志提交了一篇题为《肺炎爆发与一种可能起源于蝙蝠的新型冠状病毒有关》的文章[143]。该文于 2 月初发表。应该指出的是，提交这篇论文原稿的同一天，PRC 国家卫生健康委员会首次发布声明确认病毒正在发生人际传播，尽管地方卫生官员一个月前就已向中共发出了警告[144]。石和她的共同作者们极不可能是在提交论文的同一天才写

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[139] 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-mojiang-mine-its-role-origins-covid-19-2021-06-09/.

[140] 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-coronavirus1/.

[141] 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

[142] *Ibid.*

[143] 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

[144] Wang, Yanan. “Human-to-Human Transmission Confirmed in China Coronavirus.” *AP NEWS*, 20 Jan. 2020. https://apnews.com/14d7dcffa205d9022fa9ea593bb2a8c5

了这篇论文，这意味着他们几天甚至几周前就知道病毒正在通过人际传播扩散，但没有向世界发出警报。英国南安普顿大学研究人员的一项研究显示，若在上述论文发表的一周前就开始实施针对人际传播的恰当限制措施，武汉的病例数量本可以减少 66%[145]。这本可以对病毒的传播产生重大影响，特别是 2020 年 1 月 10 日至 1 月 23 日正值春节客运高峰。武汉在 1 月 23 日开始封城。

石正丽被列为这篇文章的通讯作者，文章称 COVID-19“现在已经发展到可以通过人与人之间的接触传播”[146]。研究人员得出结论，据称是在自然界产生的蝙蝠冠状病毒 RaTG13 是与 SARS-CoV-2 最接近的近亲（强调为报告作者所加）：

> **我们然后发现先前在云南省的中华菊头蝠标本中检测到的蝙蝠冠状病毒（BatCoV RaTG13）的 RNA 依赖性 RNA 聚合酶（RdRp）的一小段序列**与 2019-nCoV 有很高的序列同源性。我们对该样本（GISAID 登录号：EPI_ISL_402131）进行了全长测序。Simplot 软件基因重组分析显示，2019-nCoV 的整个基因组与 RaTG13 的基因组（图 1c）高度相似，总基因组序列同源性为 96.2%。通过比对 2019-nCoV、RaTG13、SARS-CoV 和之前报告的蝙蝠 SARSr-CoVs 的基因组序列，2019-nCoV 的基因组中没有检测到重组事件的证据。通过对 RaTG13 的 RdRp 和其刺突蛋白的全长基因组和基因序列进行系统发育分析，发现相比其它病毒的基因组序列，**RaTG13 是与 2019-nCoV 最接近的近亲，这两者组成了不同于其它 SARSr-CoVs 的谱系**（图 1d 和扩展数据图表 2）… **与 RaTG13 密切的系统发育关系为 2019-nCoV 可能起源于蝙蝠提供了证据[147]。**

对这篇论文的仔细审阅及论文作者几个月后发表的更正显示了这些研究人员说法中的不一致之处。上面所引述中的说法当中，有几个完全是错误的。这项有关 RaTG13 的研究受到持续几个月的批评和质疑后，石和其他研究人员不得不在 2020 年 11 月 17 日发表一份补充报告。**这份补充报告显示，RaTG13 实际上是 ID4991，这是在 2012 或 2013 年之前收集的样本，其全长基因组序列则是在 2018 年获得的，而不是像论文中最初说的那样是在 2020 年 1 月获得的[148]。**

不幸的是，没有其他实验室可以确认 RaTG13 的基因组序列。在发表于《科学》杂志的一

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[145] 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.

[146] Zhou (2020).

[147] *Ibid.*

[148] 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

次采访中，石正丽说整个样本已经在基因组测序中用完了[149]。外部研究人员无法去验证RaTG13的基因组序列，而武汉病毒所在何时收集并测序 RaTG13 的问题上刻意加以混淆，这引发了多个疑问：

- 为什么在 2020 年 2 月的那篇论文中不提及病毒序列已被重新命名？
- 为什么要谎报获得病毒全长序列的时间？
- 为什么要在论文发表近十个月后才发布内容更正？
- 为什么就只有这个样本在测序中被销毁了，而其它样本则没有？

2020 年 12 月，BBC 新闻台的几名记者试图探访云南那个收集到 RaTG13 蝙蝠病毒的洞穴。他们发现自己被便衣警察尾随，并在一些检查站被阻拦下来，他们在那里被告知不要进入那一地区[150]。法国电视节目"特派记者"（Envoye Special）制作了一段视频，他们报道了与住在矿井附近的村民的对话。据其中一位村民说，这个矿井已被关闭，还有监控摄像头。那个村民还声称有几个人因冒险太靠近矿井而被捕[151]。

必须指出的是，2020 年 3 月，美国、英国和澳大利亚的研究人员在《自然-医学》（Nature Medicine）上发表了《SARS-CoV-2 的近端起源》[152]。就 RaTG13 而言，他们发现，"虽然从中华菊头蝠中提取的 RaTG13 与 SARS-CoV-2 总体上有~96%的同源性，但其刺突蛋白在 RBD 方面出现偏离，这似乎表明它可能无法有效地与人 ACE2 受体蛋白结合"[153]。RBD 是受体结合域（receptor-binding domain）的缩写，是病毒刺突蛋白的一部分。**这正是石正丽、胡犇和其他武汉病毒所研究人员早在 2015 年就进行基因改造和基因替换的同一部分病毒基因组。**

如果 SARS-CoV-2 是经过基因改造的，这可能就是如何这样做的一个可行的模式。RaTG13 的 RBD 或其整个刺突蛋白都可以用武汉病毒所内的反向遗传学系统进行替换。如果对武汉病毒所拥有的多种尚未发表的冠状病毒中的其中一种进行基因改造，然后让改造后产生的嵌合病毒进入能表达人 ACE2 受体蛋白的小鼠或果子狸体内，由此产生的病毒可能会变得更适应于感染人类——就像 SARS-CoV-2 一样。

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[149] Shi, Zheng-li. "Reply to Science Magazine." *Science Magazine,* https://www.sciencemag.org/sites/default/files/Shi%20Zhengli%20Q%26A.pdf

[150] 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.

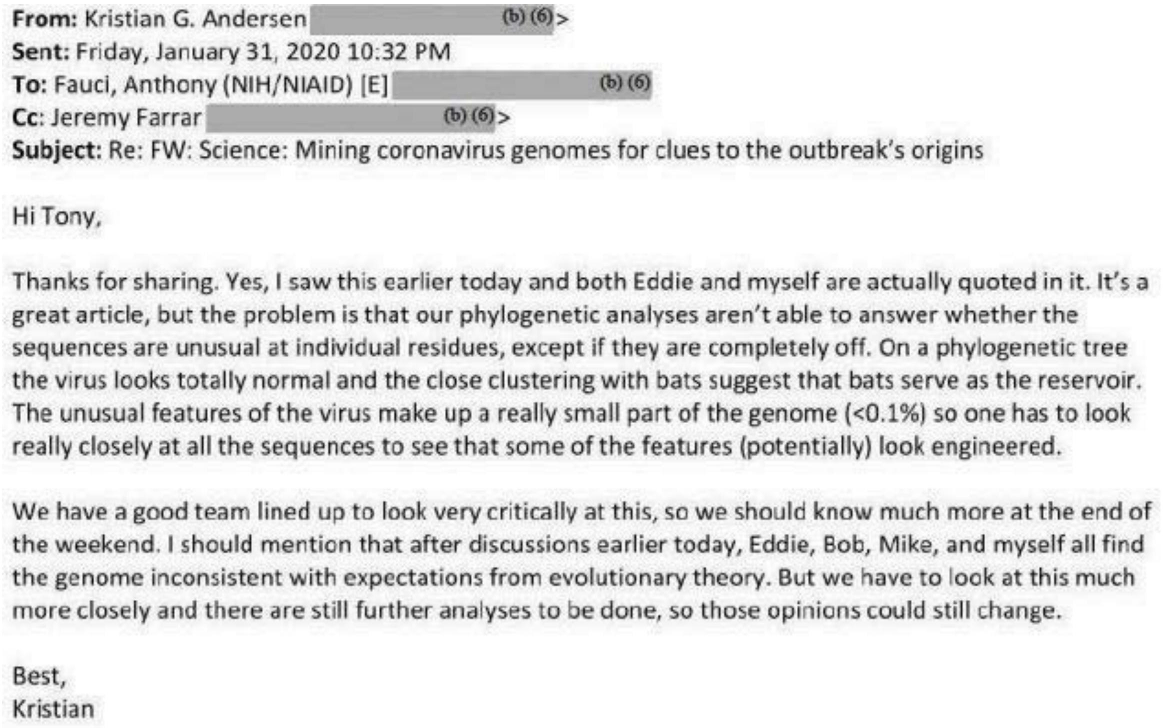
[151] Asis, Francisco de. "Quite Important the Conversation with Danaoshan Inhabitant.- He Pointed towards the Location We Already Knew for the Mine.- The Roadblocks Are Probably the Diverted Traffic We Already Observed Too.Rest of the Story Is Just Incredible! Pic.twitter.com/kzHz7v5rSg." *Twitter*, Twitter, 12 Mar. 2021, https://twitter.com/franciscodeasis/status/1370183826731888641?s=20.

[152] Andersen, Kristian G et al. "The proximal origin of SARS-CoV-2." *Nature Medicine*, 17 March 2002, 26(4):450-452. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7095063/

[153] *Ibid.*

根据科学家们的说法，包括那些在武汉病毒所工作的人，ID4991/RaTG13 与 SARS-CoV-2 的接近程度超过其它任何已被公开识别的病毒。现已很清楚的是，武汉病毒所的研究人员早在 2013 年就已获取这种病毒，这比该所开始对野外发现的其他冠状病毒进行基因改造还要早几年。**鉴于 RaTG13 和 SARS-CoV-2 之间最大的区别在于刺突蛋白——而这恰恰就是武汉病毒所多年来对各种冠状病毒进行修改的部分——再加之研究人员对该病毒重新命名并谎报对之测序的时间，那么，如果 SARS-CoV-2 确实是经过基因改造的，ID4991/RaTG13 可能就是其原始基因材料的来源。**

根据 Buzzfeed 新闻网获取的电子邮件，看起来，上述论文的第一作者兼通讯作者克里斯蒂安 · G · 安德森（Kristian G. Andersen）最初认为这是一个有可能成立的理论。在 2020 年 1 月 31 日发给美国国家过敏和传染病研究所所长安东尼 · 弗契（Anthony Fauci）医生的一封电子邮件中，安德森表示，这个病毒的某些部分可能经过改造，与病毒进化理论不符。



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

发件人：克里斯蒂安·G·安德森[redacted]
发件时间：2020 年 1 月 31 日 10:32 PM
收件人：安东尼·弗契（NIH/NIAID）【E】[redacted]
抄送：杰瑞米·法拉尔[redacted]
主题：回复：转发：深挖新冠病毒基因组以寻找疫情爆发源头

你好托尼，

> 谢谢分享。是的，今天早些时候我也看到这文章了，埃迪和我都在文中被引用了。这是一篇很棒的文章，但问题是，我们的系统发育分析无法回答这些序列在单个残基上是否不寻常的问题，除非它们其实是完全不同。在系统发育树上，该病毒看起来完全正常，与蝙蝠基因序列的紧密聚类似乎表明蝙蝠是病毒的宿主。该病毒的不寻常特征只占基因组的一小部分（小于 0.1%），所以必须仔细观察所有的序列才能发现其中一些特征（可能）看起来像是经过人工设计的。
>
> 我们有一支优秀的团队接下来会开始对此进行非常审慎的探究，所以我们在周末应该会知道得更多。值得一提的是，经过今天早些时候的讨论，埃迪、鲍勃、迈克和我都发现基因组与病毒进化论的预期不符。但我们必须更仔细地研究这一点，还有更多的分析要做，所以这些观点仍有可能改变。
>
> 祝好，
> 克里斯蒂安

图 8：安德森在电邮中示意 SARS-CoV-2 是转基因的[154]

武汉病毒所发表于 2020 年 2 月的那篇关于 RaTG13 的有意误导的论文在 1 月 23 日就作为预印本上传[155]。鉴于安德森及他的共同作者们在他们 2020 年 3 月发表的论文中引用了那篇论文，几乎可以肯定的是，安德森、弗契医生和其他人在安德森发送这封电子邮件之前就已看到过那篇论文。2020 年 2 月 1 日，也就是安德森给弗契医生发电子邮件的第二天，弗契医生、安德森和其他人通过电话会议就上述问题进行了辩论。会议之前，他们都事先同意对这场辩论保密。在会议讨论之后，安德森放弃了他有关病毒经过基因改造的说法[156]。目前尚不清楚那场电话会议上说了什么导致安德森这样做。

武汉病毒所科学家们的更多掩盖行为

随着武汉病毒所正进行的研究类型受到更多的调查，中共文字审查人员和武汉病毒所研究人员一直在删除与 COVID-19 大流行病起源可能相关的冠状病毒研究，或抹去对这类研究文献的参考痕迹。如前所述，胡犇曾获青年科学基金项目奖，从 2019 年开始测试两种与 SARS 相

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[154] Andersen, Kristian G. Email to Anthony Facui and Jeremy Farrar. 31 Jan. 2020. https://s3.documentcloud.org/documents/20793561/leopold-nih-foia-anthony-fauci-emails.pdf

[155] 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

[156] 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/covid-19-fauci-lab-leaks-wuhan-china-origins/7737494002/.

近的冠状病毒的致病性。在 PRC 的一些面向公众的网站上，胡犇的名字现已经从科研基金获奖名单中删除。

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

C010802	研究杆状病毒 Ac34 蛋白抑制哺乳动物 CRM1 出核途径的机制	穆敬芳	中国科学院武汉病毒研究所
C010802	两株新型蝙蝠 SARS 相关冠状病毒对表达人 ACE2 的转基因小鼠的致病性研究		中国科学院武汉病毒研究所
H1904	肠道病毒 71 型 3A 蛋白拮抗 RNAi 抗病毒免疫机制的研究	邱洋	中国科学院武汉病毒研究所

图 9：胡犇的名字在 2019 年的科研基金名单上被删除[157]

在数据库中列出的近 80 项武汉病毒所的科研基金中，授予胡犇的那一项是唯一一笔没有指明项目负责人身份的基金。

一篇 2017 年 12 月 12 日采访胡犇的文章在推特上流传开后被下线。在这篇文章中，胡犇谈到了对云南那个蝙蝠洞中蝙蝠病毒样本的监测和采集工作，以及他使用反向遗传学方法将刺突蛋白嵌入活体冠状病毒的工作。耐人寻味的是，他还谈到石正丽是如何“经常会亲自带队采样”[158]。撤下这篇文章很可能是为避免引发人们对那个采集 RaTG13 的洞穴的关注。

同样，胡犇 2018 年发表在中国科学院武汉分院网站上的一篇文章也被移除[159]。尽管这篇

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[157] 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

[158] “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

[159] 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

文章广泛讨论了石正丽和武汉病毒所其他研究人员的工作，但文中并没给出任何独特的见解或危险研究的证据。那为何要把这篇文章移除呢？

也许最令人怀疑其中必有隐情的还是石正丽有关武汉病毒所内部活动的反复谎言。2020 年 8 月，在国会众议院外交委员会少数党幕僚中期报告发表后，中国环球电视网就我们的这份报告采访了石正丽。在随后发表的采访文章中，石正丽否认陈薇少将接管了武汉国家生物安全四级实验室：

> 刘欣：这份报告更进一步说，这个实验室已被中国军方接管了。报告称陈薇少将已接替袁志明成为武汉病毒研究所所长，而陈薇是中国军方的医学专家。
>
> 石正丽：这是个谣言，没有这回事。
>
> 刘欣：你绝对否认中国军方已接管武汉病毒研究所。
>
> 石正丽：是的，这是个谣言。[160]

这是明显错误的。就像之前所讨论过的，在受中共管控的一些论坛上，那些宣布陈薇已抵达武汉的帖子承认了她对实验室的接管。报道说："陈薇少将已在武汉十多天。她接管 P4 实验室犹如一枚'定心丸'。"[161]

在同一采访中，石正丽在回应委员会少数党幕僚在报告中提出的有关可能的实验室泄漏事件的问题时再次撒谎，声称武汉病毒所的所有研究都已经发表，而且他们的这些病毒样本可供审议：

> 我可以给你的另一个证据是，我们的实验室已经做了 15 年的研究，我们所有的研究工作都已经发表了。我们也有自己的基因序列资料库，我们有与病毒有关的所有工作的实验记录，这些都可供人们查阅[162]。

这又是明显错误的。武汉病毒所的病毒基因序列资源库已于 2019 年 9 月被下线，并不能"供人们查阅"。鉴于前文所述的那些未披露的冠状病毒研究和武汉病毒所内的军方活动，武汉病毒所并没有发表"所有"研究工作是很明显的。达萨克在接受《自然》杂志采访时证实了这一点："我们拥有在中国工作 15 年多所收集的数据——其中有五年由 NIH 之前一项拨款资助——这些数据尚未发表。[163]"

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[160] 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.

[161] Guli.

[162] Xin.

[163] 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.

在 2021 年 6 月的一次采访中，石正丽告诉《纽约时报》，“我的实验室从来没有做过或合作做过让病毒毒性增强的功能增益实验。[164]” 鉴于多年来发表的这些通常由石设计和牵头的研究明确试图让冠状病毒对人类更具传染性，她这么说很奇怪。在同一次采访中，石就武汉病毒所研究人员在 2019 年秋天生病的事情说了谎——“武汉病毒所没有发现上述情况。”而美国国务院 1 月 15 日发布的事实清单并非如此，而且世卫组织调查小组的一名荷兰病毒学家也证实曾有几名研究人员生病[165] 。

中国共产党的掩盖活动

根据世卫组织 2020 年 8 月的一份内部文件，PRC 在 2020 年 1 月之后对 SARS-CoV-2 的溯源几乎没有投入什么努力：

> 在与中国同行进行广泛的讨论并听取他们的情况介绍后，看起来，自 2020 年 1 月以来，在武汉周围的流行病学调查方面似乎没有采取什么行动。口头介绍的数据比在 2020 年 1 月突发事件委员会的会议上提交的数据提供了少许的更多细节。没有做任何 PowerPoint 演示，也没有共享任何文件[166]。

鉴于 PRC 在前几年投入了大量的财政资源来定位、采样、识别和测试冠状病毒，如果这次的病毒真是来源不明，几乎不投入多少努力来确定病毒来源是很奇怪的。

2020 年 2 月中旬，PRC 科学技术部发布了新的《关于加强新冠病毒高等级病毒微生物实验室生物安全管理的指导意见》。PRC 的官方消息人士强调：

> 科学技术部提到的实验室的生物安全和某些人提出的冠状病毒是从中国科学院武汉病毒研究所泄露出来的说法这两者之间没有关联[167] 。

2020 年 2 月接受《环球时报》采访的专家们表示，PRC 的实验室“对生物废料处理的重视不够”[168]。这包括将实验室材料排放到污水处理系统中[169]。鉴于上述新的指导意见是在 PRC 停

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[164] 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

[165] 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.

[166] 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

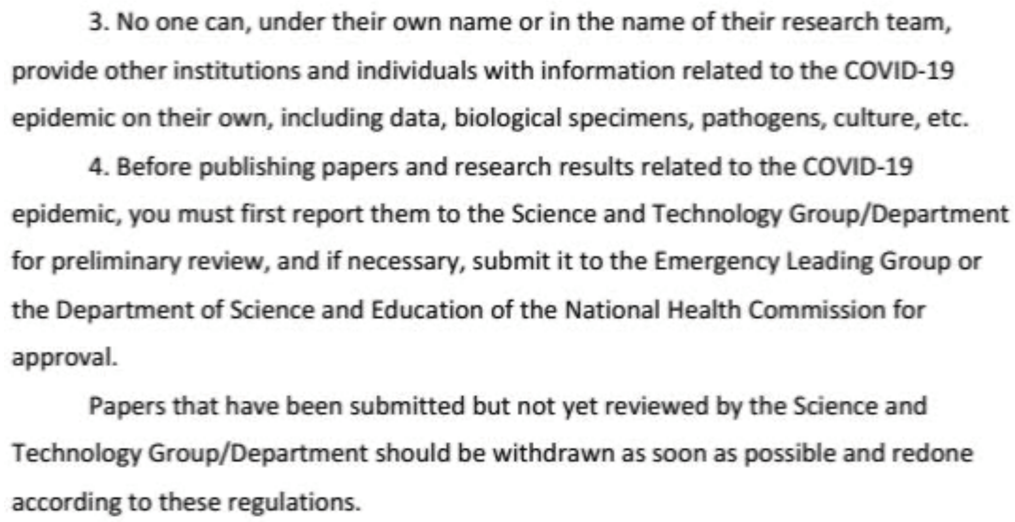
[167] Caiyu, Liu, and Leng Shumei. “Biosafety Guideline Issued to Fix Chronic Management Loopholes at Virus Labs.” *Global Times*, 16 Feb. 2020, www.globaltimes.cn/content/1179747.shtml.

[168] *Ibid*.

[169] *Ibid*.

止寻找疫情源头之后发布的，这就让人产生疑问，是什么促使 PRC 停止了溯源。

此后不久的 2020 年 2 月 25 日，中国疾病预防控制中心发布了影响到 PRC 科学家如何从事 COVID-19 相关研究的《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》。这份补充规定禁止研究人员分享数据或样本，并要求他们在进行研究或发布结果之前先获得许可。



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.

图 10：中国疾控中心 2 月 25 日发布的《规定》节选[170]

这份补充规定的完整文本已包含在本报告附录中。

2020 年 2 月 27 日，《健康时报》刊登了对宇传华的采访，他当中引用了 2 月 25 日的卫生数据。宇传华是湖北省卫生统计与信息学会副会长及武汉大学流行病与卫生统计学教授，并在 2020 年初管理一个 COVID-19 确诊病例数据库。宇传华在采访中表示，他早在 2019 年 9 月就有了 COVID-19 病例的证据：

> 宇传华教授介绍，“比如有一个 9 月 29 日发病的患者数据，数据显示患者没有进行核酸检测，临床诊断（CT 诊断）为疑似病例，患者已死亡，这个数据没有核实，也没有死亡时间，也有可能是错误的数据。”随着对这个数据库进行研究，宇传华教授发现了越来越多 12 月 8 日之前的病例数据。11 月有两个患者病例，发病时间分别是 2019 年 11 月 14 日和 11 月 21 日，12 月 8 日之前，也有五六个病例。其中

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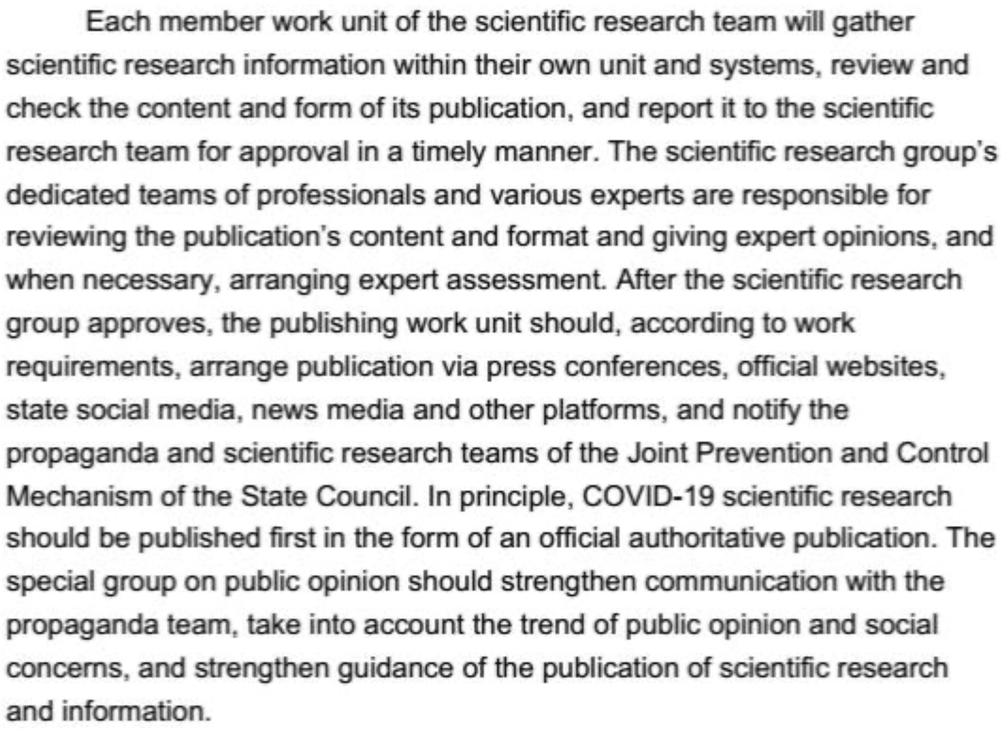
[170] Chinese Center for Disease Control and Prevention. “On the Supplementary Regulations on Strengthening the Management of Science and Technology During the Emergency Response to the Novel Coronavirus.” 25 Feb. 2020. https://www.documentcloud.org/documents/7340336-China-CDC-Sup-Regs.html

一位在 11 月底发病的患者 12 月 2 号住院并被临床诊断为肺炎[171] 。

在这个采访 2 月 27 日发表之前，宇传华联系了记者，试图撤回有关 11 月份那两名患者的信息[172]。这很可能是为了遵守中国疾控中心 2 月 25 日发布的补充条例中的封口令。

九天后，也就是 2020 年 3 月 5 日，中国国务院的应对新型冠状病毒肺炎疫情联防联控机制科研攻关组（JPCM）发布了一份机密备忘录，题为《关于规范新型冠状病毒科研管理和出版工作的通知》，美联社得到了这份文件[173]。该通知宣布，由该科研攻关组管控所有疫情相关的科研成果的发布工作，以便“统一部署” [174]。通知还要求发表研究成果的单位通知 JPCM 的宣传组，宣传组的任务是与一个舆论专班合作，结合舆情动态和“社会关切”统一协调科研成果的发布[175] 。



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.

图 11：中国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的备忘录节选

备忘录末尾警告称：“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

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[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.

[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.*

重不良社会影响的，要追究责任。[176]”该备忘录的全文已包含在本报告附录中。这些文件清楚地证明了中共努力限制 SARS-CoV-2 相关的研究，以便被发表的研究都支持有关 COVID-19 起源和出现的中共官方叙事。

在委员会少数党幕僚中期报告发布后，PRC 国有媒体中国环球电视网发布了一段旨在破坏本项调查可信度的宣传视频。题为“澄清麦考尔新冠肺炎报告中的疑惑”，这段长约 45 分钟的视频给这份报告贴上了“错误信息”的标签[177]。视频中还谈及他们所说的“病毒可能是从实验室泄露这种陈腐的旧理论”[178]，并透露石正丽就本报告接受了采访。这则视频还声称位于武汉病毒所的武汉国家生物安全四级实验室从未被陈薇将军接管[179]。如前所述，这种说法显然是不正确的。

2021 年 6 月，杰西 ·布鲁姆（Jesse Bloom）出版了题为《恢复删除的深度测序数据为 SARS-CoV-2 在武汉的早期流行提供了更多信息》的论文预印本。布鲁姆是弗雷德 · 哈钦森癌症研究中心（Fred Hutchinson Cancer Research Center）基础科学和赫伯特计算生物学项目的实验室项目负责人和副教授。布鲁姆于 2020 年 12 月初恢复了从武汉患者身上收集的多个被删除的病毒序列。这些序列最初是由武汉的研究人员上传到 NIH 的“序列读取档案”（Sequence Read Archive，SRA）数据库，但后来又应他们的要求被删除了。奇怪的是，这些样本与 SARS-CoV-2 的祖先蝙蝠冠状病毒的差异更大——“最早的 SARSCoV-2 基因序列是去年 12 月在武汉收集的，但这些基因序列相比今年 1 月从中国其他地方甚至其他国家收集的病毒基因序列，与 RaTG13 相差更远。[180]”布鲁姆总结道（强调为报告作者所加）：

> **这个信息丰富的数据集被删除这一事实所暗示的含义超越了从被恢复的病毒基因序列中直接窥见的含义。**对于任何想要了解病毒传播的人来说，早期患病的武汉门诊患者身上的病毒样本是一座金矿。连我对 13 个部分基因序列的分析都很能说明问题，那么对全部 34 个样本进行完整测序显然比删除部分基因序列后的测序能提供更多的科学信息。**数据集的删除没有明显的科学原因：**这当中的病毒基因序列与汪明等人（2020a, b）所描述的病毒样本的基因序列是一致的，而这篇论文并没有任何更正，论文也称该研究被批准使用人类受试者，而且测序并没显示质粒污染或样本间污染的证据 … 尽管测序数据在谷歌云端平台上（如

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[176] *Ibid.*
[177] “The Point: Clearing up Confusion in the McCaul Report On Covid-19.” *CCTV News*, 25 July 2020, www.youtube.com/watch?v=n5qYogMTZOw.
[178] *Ibid.*
[179] *Ibid.*
[180] 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

> 上所述），而且突变信息列在了汪明等人发表在《Small》期刊上的同篇论文的表格中（2020b），**从 SRA 数据库中删除数据的实际后果就是没有人知道这些病毒基因序列的存在。**尤其是考虑到那些让实验室销毁早期样本的指令（庄屏卉，2020）和 COVID-19 相关研究的出版需获批准的多条命令（中国疾控中心，2020；姜大翼等人，2020a），**上述情况似乎表明，没有做出全心全意地努力来最大限度地获取武汉疫情早期有关病毒序列的信息[181]。**

PRC 混淆 COVID-19 起源的努力并不限于销毁病毒样本和对医生进行封口，它还持续上演了一场虚假信息攻势。正如我们在上一份报告中谈到的，PRC 外交部官员赵立坚在推特上分享了一篇文章，当中声称病毒是由美军带到中国的[182]。这篇文章来自全球研究（globalresearch.ca）网站，这是一个推动亲普京宣传内容的网站，而且据报与俄罗斯国家媒体有关联[183]。他的推文还被中国驻南非大使馆转推以扩大影响[184] 。

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[181] *Ibid*.

[182] 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

[183] 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/.

[184] 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/8cRxkSZB3z.” *Twitter*, 16 Mar. 2020, www.twitter.com/ChineseEmbSA/status/1239453193689587712

Lijian Zhao 赵立坚 @zlj517 · Mar 12, 2020

China government official

2/2 CDC was caught on the spot. When did patient zero begin in US? How many people are infected? What are the names of the hospitals? It might be US army who brought the epidemic to Wuhan. Be transparent! Make public your data! US owe us an explanation!

图 12： PRC 外交部发言人推特上暗示 COVID-19 通过世界军人运动会进入武汉

> 赵立坚的推文译文：美国疾控中心主任被抓了个现行。零号病人是什么时候在美国出现的？有多少人被感染？医院的名字是什么？可能是美军把疫情带到了武汉。美国要透明！要公开数据！美国欠我们一个解释！

为进一步推动这一说法，中共控制的媒体称美国陆军预备役成员玛特捷 · 贝纳西（Maatje Benassi）是“零号病人”。贝纳西参加了世界军人运动会，但并没因此生病，然而她仍多次成为谎言骚扰的目标。宣扬上述说法的视频被上传到了微信、微博和西瓜视频这些位于 PRC 的网络平台上。在赵立坚发推称是美军把病毒带到武汉的两周后，《环球时报》放大了这一说法，敦促美国政府公布运动员的健康信息，并重复了关于贝纳西的说法[185] 。

和本补充报告中所示意的一样，赵立坚的另一条推文其实也示意大流行病确实是从 2019

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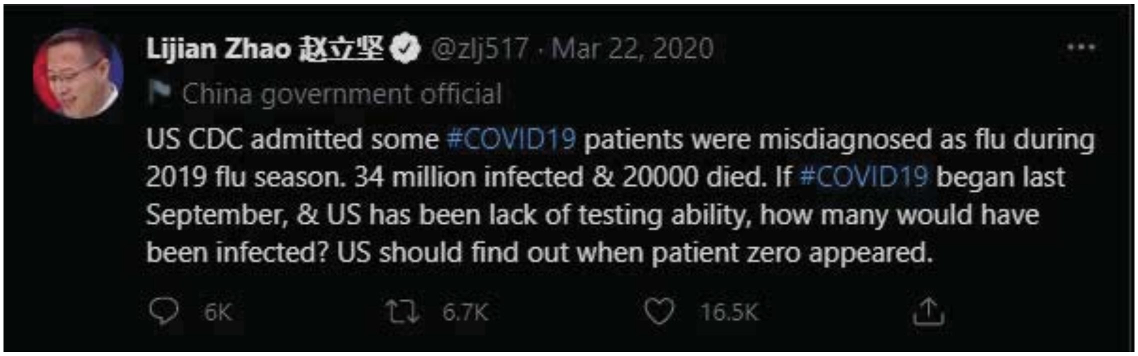
[185] Shumei, Leng, and Wan Lin. “US Urged to Release Health Info of Military Athletes Who Came to Wuhan in October 2019.” *Global Times*, 25 Mar. 2020, www.globaltimes.cn/content/1183658.shtml.

年 9 月份开始的，只不过是始于美国[186]。



Lijian Zhao 赵立坚 @zlj517 · Mar 22, 2020

China government official

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.

图 13：PRC 外交部发言人在推特上表示，COVID-19 大流行病始于 2019 年 9 月

> 赵立坚的推文译文：美国疾控中心（CDC）承认，2019 年流感季期间，有 19 名患者被误诊为流感。3,400 万人感染，20,000 人死亡。如果新冠肺炎从去年 9 月就已爆发，而美国一直缺乏检测能力，有多少人会被感染？美国应该找出零号病人是什么时候出现的。

需要指出的是，这条推文是在 2020 年 3 月发送的——前文提到的暗示大流行病始于 2019 年 9 月的那项哈佛大学的研究是在 2020 年下半年才发表的。赵立坚的上述指控是在他重复是美军将 COVID-19 带到武汉这一说法的 10 天之后发布的。如果中共那时意识到了调查将显示出现类似 COVID-19 症状的患者就诊人数在 2019 年 9 月、10 月和 11 月就已上升，这很可能是他们会为掩盖这些疾病的源头而采取的行动。

牵涉彼得·达萨克的武汉病毒所虚假信息攻势

如我们前文所解释的，彼得·达萨克深度参与了在武汉病毒所进行的功能增益研究，其中包括在美国宣布暂停资助功能增益研究的情况下以二级生物安全水平进行的研究。此外，我们还发现了强有力的证据，似乎表明彼得·达萨克是中共虚假信息攻势的公开面孔，该虚假信息攻势旨在压制有关潜在实验室泄漏事故的公开讨论。一家第三方组织获得的电子邮件显示，达萨克曾组织发表一份于 2020 年 2 月 19 日刊登在《柳叶刀》（The Lancet）上的声明，“谴责暗示 COVID-19 没有自然来源的阴谋论”[187]。声明接着表示，“阴谋论只会制造恐慌、谣言和偏

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[186] 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.

[187] 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/

见，破坏我们在对抗这个病毒时的全球合作。” 这些电子邮件显示了达萨克为组织一大批科学家在他亲自起草的一份声明上签名所做的努力。达萨克在其中一封电子邮件的结尾宣称，“请注意，这份声明上不会有生态健康联盟的标志，也不会被识别为来自任何一个组织或个人，声明的用意是让大家作为一个社区来支持我们的同事们。[188]”

这些从达萨克的生态健康联盟电邮账户发出的电子邮件还显示，这份声明是达萨克应之前曾与他共事过的武汉病毒所研究人员的请求而起草的（强调为报告作者所加）：

> 你应当知道，阴谋论者非常活跃，用一些令人极其不愉快的网页攻击我们在中国的合作者，一些人现在甚至收到了对他们和他们家人的死亡威胁。**他们请求我们给予他们任何我们能够给予的支持[189]。**

在另一封电子邮件中，达萨克表示，王林发（王没有签署声明）敦促达萨克和巴里克不要签署声明，实际上是掩盖他们的参与。如前所述，王林发与达萨克、石正丽和胡犇合著多篇论文，其他几封关于这份声明的电子邮件中也都抄送了他。王现为新加坡杜克-新加坡国立大学医学院新发传染病项目主任兼教授。他是中国公民，在 PRC 的上海华东师范大学获得生物化学学士学位[190]，之后在美国加州大学戴维斯分校获得分子生物学博士学位。2020 年 1 月，王在武汉的武汉病毒所拜访与他共事的研究人员。鉴于他之前发表的那些论文，他拜访的人当中很可能包括胡犇和石正丽，王和他俩一起合著了几十篇论文。他于 1 月 18 日离开武汉，不到三个星期后，达萨克就对外传阅了他投稿给《柳叶刀》的声明的草稿。王林发被包括在达萨克征集共同签名者的电子邮件收件人中[191] 。

在电子邮件中，达萨克说（强调为报告作者所加）：

> 我昨晚和林发谈了我们发的那个声明。他认为，我也同意，**你、我和他不应该签署这个声明，这样这个声明和我们保持一定距离**，因此不会起反作用…**然后，我们会以一种不会将它与我们的合作联系起来的方式发布它，这样我们可以让独立的声音最大化[192]。**

这些电子邮件的副本已包含在本报告附录中。

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[188] 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

[189] 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

[190] Wang, Linfa. “Curicullum Vitae.” https://globalhealth.duke.edu/sites/default/files/cv/cv-linfa_wang-jan2017.pdf

[191] Daszak (6 Feb.)

[192] 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

推动达萨克和巴里克这两名武汉病毒所最重要的美国合作者掩藏他们为组织这份声明所做努力的同时，王林发当时还担任着武汉病毒研究所新发传染病中心科学顾问委员会主任一职，石正丽是该中心的负责人[193]。

巴里克表示同意，并选择不签字。目前尚不清楚为什么达萨克最终改变了主意，签署了这份声明。虽然达萨克是《柳叶刀》这份声明的组织者，但被列为通讯作者的却是查尔斯 · 卡利舍（Charles Calisher）。奇怪的是，所列出来的联系卡利舍的电子邮件地址是个通用地址（COVID19Statement@gmail.com[194]），该邮件地址看上去像是专为这一声明所创建的，这不是发表科学文章的寻常做法。

2020 年 2 月发表在《柳叶刀》上的声明宣称，作者们"没有利益冲突"，尽管代表武汉病毒所研究人员组织发表这份声明的达萨克也资助并参与了与武汉病毒所研究人员的项目合作。2020 年 6 月，在公众对达萨克与武汉病毒所之间的联系表示关注的背景下，"《柳叶刀》邀请该声明的 27 名作者重新评估他们间的利益冲突"[195]。**达萨克提交了一份经过修改的披露声明，尽管他在这份披露声明中对自己与 PRC 研究人员的合作予以透明披露，但他没有提到武汉病毒所，也没有披露他是应 PRC 研究人员的要求而起草了这份声明[196]。**

这些电子邮件还显示，达萨克帮助编辑了美国国家科学院、国家工程院、国家医学院三名院长于 2020 年 2 月 6 日发给白宫科学和技术政策办公室的一封有关 COVID-19 起源的信[197]。尽管未被包括在这封信的最终成稿中，但达萨克与其他被咨询的专家们所编辑的最后一版草稿中有一句话说，"专家们的初步观点是，现有的基因组数据与自然进化一致，目前没有证据表明该病毒被经过设计以便在人群中能更快速地传播"[198]。达萨克当时其实还推动使用更广义的措辞，因为他认为"这个有点太具体了，因为还有其他阴谋论存在"[199]。目前尚不清楚为什么美国三院的院长们在这封信递给白宫之前移除了上面这句话。达萨克特地寻求在这封信发布之

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[193] Wang.

[194] Calisher.

[195] 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

[196] *Ibid.*

[197] 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

[198] 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

[199] *Ibid.*

后再发表他的《柳叶刀》声明，这样他在声明中就引用这封信作为病毒自然起源的证据，但他没有在声明中透露他本人帮助编辑了这封信。包括弗契医生在内的政府高级官员当时极有可能看到了美国国家科学院、国家工程院和国家医学院的这封信以及发表在《柳叶刀》上的声明，从而形成了他们的观点，并扼杀了美国联邦政府内部关于 COVID-19 起源的辩论。

在发出最初这封信的 16 个月后，美国国家科学院、国家工程院和国家医学院的院长们于 2021 年 6 月 15 日发表了一份最新声明，题为《美国三院院长敦促，让科学证据来确定 SARS-CoV-2 的起源》[200]。这份经过更新的声明承认，大流行病的源头在某些情况下也可能是实验室泄漏造成的。声明说：

> 然而，围绕病毒起源的不同理论，错误信息、未经证实的宣称和对科学家的人身攻击是不可接受的，这正在公众间散播困惑，并有可能破坏公众对科学和科学家的信任，包括那些仍在引领控制大流行病相关努力的科学家们…就 SARS-CoV-2 而言，根据我们目前的理解，有多种可信度各不相同的设想能从原则上解释其起源。**这些各种各样的设想从人畜共患病毒的自然溢出（即病毒从非人类动物传播到人类）到与实验室工作相关的情况，不一而足[201]。**

与致白宫的那封信不同，这份声明没有说明，在起草过程中如果咨询了任何外部专家，这些专家都是谁。

耐人寻味的是，三个星期后，在 2021 年 7 月，达萨克和他的同事们发布了 2020 年 2 月声明的更新版本，标题非常相似：《科学而非猜测对确定 SARS-CoV-2 如何感染人类至关重要》。最初那份声明的 27 名作者中有 24 人签署了这份第二版声明，声明内容相比这些作者的最初立场作出了重大退让（强调为报告作者所加）：

> **我们最初那份声明的第二个目的是表达我们的工作观点，即 SARS-CoV-2 最有可能起源于自然界而非实验室，**这是基于对新病毒的早期基因分析和从以往的新兴传染病——包括导致普通感冒的冠状病毒以及最初的 SARS-CoV 和 MERS-CoV——中得到的确凿证据。**然而，观点既非数据也非结论。**必须通过以科学方法获得的证据来为我们的理解提供信息，并作为解读现有信息的基

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[200] McNutt, Marcia, et al. “Let Scientific Evidence Determine Origin of SARS-CoV-2, Urge Presidents of the National Academies.” *The National Academies of Sciences, Engineering, and Medicine*, 15 June 2021, www.nationalacademies.org/news/2021/06/let-scientific-evidence-determine-origin-of-sars-cov-2-urge-presidents-of-the-national-academies.

[201] *Ibid.*

础[202]。

这与达萨克在其第一份几乎像是宣传材料的声明所说的话非常不同，当初是“谴责暗示COVID-19 没有自然来源的阴谋论”[203]。尽管态度有所软化，但这些作者继续指责那些寻求调查实验室泄漏假说的人，称这些人是 PRC 不愿配合国际调查的根源：

> 指控和猜测无济于事，因为它们不利于获取信息和客观评估从蝙蝠病毒到人类病原体的演变途径，而这些信息可能有助于防范未来的大流行病。相互指责没有、也不会鼓励国际合作与协作[204]。

他们的第一份声明引用了美国国家科学院、国家工程院和国家医学院院长们的信（达萨克帮助编辑了该信），第二份声明则引用了他们发声明的几周前刚发布的美国三院院长声明。这就引出了一个问题：达萨克或声明的任何一位作者是否协助起草或编辑了美国三院院长们在 6 月 15 日发布的这封信。

还应该指出的是，达萨克是2021 早期派遣的世卫组织-中国联合考察团中唯一的美国代表。美国提出了一份供考虑的专家名单，但没有一人被选中。达萨克不在这份名单上，但仍被中共选中并批准[205]。世卫组织于 2021 年 3 月发布的 COVID-19 起源报告的附件中，有数条被达萨克重复过的中共虚假信息。这当中包括一项对“阴谋论”的讨论[206]，“阴谋论”包括实验室泄漏假说和 SARS-CoV-2 可能具有转基因属性的相关疑问。讨论中还把武汉病毒所病毒数据库的下线说成是“有关数据丢失的谣言”[207]——达萨克在接受英国皇家国际事务研究所（Chatham House）采访时也使用了类似的措辞——尽管该数据库仍处于离线状态[208]。委员会少数党幕僚无法确定达萨克是否协助起草或编辑了世卫组织的这份报告。

在 COVID-19 的起源问题上，彼得·达萨克还采取了更多令人关切的行动，其中包括莫名其妙地谎报生态健康联盟在 SARS-CoV-2 出现后的几个月里所做的工作。在 NIH 暂停了他用于资助武汉病毒所研究的拨款后，达萨克在 2020 年 8 月 21 日接受《自然》杂志的采访，他声称“这笔拨款没有被用来资助 SARS-CoV-2 研究。我们的组织还没有实际上发表任何 SARS-CoV-2 相关的数据”[209]。但四天后，《自然-通讯》（Nature Communications）就发表了《蝙蝠冠

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[202] 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/
[203] Calisher (Feb.)
[204] Calisher (July)
[205] Testimony from former senior U.S. official received by Committee Minority Staff.
[206] Joint Report - ANNEXES.
[207] *Ibid.*
[208] *Ibid.*
[209] Subbaraman.

状病毒在中国的起源和跨物种传播》[210]。达萨克、石正丽、胡犇和王林发全部被列为作者，石正丽和达萨克都被列为通讯作者。这篇论文的预印本是在2020年5月31日上传的，比达萨克接受《自然》采访早了近三个月。这篇论文中包括了一项“似乎表明SARS-CoV-2很可能起源于菊头蝠属蝙蝠”的系统发育分析[211]。达萨克、石正丽、三名与生态健康联盟有关的研究人员与王林发被列出的贡献是设计研究、展开实地考察以及建立样本收集和测试规程。

这项研究的经费来自NIH（拨款项目编号：R01AI110964）、USAID“预测”项目（合作协议号GUN-A-OO-09-00010-00）以及石正丽负责的中国科学院战略性先导科技专项（项目编号：XDB29010101）。该研究还获得了中国国家自然科学基金（项目编号：31770175和31830096）的资助。论文中指出：

> 生态健康联盟的员工在2020年4月24日之后开展的所有工作都得到了塞缪尔·弗里曼慈善信托基金（Samuel Freeman Charitable Trust）、帕梅拉·泰（Pamela Thye）、华莱士基金会（Wallace Fund）和一匿名捐赠者转交施瓦布慈善基金（Schwab Charitable）的慷慨资助[212]。

NIH是在4月24日终止了“了解蝙蝠冠状病毒出现风险”项目，该项目由编号为R01AI110964的科研基金资助[213]，论文中也将该笔基金列为项目资助[214]。也就是说，这笔达萨克告诉《自然》杂志并没被用于资助SARS-CoV-2相关研究工作的科研基金在一篇介绍SARS-CoV-2相关研究的论文中被列为资助来源。

此前，彼得·达萨克和另两名与生态健康联盟有关的研究人员在2020年3月发表了《预防类似2019-nCoV的未来流行病的策略》[215]。虽然这篇论文中没有进行实验室实验，但它仍讨论了SARS-CoV-2，并声称“野生动物贸易显然在（该病毒的）出现中起了作用”。这篇论文也由同一笔NIH科研基金（编号：R01AI110964）和与美国国际发展署“预测”项目的合作协议资助。

2020年12月，达萨克在推特上表示，上述的NIH科研基金的暂停直接阻止了他从武汉病毒所获取样本。如果这笔拨款并非用来资助生态健康联盟在SARS-CoV-2方面的工作，那这笔拨款的暂停与他们无法获取SARS-CoV-2样本有什么关系？为什么达萨克在声称NIH这笔科

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[210] 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/

[211] *Ibid.*

[212] *Ibid.*

[213] 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

[214] Latinne

[215] 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/

研资金“没有被用来资助 SARS-CoV-2 研究[216]”的同时，他自己发表的研究和自己这些说法都表明，这笔钱就是用来资助 SARS-CoV-2 研究的?

达萨克的行为中另一个令人关切的例子来自于 2021 年 3 月 10 日英国皇家国际事务研究所的一次讨论。对于武汉病毒所关闭病毒基因序列和病毒样本数据库以及世卫组织调查小组是否提了要求查看那些数据的问题，彼得·达萨克回应说（强调为报告作者所加）：

> 当我们在武汉病毒研究所的时候，我在双方都在场的整个团队面前问了有关**所谓的失踪数据库**的问题。石正丽告诉我们，当时数据库一直遭黑客的攻击尝试，约有 3000 次，于是他们关闭了这个基于 EXCEL 电子表格的数据库。绝对合理。**我们没有要求查看数据，**如你所知，这当中的很多工作是与生态健康联盟一起做的工作，我也是那些数据的一部分，**我们基本上知道那些数据库里有什么。**我分享了，**我向双方做了一次演讲，介绍我们与武汉病毒研究所一起所做的工作，并解释了其中的内容。在那些数据库中，没有证据表明有比 RaTG13 更接近 SARS-CoV-2 的病毒。就这么简单[217]。**

这是一个令人震惊的说法，因为那个数据库包含有 2.2 万多个样本，而且在 2019 年 9 月之后，武汉病毒所外的任何人都无法访问。SARS-CoV-2 的基因组序列在 2020 年 1 月公布后，就物理手段而言，达萨克不可能通过远程访问数据库将 SARS-CoV-2 的基因组序列与数据库中的所以样本进行比较。**如果做不到，鉴于在 2020 年 2 月发表论文前武汉病毒所以外的人都不知道 RaTG13 与 SARS-CoV-2 密切相关，那达萨克怎么能在无法获取数据的情况下声称自己知道在 2.2 万多个病毒样本中没有一个更接近的匹配呢？这就产生了有关他是否拥有数据库副本的疑问。**

在武汉病毒所如何交出 RaTG13 的问题上，达萨克往最好里说也是不正确的。在 2020 年 4 月 21 日接受《纽约时报》（The New York Times）采访时，他表示（强调为报告作者所加）：

> 2013 年，我们在中国的一只蝙蝠身上发现了与目前 SARS-CoV-2 最接近的近亲。**我们对病毒的一小部分基因组进行了测序，之后就将其放入了冷冻柜；**因为它看起来不像 SARS，我们就以为它成为新发疾病的风险较低。有全球病毒组项目的存在，我们本可以对这个病毒的整个基因组进行测序，然后发现它能与人类细胞结合，从而对之提高风险等级。也许我们当时为 SARS 设计疫苗的时候，本可以也让那些疫苗能够针对这个病毒，那么一旦它成了新发疾病，

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[216] Subbaraman.

[217] “Sustaining the Response: Inside the WHO-China Mission.” *Chatham House*, 10 March 2021, https://www.youtube.com/watch?v=GMlIEF58944&t=3249s.

> 我们本可以在冷冻柜里就有现成的东西可用[218]。

这当然不对——武汉病毒所的研究人员在2018年就对RaTG13的基因组进行完全测序[219]。要么就是达萨克知道这不是真的，并对《纽约时报》撒了谎，要么就是他被蒙在鼓里，不知道武汉病毒所正在进行的工作。如果是后面这种情况，那么达萨克在2021年3月声称自己知道武汉病毒所那个被下线的数据库中的一切，就更令人生疑了。

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[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.

[219] Zhou, (Nov. 2020).

V. 假说：引发大流行病的实验室泄漏

在审议了本补充报告中所讨论过的证据之后，委员会少数党幕僚总结出下述假说，该假说能够合理体现在 COVID-19 大流行病最初几个月可能发生的情况。

在 SARS-CoV-2 被意外释放的几个月前，武汉国家生物安全实验室的危废处理系统正在维修。其中一个设施的中央空调系统需要翻修，可能因此导致空气循环低于理想状态，使病毒颗粒在空气中悬浮更长时间。在 2019 年 7 月 4 日中国科学技术部发出通知，直到 9 月 30 日截止时间前，武汉病毒所的研究人员正在审核一个资助项目所采集到的样本，这个项目的编号为 2013FY113500，负责人是武汉国家生物安全实验室主任袁志明[220]。这个相同的拨款项目还资助了：

- 2013 年发表的论文，该论文报告在昆明山洞取样后首次分离出一株活体 SARS 样冠状病毒[221]。
- 2014 年发表的论文，该论文是从广西省和云南省 39 种小型哺乳动物身上采集 986 个样本后的结果。
- 2016 年发表的论文，该论文表示成功分离出第二株活体冠状病毒。
- 2017 年发表的论文，该论文表示分离出第三株活体 SARS 样冠状病毒，而且武汉病毒所研究人员创造了八个改变了刺突蛋白的嵌合冠状病毒。

胡犇、石正丽和武汉病毒所其他人在二级生物安全水平和三级生物安全水平条件下，积极地在表达 hACE2 的小鼠和果子狸身上测试新的并且进行过基因操作的冠状病毒，包括从云南矿工曾经患病的洞穴中采集到的病毒。有缺陷的危险废物处理系统和中央空调系统会导致实验室一名（或多名）雇员感染 SARS-CoV-2 的可能性增加，因为病毒颗粒更可能会在空气中停留更长时间。如前面所讨论的，武汉病毒所为雇员提供班车，接送他们往返于武汉病毒所位于武昌的老楼附近和武汉国家生物安全实验室。受感染的雇员（不管是从武汉国家生物安全实验室还是从武汉病毒所总部）随后很可能通过地铁穿越武汉市中心，传播了病毒。

9 月初，已经清楚的是发生了一次意外释放。最初，由于不清楚 SARS-CoV-2 会人传人，也不清楚无症状人群会造成大量新增病例，对此的担忧不高。由于此前病毒从实验室被意外释放只导致少数人感染，担忧更加缓解了。但是还是下达了采取应对措施的命令。当地时间 9 月 12 日零点，距离武汉病毒所一英里不到的武汉大学发出一则要求在 9 月底进行实验室安全检

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[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.

查的通知[222]。武汉大学医学院配备有生物安全三级实验室，具有动物实验资质[223]。很可能官员也向该区域其它实验室下发了类似命令。两三个小时之后，武汉病毒所病毒基因序列数据库被撤下线[224]。大概 17 个小时之后，在当地时间晚 7:09，武汉病毒所发布了一个武汉国家生物安全实验室“保安服务”采购公告。采购服务包括门防、保安、视频监控、安全巡逻和处理“外来人员来访登记和接待”的人员[225]。预算金额超过 120 万美元[226]。

为了不让国家丢脸，仍然决定继续召开 2019 年世界军人运动会。观众不允许入场观看比赛，但是国际运动员和 23.6 万名志愿者中的一些人被感染，使病毒在城市扩散。数十名运动员患病并伴有症状。由于人感染 COVID-19 后可能不出现症状，不知道有多少运动员和志愿者虽被感染但因无症状而不知道自己感染了。

运动员们 10 月底返回自己国家，带着 SARS-CoV-2 去了世界各地。正如 2002 年的 SARS 疫情一样[227]，中共试图掩盖这场疫情，浪费了本可以用来防止全球大流行病发生的宝贵时间。等到全球对病毒在武汉的传播感到警惕之时，病毒已经开始在世界各地扩散了。

12 月，当病例开始让当地医院超负荷运转，想要掩盖疫情已经变得不可能了。2019 年末的某个时间，陈薇少将被调去接管武汉国家生物安全实验室的生物安全四级实验室，并领导响应工作。中国疾控中心的武汉分部对 COVID-19 病例的定义只包含去过华南海鲜市场的人，意思就是只有与这个市场有关联的人才被认定为感染 COVID-19。这进一步遮掩了病毒的真正起源。

与武汉病毒所有联系并与石正丽、胡犇和达萨克合作研究冠状病毒基因改造的科学家王林发 2020 年 1 月初在武汉。他在武汉时访问了武汉病毒所，可能也见了石正丽、胡犇和其他人。在他访问之后到 2 月 6 日前的这段时间里，武汉病毒所研究人员请求达萨克筹组一项公开声明，压制有关实验室是 SARS-CoV-2 源头的讨论。1 月 20 日，武汉病毒所提交了一篇文章，这篇文章在 2020 年 2 月发表，文中 ID4991 被重新命名为 RaTG13，文章中有关病毒基因序列何

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[222] “Notice on the implementation of laboratory safety inspections in 2019.” *Wuhan University*, http://simlab.whu.edu.cn/info/1107/1018.htm

[223] “About Wuhan University School of Medicine (WUSM).” *Wuhan University School of Medicine*, 23 Apr. 2013, https://wsm70.whu.edu.cn/English_Site/About.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/jzxcs/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.

时获得的信息也是不实的。

2 月 6 日凌晨 12: 43，达萨克给王林发、巴里克和其他人发了声明草稿，让他们加入联署。当天晚上在达萨克睡觉之前，王林发给他打了电话，要求不要让他、达萨克和巴里克在声明上署名，以便遮掩他们与武汉病毒所之间的关联。巴里克表示同意，他和王林发都没有在声明上签名。声明在 2 月 19 日发表，宣称有关实验室泄漏的讨论是阴谋论，并压制有关 COVID-19 起源的公开辩论。

VI. 建议

在先前发布的报告中，委员会少数党幕僚为美国应对 COVID-19 采取的行动提出了几项建议，包括寻求在世卫组织建立新的，寻求世卫组织把台湾重新接纳为观察员，与志同道合的世卫组织成员国对 COVID-19 初期阶段的有关问题展开国际调查，并支持对《国际卫生条例》作出具体改革。这些建议仍然具有现实意义。

本委员会、全体国会和行政分支在这个问题上还能够采取更多的步骤。有鉴于先前详细指出的不一致之处和中共在有关实验室泄露可能性问题上的虚假信息活动，必须传唤彼得 · 达萨克作为本项调查的重要证人前来众议院外交委员会和参议院外交委员会作证。委员会少数党幕僚在多次场合曾试图与达萨克联系并给出了一份与本报告有关的问题清单。他从未回复。与此形成对照的是，拉尔夫 · 巴里克对委员会少数党幕僚提出的问题清单作出了答复。我们感谢他的协助，并相信他的证词将是有益的。达萨克和巴里克应当提供专家证词，所涉及的问题包括但不限于：

- 在 2018 年和 2019 年，武汉病毒所对冠状病毒的基因操作及其针对人类免疫系统的测试到了什么程度？
- 是谁要求在《柳叶刀》发布支持声明？
- 这一要求是否包括把讨论实验室泄露的可能性贴上阴谋论的标签？
- 王林发在 2020 年 2 月 6 日清晨给达萨克打的电话的性质和内容是什么？
- 在有关 2020 年被终止的国立卫生研究院（NIH）拨款的问题上，达萨克为什么作出自相抵触而且显然不实的陈述？
- 如果 RaTG13 在 2019 年 9 月被撤下线，达萨克如何能够证实它是在武汉病毒所数据库中与 SARS-CoV-2 最为接近的匹配？
- 达萨克是否有被撤下线的武汉病毒所数据库的副本？
- 是谁把达萨克的名字纳入了世卫组织-中国联合考察组？
- 达萨克是否知道，通过为收集武汉病毒所后来进行实验的病毒支付经费，他所提供的资金直接支持了功能增益研究，尽管联邦政府要求从 2014 年到 2017 年暂停这类研究？
- 他们是否相信 SARS-CoV-2 有可能是受过基因操作的病毒，并通过类似于他的“无痕”方式制造从而未留下任何操作证据？

作为对大流行病的回应，委员会少数党幕僚还建议国会寻求立法，落实下列限制和制裁措施：

- 制定禁令，不得从事和资助任何包括功能增益研究在内的工作，直到制定出国际性并

且具有法律约束力的标准之后，而且必须是在该标准以可证实的方式得到遵守的条件下，该禁令方可取消。

- 授权并资助一个目的在于大流行病预防、警告和早期发现的公-私合作伙伴。
- 制裁中国科学院及相关实体。
- 将武汉病毒研究所及其领导层列入“特别被指定国民和被封锁人员名单”，并实施额外和恰当的次级制裁。
- 扩展法律和行政制裁机制，以遏制对两用技术的滥用。
- 授权对未能确保恰当安全水平和信息分享的学术、政府与军事生物研究设施实施新的制裁。
- 出于可能吊销的目的，对在美国从事生物、化学或相关研究的中国公民的所有 H-2B 签证进行审核。
- 出于可能吊销的目的，对在美国学术机构学习的中国公民的所有学生签证进行审核。

此外，行政分支应当展开国际谈判，以便为实验室生物安全建立一个具有法律约束力的国际标准，包括由一个与国际原子能机构类似的国际组织予以认证和检查。

鼓励面临经济萎缩、按照 PRC“一带一路”倡议而签署协议的外国政府审视双边协议的条款，特别是促进中国政府获取这个国家所特有的自然资源、矿产、植物和动物的联合科学与学术研究的协议或谅解备忘录。有些协议推动实行将所有地方、市或省级控制权中央集权化的治理结构，这会增加建立对本国公民进行操弄、误报、误导和哄骗的国家治理结构的风险。

建议考虑与 PRC 签署双边协议的外国政府意识到，基于本报告所包含的信息，PRC 在无视现有安全程序的情况下进行科学研究，其方式与国际安全标准不符，并且没有充分评估科学研究有可能对环境、试验对象或人类所构成的风险。本委员会少数党幕僚建议避免签署这类协议。

VII. 结论

情报界按照拜登总统的命令对 COVID-19 起源所进行的 90 天审议报告定于 2021 年 8 月 24 日之前完成。虽然是基于开源信息，但委员会少数党幕僚希望，在资深成员迈克尔 · T · 麦考尔指示下制定的本补充报告所包含的汇总和分析将帮助为有关 SARS-CoV-2 源自实验室意外泄露的可能性的公开辩论提供信息。至关重要的是，围绕武汉病毒研究所的公开讨论必须是透明、诚实和详尽的。

委员会少数党幕僚的意见是：基于现有的优势信息、有文献可查的混淆、隐藏和销毁证据的努力以及缺乏与此相反的实际证据，SARS-CoV-2 是由武汉病毒研究所在 2019 年 9 月 12 日之前的某个时候意外释放的。该病毒有可能是天然的，也有可能是基因操作的结果，有可能是在 2012 年至 2015 年期间在 PRC 云南省的已被确认的洞穴收集的。病毒被释放是由于糟糕的实验室安全标准和操作，在包括二级生物安全水平在内的并不充足的生物安全水平下从事危险和不当的功能增益研究使得问题更加严重。该病毒随后在世界军人运动会之前几个星期在武汉市中心扩散，很可能是通过武汉地铁。这场运动会成为国际媒介，把病毒扩散到世界各个大陆。

本报告指出的各方有责任对本报告提出的问题作出回应并尽快加以澄清并提供任何新的或额外的证据。委员会少数党幕僚一如既往地做好了接收支持或反驳本报告的证据或证词的准备。在中国共产党揭开其自行盖上的保密面纱，解释其有关大流行病初期的谎言并允许查阅武汉病毒所的档案和样本数据库之前，有关 SARS-CoV-2 和 COVID-19 大流行病起源的问题将挥之不去。在那一天到来之前，美国和世界各地志同道合的国家有责任确保必要的追责和改革，以防止中共的渎职行为酿成 21 世纪的第三场大流行病。

VIII.　附录

武汉病毒研究所实验室泄露与 COVID-19 大流行病爆发时间线

2012 年 4 月：六名在 PRC 云南省位于一处洞穴内的铜矿工作的矿工患病。年龄在 30 岁到 63 岁之间的这些矿工被送往昆明一个医院时有持续的咳嗽、发烧、头痛、胸痛和呼吸困难。六人中有三人死亡。

2012 年末—2015 年：武汉病毒研究所的研究人员在这个洞穴中搜集蝙蝠的样本。

2015 年—2017 年：石正丽、胡犇、彼得 · 达萨克和王林发联合发表分离出新冠状病毒的研究。他们开展了功能增益研究，将新的和经过基因操作的冠状病毒在表达人类免疫系统的小鼠和其它动物身上实验。他们有时与拉尔夫 · 巴里克合作。

2018 年—2019 年：石正丽、胡犇和武汉病毒所其他研究人员让表达人类免疫系统的转基因小鼠和果子狸感染未发布的新的而且经过基因改造的冠状病毒。

2019 年 7 月 4 日：PRC 科技部下令审查几个项目资助，包括编号为 2013FY113500 的资助项目。这个项目为在云南省收集数百个冠状病毒和蝙蝠样本提供资金。

2019 年 7 月 16 日：武汉病毒所发布武汉国家生物安全实验室危废处理系统改造工程招标公告。招标结束日期为 7 月 31 日。

2019 年 8 月末/9 月初：一名或多名研究人员意外感染 SARS-CoV-2。该病毒或者是从云南洞穴中收集而来的，或者是武汉病毒所功能增益研究的结果。这些研究人员乘坐地铁在武汉市中心出行，将病毒扩散。

2019 年 9 月 12 日：当地时间 12:00am，武汉大学发布一份声明，宣布进行实验室检查。2:00am 到 3:00am 间，武汉病毒所的病毒基因序列和样本数据库被撤下线。7:09pm，武汉病毒所发布武汉国家生物安全实验室保安服务采购项目招标公告。

2019 年 9 月—10 月：武汉病毒所总部以及武汉国家生物安全实验室班车站点附近医院的车流量稳步增加，直至到达两年半来的最高水平。百度上与 COVID-19 症状有关词条的搜索量也相应增加。

2019 年 10 月 18 日—27 日：世界军人运动会在武汉召开，观众人数为零。国际运动员描述说这个城市是一座鬼城，并目睹武汉周围设有军事路障。数十名运动员病得很厉害。

2019 年 10 月末—11 月初：国际运动员返家，带着 SARS-CoV-2 前往世界各地。

2019 年 11 月 21 日：意大利米兰的一名四岁男童出现咳嗽。他的样本后来检测 COVID-19 呈阳性。

2019 年 11 月 27 日：巴西采集了废水样本，这些样本之后被检测出含有 SARS-CoV-2 的 RNA。

2019 年 12 月 1 日：中共第一例"官方"COVID-19 感染病例。

2019 年底：陈薇少将抵达武汉，接管武汉国家生物安全实验室生物安全四级实验室。

2019 年 12 月 27 日：一家中国基因公司据信对武汉大多数病毒进行了测序，结果显示与 SARS 类似。湖北省中西医结合医院医生张继先告诉 PRC 卫生官员，感染了大约 180 人的新疾病是由一种新型冠状病毒引起的。

2019 年 12 月 29 日：在湖北省中西医结合医院和其他医院发现更多病例之后，武汉市疾控中心组织专家组展开调查。

2019 年 12 月 30 日：在武汉的医生向当地卫生官员汇报"SARS 冠状病毒"检查呈阳性。根据《国际卫生条例（2005 年）》，PRC 被要求在 24 小时内向世卫组织汇报这些结果。他们没有。

2019 年 12 月 31 日：位于日内瓦的世卫组织官员注意到媒体有关武汉爆发疫情的报道，指示世卫组织驻华代表处调查。

2020 年 1 月：王林发与武汉病毒所的合作者会面，很可能包括石正丽和胡犇。

2020 年 1 月 1 日：湖北省卫生健康委员会官员下令已经确认新病毒与 SARS 类似的基因测序公司和实验室停止检测并销毁现存样本。李文亮医生因"散布谣言"被拘留。

2020 年 1 月 2 日：武汉病毒研究所完成了病毒基因测序，但是中共没有分享测序信息或向世卫组织通报。PRC 严厉通报了拘留武汉医生一事。

2020 年 1 月 3 日：中国国家卫生健康委员会下令研究机构不要发布任何有关"不明疾病"的信息，并且下令实验室将样本转交到中共控制的国家机构或将样本销毁。

2020 年 1 月 11 日—12 日：在上海一位研究人员在网上透露了基因序列之后，中共向世卫组织发送了武汉病毒研究所 10 天前就已完成的基因测序信息。这位研究人员所在的上海实验室被下令关闭。

2020 年 1 月 14 日：习近平得到一名中国最高卫生官员有关大流行病正在发生的警示。

2020 年 1 月 18 日：王林发离开武汉。

2020 年 1 月 20 日：武汉病毒所提交一篇文章称 SARS-CoV-2 来源于自然。文章将 ID4991 重新命名为 RaTG13，并且包含了有关何时获得病毒基因组序列的不实信息。

2020 年 1 月 23 日：中共对武汉实行全市范围的封锁。但是，在封城措施生效之前，预计已有 500 万人离城。

2020 年 1 月最后一周：达萨克和其他外部专家编辑一封由美国国家科学院、国家工程院和国家医学院院长致白宫科技政策办公室的信。达萨克力推要求加入应对"阴谋论"的言辞。

2020 年 1 月 30 日：谭德塞宣布"国际关注的突发公共卫生事件"，而一周之前，他曾拒绝作出这样的宣布。

2020 年 1 月末—2 月初：PRC 研究人员，可能是武汉病毒所的研究人员，请求达萨克帮助回应 SARS-CoV-2 来自实验室泄漏或基因操作的说法。达萨克帮助编辑了美国国家科学院、国家工程院和国家医学院给白宫科技政策办公室的回应。

2020 年 2 月 3 日：武汉病毒所研究人员 1 月 20 日提交的论文由《自然》杂志在线发表。

2020 年 2 月 6 日 12:43:40 am：达萨克向王林发、巴里克和其他人发送了将在《柳叶刀》上发表的声明草稿，请求他们加入联署。声明中引用了武汉病毒所 2 月 3 日发表的那篇论文。几个小时内，王林发给达萨克打了电话，告诉他自己不会签名，也让达萨克和巴里克不要签名。

2020 年 2 月 6 日（下午）：3:16pm，达萨克给巴里克发了一封标注为高重要性的邮件，转达了王林发的请求，并且告诉巴里克，声明将"以一种不会与我们的合作联系起来的方式发布。" 4:01:22pm，巴里克同意不在声明上签名。

2020 年 2 月 7 日：第一位在微信上与同学分享 SARS 阳性检测结果的李医生死于 COVID-19。

2020 年 2 月 9 日：COVID-19 死亡人数超过 SARS。

2020 年 2 月 15 日：法国发生亚洲以外地区的第一例 COVID-19 死亡病例。

2020 年 2 月 16 日：世卫组织和 PRC 官员开始了为期九天的"2019 世卫组织-中国冠状病毒病联合考察"，前往 PRC 考察疫情和 COVID-19 起源问题。许多团队成员在考察期间未被允许前往武汉，其中包括至少一名美国人。

2020 年 2 月 18 日：达萨克的声明在《柳叶刀》在线发表，其中提到他协助撰写的来自美国国家科学院、国家工程院和国家医学院的那封信，以及武汉病毒所 2 月 3 日发表的那篇有关 COVID-19 起源的论文。尽管起草了这份声明信，但是达萨克没有被列为通讯作者。

2020 年 2 月 25 日： PRC 境外通报的新增感染病例首次超过境内。

2020 年 2 月 26 日： 世卫组织-中国联合考察组发布考察结果，赞扬 PRC 的疫情应对措施。

2020 年 2 月 29 日： 美国报告了第一例 COVID-19 死亡病例。

2020 年 3 月 11 日： 世卫组织官员正式宣布 COVID-19 为大流行病，此时已有 114 个国家通报了 118,000 个感染病例，包括美国的 1,000 多例。

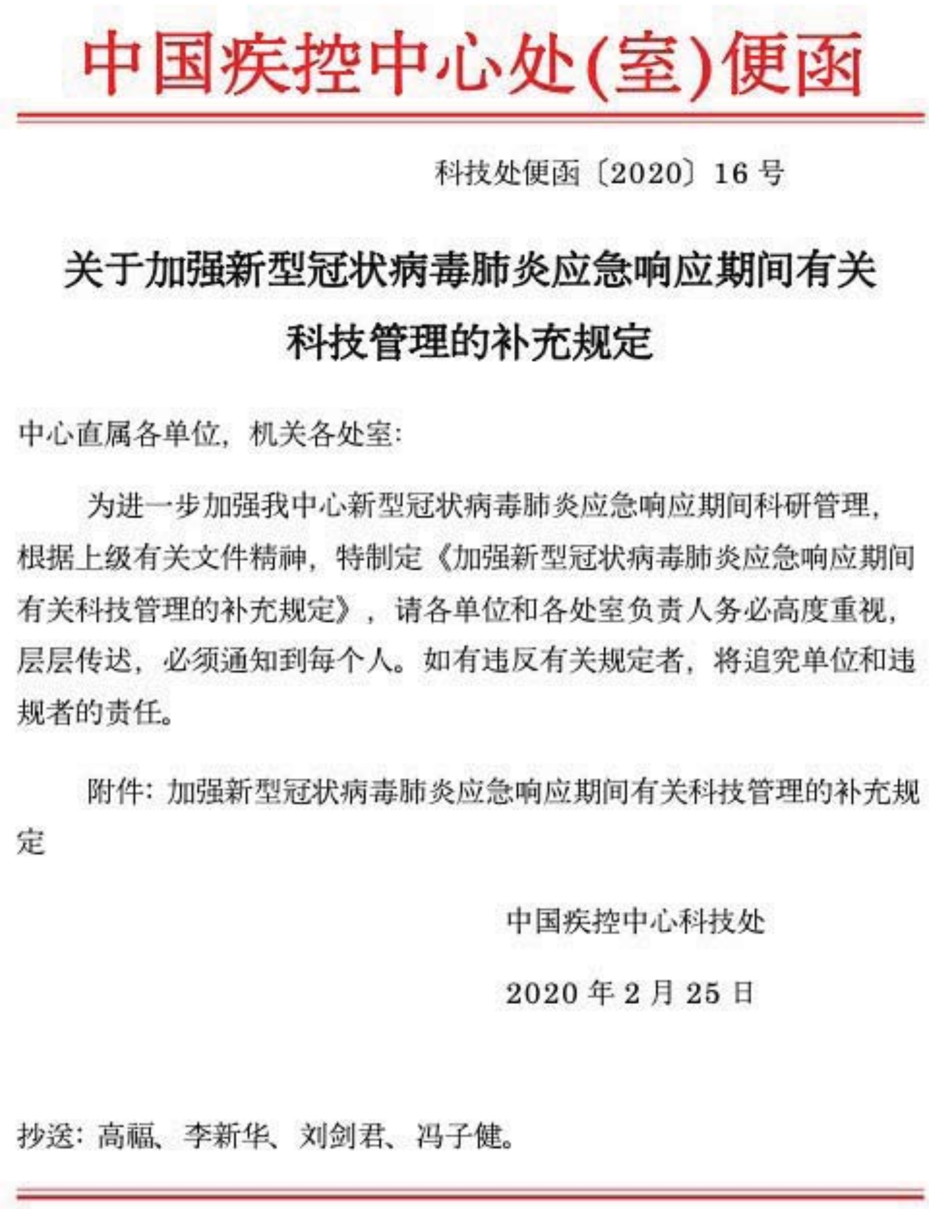
2020 年 6 月 15 日： 美国国家科学院、国家工程院和国家医学院的院长发表声明说，“让科学证据来确定 SARS-CoV-2 的起源。”

2020 年 6 月 21 日： 在面临公开压力后，达萨克更新了《柳叶刀》那份声明的公开披露表格。他没有提武汉病毒所，也没有提声明是在 PRC 研究人员的请求下起草的。

2020 年 7 月 5 日： 达萨克和 27 名最初联署者中的 23 人发布对他们 2 月声明的更新，撤回将有关病毒起源的公开辩论贴上“阴谋论”标签的做法。

2020 年 11 月 17 日： 在受到公开压力后，石正丽、胡犇和其他武汉病毒所研究人员发表一份对他们 2 月 3 日论文的补充，证实 RaTG13 是从云南洞穴中采集到的 ID4991，并且披露他们在 2012 年到 2015 年间从那个洞穴中收集了 293 个冠状病毒。

中国疾控中心有关补充规定的便函



中国疾控中心处(室)便函

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：

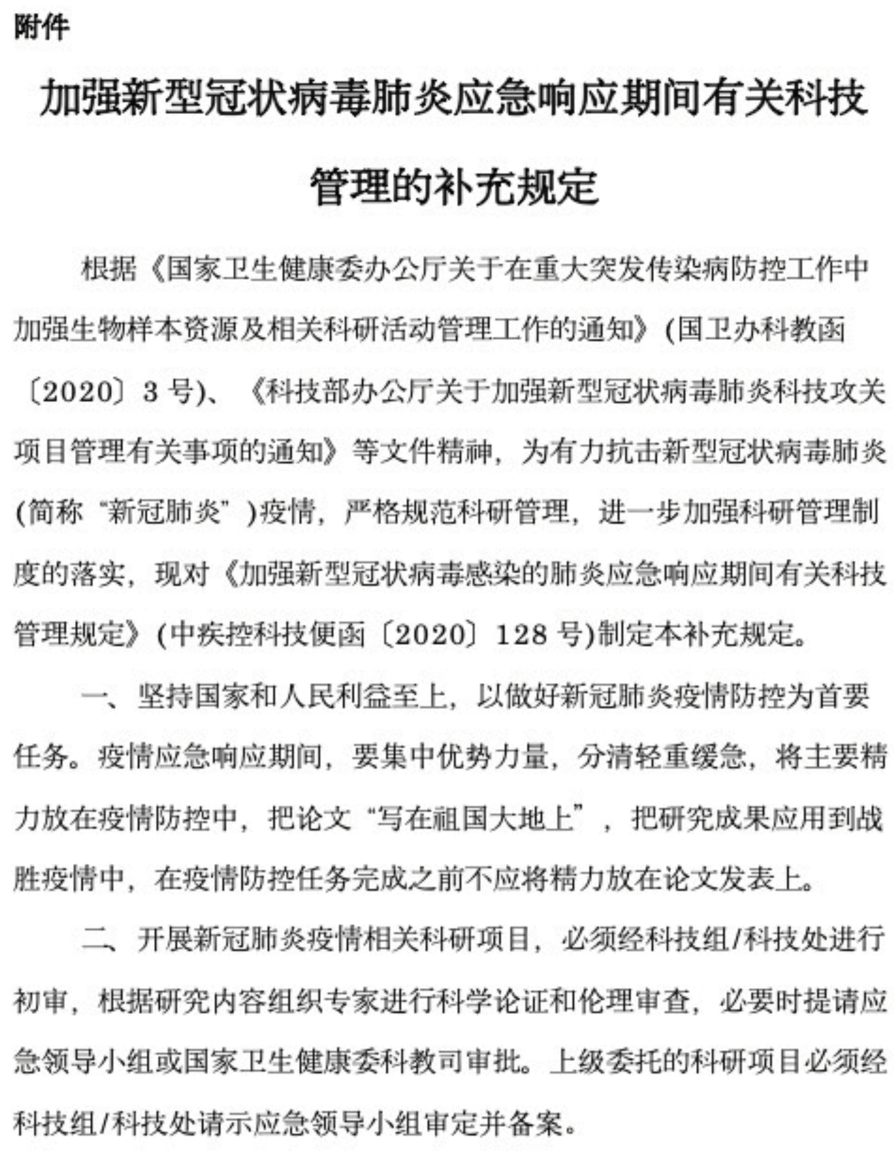
为进一步加强我中心新型冠状病毒肺炎应急响应期间科研管理，根据上级有关文件精神，特制定《加强新型冠状病毒肺炎应急响应期间有关科技管理的补充规定》，请各单位和各处室负责人务必高度重视，层层传达，必须通知到每个人。如有违反有关规定者，将追究单位和违规者的责任。

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。



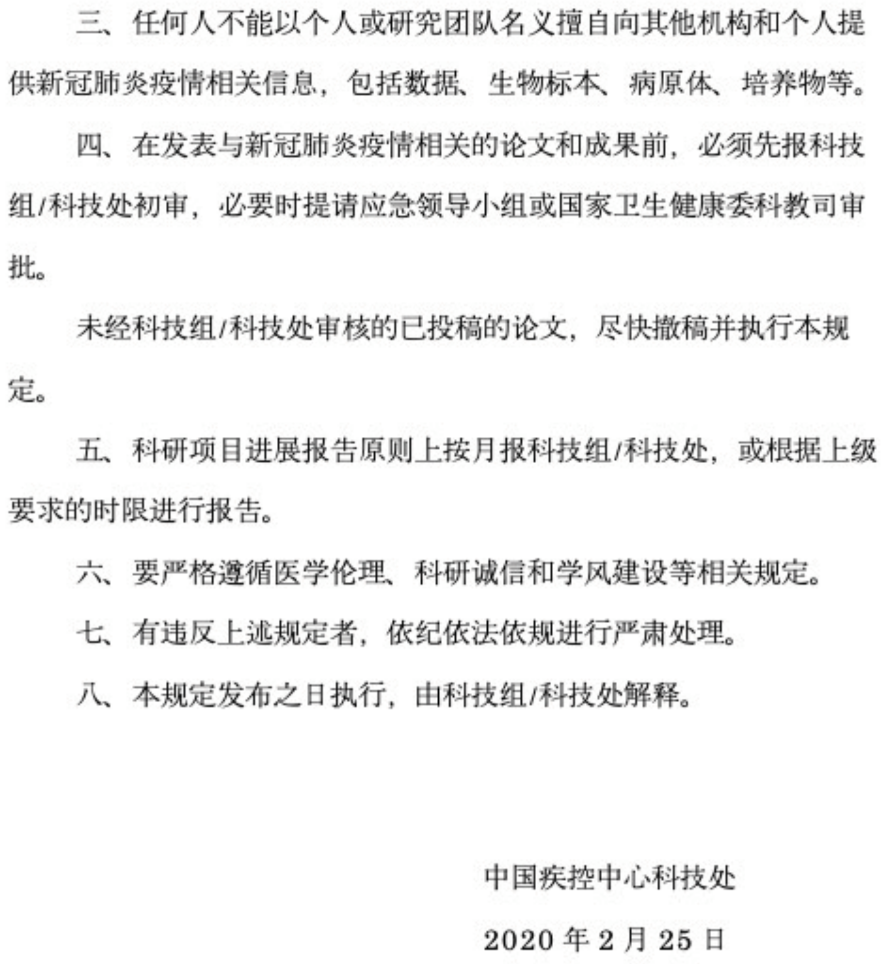
附件

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

国务院联防联控机制关于新冠肺炎科研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

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

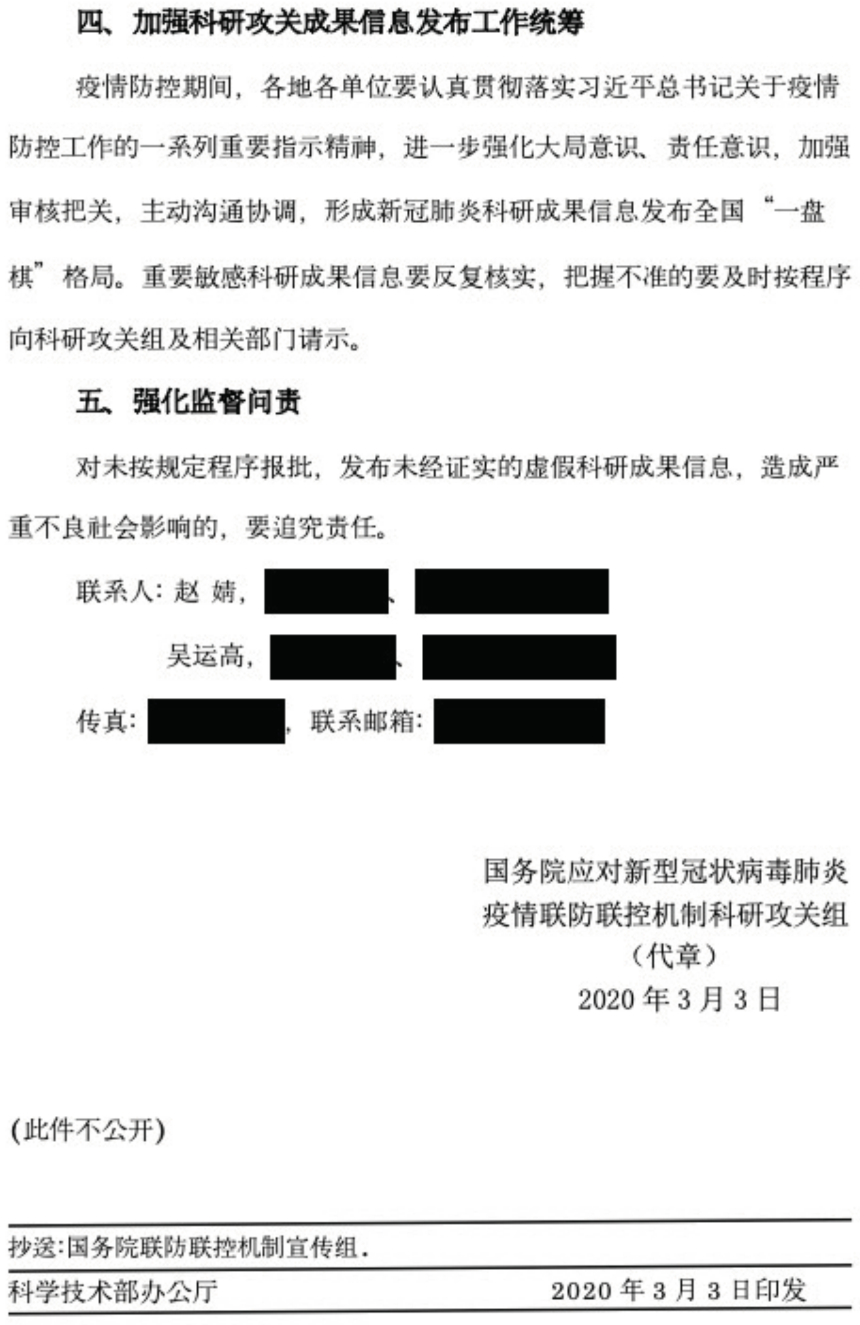
按照“依法依规、科学客观、归口管理、精准发布”的原则，把新冠肺炎治疗药物、疫苗、病毒溯源、病毒传播途径、检测试剂等各类疫情防控科研成果信息的发布工作，纳入国务院应对新型冠状病毒肺炎疫情联防联控机制科研攻关组(以下简称科研攻关组)的统一部署。科研攻关组统筹协调科研应急攻关成果信息发布，指导、协调各地各单位科研成果信息发布.

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]

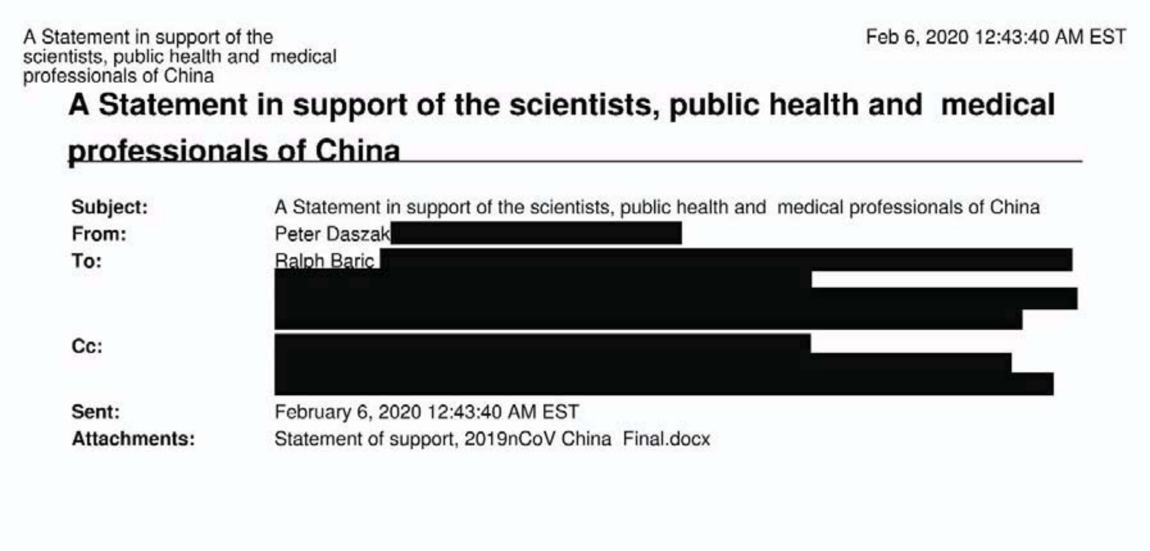
国务院应对新型冠状病毒肺炎
疫情联防联控机制科研攻关组
（代章）
2020 年 3 月 3 日

(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

2020 年 2 月 6 日 12:43am 电邮 彼得 · 达萨克致拉尔夫 · 巴里克、王林发和其他人邀请他们签署声明



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]
Cc: [redacted]
Sent: February 6, 2020 12:43:40 AM EST
Attachments: Statement of support, 2019nCoV China Final.docx

支持中国科学家、公共卫生
和医学专业人士的声明

2020 年 2 月 6 日 12:43 AM EST

支持中国科学家、公共卫生和医学专业人士的声明

主题： 支持中国科学家、公共卫生和医学专业人士的声明
发件人： 彼得·达萨克 [redacted]
收件人： 拉尔夫·巴里克 [redacted]
抄送： [redacted]
发送日期： 2020 年 2 月 6 日 12:43 AM EST
附件： Statement of support, 2019nCoV China Final.docx

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 34th Street – 17th Floor
New York, NY 10001

Tel. +1 212-380-4474
Website: www.ecohealthalliance.org
Twitter: @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.

支持中国科学家、公共卫生 2020 年 2 月 6 日 12:43 AM EST
和医学专业人士的声明

亲爱的拉尔夫、琳达、吉姆、丽塔、林发和休姆，

我一直在密切跟踪围绕中国出现新型冠状病毒的事件，并且对最近有关病毒起源的谣言、虚假信息和阴谋论的散播感到不安。这些东西如今尤其针对与我们合作多年的科学家，他们在英勇地抗击这场疫情，并以前所未有的速度、开放和透明分享数据。这些阴谋论有破坏全球合作的危险，而我们正需要这种全球合作来应对已经在各大洲传播的疾病。

我们起草了一份支持中国科学家、公共卫生和医学专业人士并与他们团结一致的简单声明，并且希望邀请你们与我们一起作为首批签署人。如果你们同意，我们还会将这封声明信发送给大约其他六名在这个领域的权威，然后我们会将其广泛传播，创建一个签名网页，让其他人士可以通过联署显示他们的支持。我还会在两星期后在马来西亚举行的 2020 年国际传染病大会上，在我的会议上亲自提出这个声明，目的也是让东南亚广泛关注我们对中国同事所做工作的支持。

我衷心希望你们能够加入我们。请审阅这封声明信，并告知我你们是否愿意与我和比利 · 卡雷什一起成为联署人。同时，请确认信中列出的你们的职位和隶属机构。我们计划在美国国家科学院、国家工程院和国家医学院院长致信的同时，将这份声明广泛传播。他们的那封信可能于明天或星期五公布。

感谢你们对此予以考虑以及对世界各地的科学和公共卫生界的支持！

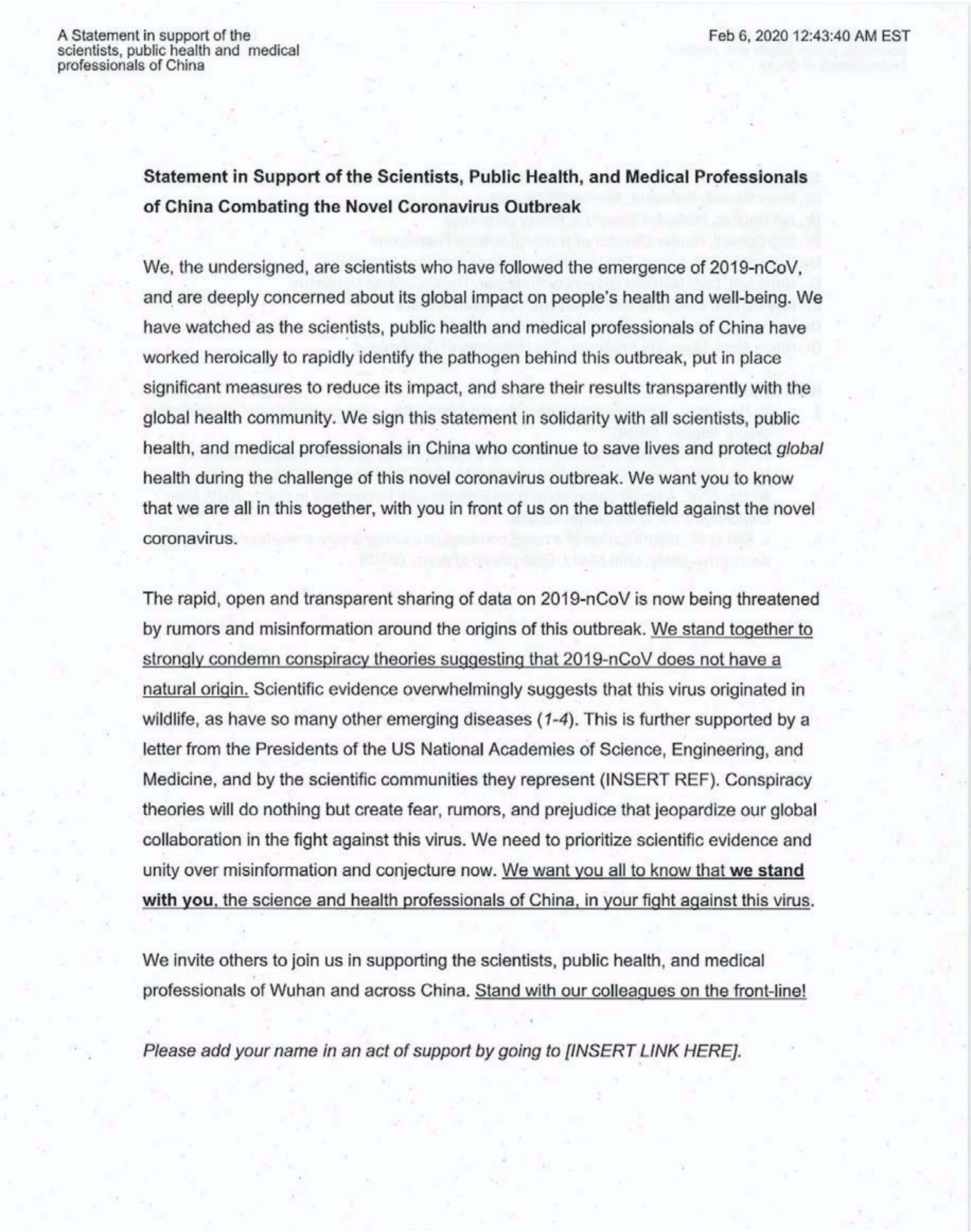
祝好！

彼得

彼得 · 达萨克
主席

生态健康联盟
西 34 街 460 号 17 楼
纽约州纽约，邮编 10001
电话: +1 212-380-4474
网址: www.ecohealthalliance.org
推特: @PeterDaszak

生态健康联盟引领有关人类与野生生物健康和脆弱生态系统的前沿研究。我们通过这一科学研发防止大流行病发生和促进自然资源保护的方案。



A Statement in support of the
scientists, public health and medical
professionals of China

Feb 6, 2020 12:43:40 AM EST

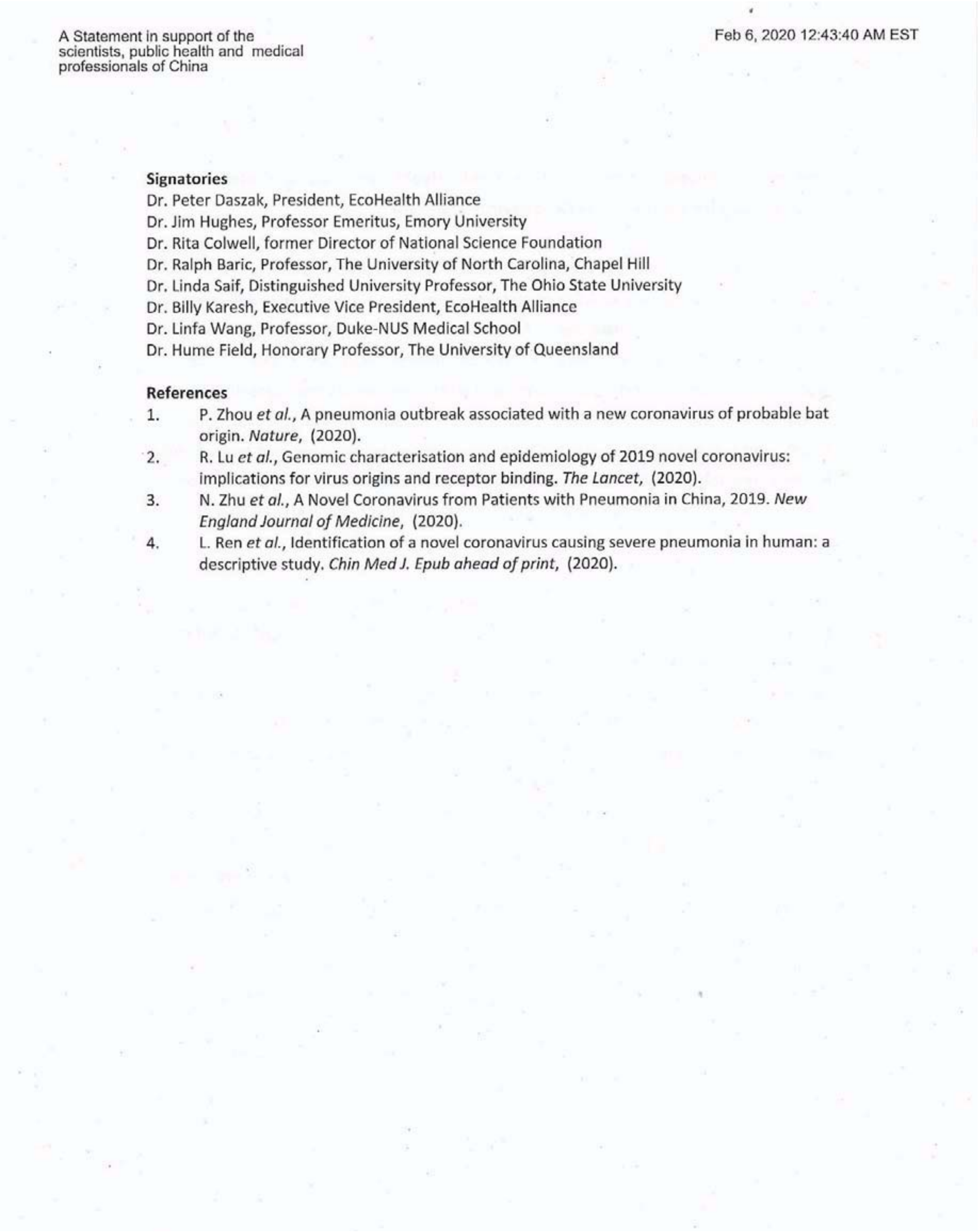
Statement in Support of the Scientists, Public Health, and Medical Professionals of China Combating the Novel Coronavirus Outbreak

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].



A Statement in support of the
scientists, public health and medical
professionals of China

Feb 6, 2020 12:43:40 AM EST

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 Karesh, Executive Vice President, EcoHealth Alliance
Dr. Linfa Wang, Professor, Duke-NUS Medical School
Dr. Hume Field, Honorary Professor, The University of Queensland

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支持中国科学家、公共卫生 2020 年 2 月 6 日 12:43 AM EST
和医学专业人士的声明

支持中国科学家、公共卫生和医学专业人士抗击新型冠状病毒疫情的声明

我们这些联署者是跟踪 2019-nCoV 出现并对它给全球人民健康和福祉造成的影响深感忧虑的科学家。我们看到中国的科学家、公共卫生和医学专业人士英勇努力，快速确定了此次疫情背后的病原体，采取重要措施缓解影响，并且以透明的方式向全球卫生界分享他们的结果。我们签署这项声明，以显示我们与在这场新型冠状病毒疫情挑战期间，继续拯救生命和保护全球健康的所有中国科学家、公共卫生和医学专业人士团结一致。我们希望你们知道，在抗击这个新型冠状病毒的战场上，你们站在我们的前面，我们与你们荣辱与共。

围绕此次疫情源头的谣言和虚假信息，现在正威胁着 2019-nCoV 数据的快速、开放和透明分享。我们站在一起，强烈谴责暗示 2019-nCoV 没有自然来源的阴谋论。科学证据压倒性地显示，这个病毒与其它许多新发疾病一样起源于野生生物（*1-4*）。美国国家科学院、国家工程院和国家医学院院长的一封信，以及他们所代表的科学界，为此提供了进一步的支持（插入参考文献）。阴谋论只会制造恐慌、谣言和偏见，破坏我们在对抗这个病毒时的全球合作。相对于虚假信息和猜测，我们现在需要优先强调科学证据和团结。我们希望你们所有人知道，在对抗这个病毒的战斗中，我们与你们站在一起，与中国的科学和卫生专业人士站在一起。

我们邀请其他人加入我们，对武汉和中国各地的科学家、公共卫生和医学专业人士表示支持。与我们在第一线的同事站在一起！

请前往【在此处插入链接】加上您的名字，以示支持。

支持中国科学家、公共卫生 2020 年 2 月 6 日 12:43 AM EST
和医学专业人士的声明

签署人

彼得 · 达萨克博士，生态健康联盟主席
吉姆 · 休斯博士，埃默里大学荣休教授
丽塔 · 科尔威尔博士，前国家科学基金会理事长
拉尔夫 · 巴里克博士，北卡罗莱纳大学教堂山分校教授
琳达 · 赛义夫博士，俄亥俄州立大学杰出教授
比利 · 卡雷什博士，生态健康联盟副执行长
王林发博士，杜克-新加坡国立大学医学院教授
休姆 · 菲尔德博士，昆士兰大学荣誉教授

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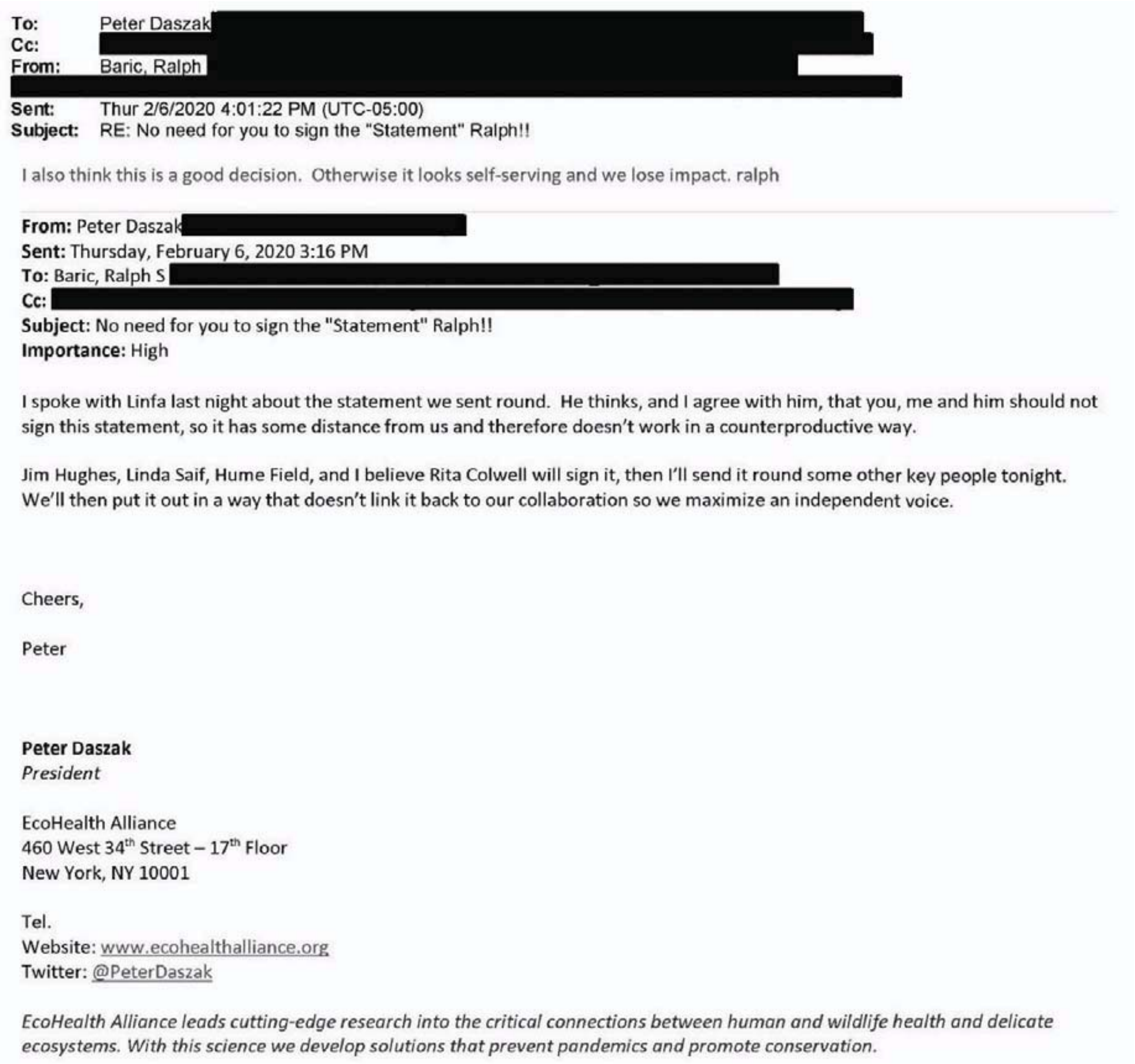
2020 年 2 月 6 日 3:16pm 电邮 彼得·达萨克致拉尔夫·巴里克转达王不签署声明的要求



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!!

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 34th Street – 17th Floor
New York, NY 10001

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

收件人：彼得 · 达萨克[redacted]
抄送：[redacted]
寄件人：巴里克，拉尔夫[redacted]
发送日期：2020/2/6 星期四 4:01:22 PM (UTC-05:00)
主题： 回复：不需要你签署“声明”了拉尔夫！!

我也认为这是个好决定。否则会看起来我们是在为自己服务，这会失去影响力。拉尔夫

发件人： 彼得 · 达萨克[redacted]
发送日期：2020 年 2 月 6 日星期四 3:16 PM
收件人：巴里克，拉尔夫 S[redacted]
抄送：[redacted]
主题：不需要你签署“声明”了拉尔夫！!
重要性：高

我昨晚和林发谈了我们发的那个声明。他认为，我也同意，你、我和他不应该签署这个声明，这样这个声明和我们保持一定距离，因此不会起反作用。

吉姆 · 休斯、琳达 · 赛义夫、休姆 · 菲尔德和我认为，丽塔 · 科尔威尔会签署。然后我今晚会把它发给其他一些关键人物。然后，我们会以一种不会将它与我们的合作联系起来的方式发布它，这样我们可以让独立的声音最大化。

祝好！

彼得

彼得 · 达萨克

主席

生态健康联盟
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纽约州纽约，邮编 10001
电话: +1 212-380-4474
网址: www.ecohealthalliance.org
推特: @PeterDaszak

生态健康联盟引领有关人类与野生生物健康和脆弱生态系统的前沿研究。我们通过这一科学研发防止大流行病发生和促进自然资源保护的方案。

2020 年 2 月 8 日 8:52pm 电邮 彼得·达萨克致丽塔·科尔威尔声称武汉病毒所研究人员要求发表声明

From: Peter Daszak [redacted]
Sent: Saturday, February 08, 2020 8:52 PM
To: Rita Colwell [redacted]
Cc: Rita Colwell [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 34th Street – 17th Floor
New York, NY 10001

发件人：彼得 · 达萨克[redacted]
发送日期： 2020 年 2 月 8 日星期六 8:52 PM
收件人：丽塔 · 科尔威尔[redacted]
抄送：丽塔 · 科尔威尔[redacted]
主题：回复：冠状病毒声明
重要性：高

丽塔你好，

感谢你的评论。我认为目前那项工作已经完成了，12 个国家发布了>50 个基因组，多个国家的作者发表了系统发育分析。我尝试将此说得更明确一点，对声明信做了以下修改，希望可以解答你的置评。

1）我加入了 GISAID 网页作为参考，网页上有 12 个国家发布和分析的 57 个（截至目前）2019-nCoV 全长基因组序列
2）我加入了 CDC 有关 2019-nCoV 的网页作为参考，网页上有以下与我们声明信完全一致的陈述：
“2019-nCoV 是一种乙型冠状病毒，类似 MERS 和 SARS，后两者来源于蝙蝠。来自美国患者的序列与中国最初发布的序列相似，似乎表明这个病毒可能是最近而且单一地出现自一个动物宿主。”

此外，请注意，我们不会将这个称为“请愿”，而是称为“支持声明”——这出现在标题当中，也会出现在我们发送出去的所有材料中。这是为了避免它看起来是一个政治性的声明——这只是顶级的科学家对目前处在重压之下的其他科学家和卫生专业人士表示支持的一封信。

我希望你愿意做这件事——你的声音将非常具有影响力，尤其是在让美国和中国之间这些关键桥梁保持开放方面。你应当知道，阴谋论者非常活跃，用一些令人极其不愉快的网页攻击我们在中国的合作者，一些人现在甚至收到了对他们和他们家人的死亡威胁。他们请求我们给予他们任何我们能够给予的支持。

一旦我们收到你的回复，我们就准备好将此发送给我们有更多人的一个名单（名单

随附），不过当然，如果你对此感到不安，我会确保你的名字不会与此联系起来。

祝好！

彼得

彼得 · 达萨克
主席

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生态健康联盟引领有关人类与野生生物健康和脆弱生态系统的前沿研究。我们通过这一科学研发防止大流行病发生和促进自然资源保护的方案。

Watch Live: Trump, First Lady participate in Memorial Day event at Fort McHenry

Wuhan lab had three live bat coronaviruses: Chinese state media

AFP • May 24, 2020

Scroll back up to restore default view.

The Chinese virology institute at the centre of US allegations it may have been the source of the COVID-19 pandemic has three live strains of bat coronavirus on-site, but none match the new global contagion, its director has said.

Scientists think COVID-19 -- which first emerged in the central Chinese city of Wuhan and has killed more than 340,000 people worldwide -- originated in bats and could have been transmitted to people via another mammal.

But the director of the Wuhan Institute of Virology told state broadcaster CGTN that claims made by US President Donald Trump and others the virus could have leaked from the facility were "pure fabrication".

What to Read Next

Trump commemorates Memorial Day, defends decision to play golf
Reuters

In the interview filmed on May 13 but broadcast Saturday night, Wang Yanyi said the centre has "isolated and obtained some coronaviruses from bats".

"Now we have three strains of live viruses... But their highest similarity to SARS-CoV-2 only reaches 79.8 percent," she said, referring to the coronavirus strain that causes COVID-19.

Related Video: Vaccination and the Immune System

One of their research teams, led by Professor Shi Zhengli, has been researching bat coronaviruses since 2004 and focused on the "source tracing of SARS", the strain behind another virus outbreak nearly two decades ago.

"We know that the whole genome of SARS-CoV-2 is only 80 percent similar to that of SARS. It's an obvious difference," she said.

"So, in Professor Shi's past research, they didn't pay attention to such viruses which are less similar to the SARS virus."

- Plans for more labs -

Conspiracy rumours that the biosafety lab was involved in the outbreak swirled online for months before Trump and US Secretary of State Mike Pompeo brought the theory into the mainstream by claiming that there is evidence the pathogen came from the institute.

The United States and Australia have called in recent weeks for an investigation into the origins of the pandemic.

Chinese scientists have said that the virus first emerged at a market selling live animals in Wuhan, though officials in Beijing more recently cast doubt about its origins.

Chinese Foreign minister Wang Yi on Sunday blasted what he called efforts by US politicians to "fabricate rumours" about the pathogen's origins and "stigmatise China".

He said China would be "open" to international cooperation to identify the source of the novel coronavirus, as long as any investigation is "free of political interference".

The World Health Organization has said Washington offered no evidence to support the "speculative" claims about the Wuhan lab.

The Wuhan lab has said it received samples of the then-unknown virus on December 30, determined the viral genome sequence on January 2 and submitted information on the pathogen to the WHO on January 11.

Wang Yanyi said in the interview that before it received samples in December, their team had never "encountered, researched or kept the virus".

"In fact, like everyone else, we didn't even know the virus existed," she said. "How could it have leaked from our lab when we never had it?"

At a press conference Sunday, Zhao Chenxin, deputy secretary-general of the National Development and Reform Commission, said every Chinese prefecture must have its own P3 laboratory to ramp up preparations against infectious diseases.

Apart from the P3 lab plans -- the second-highest biosafety classification for labs handling pathogens -- Zhao said each city should also have a lower-level P2 laboratory so they could "quickly respond in a major epidemic".

The Wuhan institute has both P3 and P4 labs.

中国的低人工、低人权“优势”才是无解的！

(美国撤了，中国漏了。- USA quits, China leaks.)
(Why carry out such kind of virus research? Why???)

刚才看到有人说，为什么外媒这次反应平淡为什么大家都觉得这是人工病毒泄漏，生化武器事故，但是没有国家管这个事情，任由武汉人死亡

我的思路是这样的
中国作为世界工厂，就是靠着低人工低人权换外汇；
中国上马了大量的五毒所这样的生物科研机构，我认为它们主营业务是外包各种生物实验把国外做不了的实验，动物实验，甚至人体药物实验拿到中国做
比如比尔盖茨的基金就和武毒所有联系
比如各个城市的三河大神会去试药挣钱。一天两、三百，实验各种药物，还不用害怕试药者出了事儿天价起诉。
开脑洞说，这是武汉的国际产业，什么默克尔老妖婆，莫迪，梅姨都在近一年“特地”到访武汉。说真的，武汉特殊在哪里？比如习进平访美两天，特地跑到伊利诺伊州或者阿肯色州一个城市去干嘛？

所以我觉得石正丽的研究，一开始确实也和国外合作这是事实，后来国外专家说很危险，所以撤出了，但是也沾了浑水。或者说武毒所，也和国外的机构合作其他项目！这就是某种意义上的生物项目外包。现在中国军方也好，石正丽也好，出了泄漏的事儿，国外也不知如何指责！武毒所也有一些国外公司或机构做一些低人权实验的证据！总之，武毒所是厚着脸皮油盐不进。国外科研界或者媒体也无从下嘴鸟。

再说武汉市。我是很悲观的。咱们只看事实。是不是 12 月发行了泄漏通告了全世界却继续瞒着国内。是不是等到春运基本结束，武汉的流动人口散去，才封城。是不是医生护士没有药也没有防护。是不是现在全世界都找到特效药了还拖延着不用？火神山医院、方舱的意义无非是换个地方等死。这是将计就计，自残一下，或者说是放血疗法，或者说是人口优化计划。反正有枪杆子和笔杆子，一切都稳，就让子弹再飞一下。正好搞搞压力测试嘛！习进平连面都不露又怎样！这几天各种大外宣大内宣的功力，大家想必也体会到了，可谓炉火纯青。

国际舆论估计也就这样了，毕竟作为世界工厂，中国还很有价值。就好像原来中国焚烧国外的塑料垃圾，很多村民得了癌症，国外怎么办呢？塑料王国那部纪录片大家可以去看看，低人权低人工是无解的

我觉得中国几千年的历史就是这样了，能推翻中共的只有中国人，伴随着流血，伴随着牺牲，就像几千年来无数的朝代更迭一样。这次中共还稳的很，机会可能要 20 年以后，习近平老朽的时候。各位已经移民出来的，好好捍卫各自国家的自由世界，可能的话，把自己父母或者家族里的小辈带出来，也就这样了。或者还有一点希望，就是全民不合作，像三和大神一样，拒绝做流水线人肉机械手臂：“兄弟，这家是黑厂不要去，不如我们去打游戏”。三和大神这一刻，比华为 996ICU 党都充满了人性的光辉！

Understanding the Risk of Bat Coronavirus Emergence

Daszak, Peter

Ecohealth Alliance, Inc., New York, NY, United States

Abstract

This project will examine the risk of future coronavirus (CoV) emergence from wildlife using in-depth field investigations across the human-wildlife interface in China, molecular characterization of novel CoVs and host receptor binding domain genes, mathematical models of transmission and evolution, and in vitro and in vivo laboratory studies of host range. Zoonotic CoVs are a significant threat to global health, as demonstrated with the emergence of pandemic severe acute respiratory syndrome coronavirus (SARS-CoV) in China in 2002, and the recent and ongoing emergence of Middle East Respiratory Syndrome (MERS-CoV). Bats appear to be the natural reservoir of these viruses, and hundreds of novel bat-CoVs have been discovered in the last two decades. Bats, and other wildlife species, are hunted, traded, butchered and consumed across Asia, creating a large scale human-wildlife interface, and high risk of future emergence of novel CoVs. This project aims to understand what factors increase the risk of the next CoV emerging in people by studying CoV diversity in a critical zoonotic reservoir (bats), at sites of high risk for emergence (wildlife markets) in an emerging disease hotspot (China). The three specific aims of this project are to: 1. Assess CoV spillover potential at high risk human-wildlife interfaces in China. This will include quantifying he nature and frequency of contact people have with bats and other wildlife; serological and molecular screening of people working in wet markets and highly exposed to wildlife; screening wild-caught and market sampled bats from 30+ species for CoVs using molecular assays; and genomic characterization and isolation of novel CoVs. 2. Develop predictive models of bat CoV emergence risk and host range. A combined modeling approach will include phylogenetic analyses of host receptors and novel CoV genes (including functional receptor binding domains); a fused ecological and evolutionary model to predict host-range and viral sharing; and mathematical matrix

models to examine evolutionary and transmission dynamics. 3. Test predictions of CoV inter-species transmission. Predictive models of host range (i.e. emergence potential) will be tested experimentally using reverse genetics, pseudovirus and receptor binding assays, and virus infection experiments across a range of cell cultures from different species and humanized mice.

Public Health Relevance

Most emerging human viruses come from wildlife, and these represent a significant threat to global public health and biosecurity - as demonstrated by the SARS coronavirus pandemic of 2002-03 and an ongoing SARS-like epidemic in the Middle East. This project seeks to understand what factors allow animal Coronaviruses to evolve and jump into the human population by studying virus diversity in a critical group of animals (bats), a sites of high risk for emergence (wildlife markets) in an emerging disease hotspot (China).

Funding Agency

Agency	National Institute of Health (NIH)
Institute	National Institute of Allergy and Infectious Diseases (NIAID)
Type	Research Project (R01)
Project #	5R01AI110964-03
Application #	9086286
Study Section	Clinical Research and Field Studies of Infectious Diseases Study Section (CRFS)
Program Officer	Stemmy, Erik J
Project Start	2014-06-01
Project End	2019-05-31
Budget Start	2016-06-01
Budget End	2017-05-31
Support Year	3
Fiscal Year	2016
Total Cost	
Indirect Cost	

Institution

Name	Ecohealth Alliance, Inc.

Department	
Type	
DUNS #	077090066
City	New York
State	NY
Country	United States
Zip Code	10001

Related projects

NIH 2019 R01 AI	Understanding the Risk of Bat Coronavirus Emergence Daszak, Peter / Ecohealth Alliance, Inc.	
NIH 2018 R01 AI	Understanding the Risk of Bat Coronavirus Emergence Daszak, Peter / Ecohealth Alliance, Inc.	
NIH 2017 R01 AI	Understanding the Risk of Bat Coronavirus Emergence Daszak, Peter / Ecohealth Alliance, Inc.	$597,112
NIH 2016 R01 AI	Understanding the Risk of Bat Coronavirus Emergence Daszak, Peter / Ecohealth Alliance, Inc.	
NIH 2015 R01 AI	Understanding the Risk of Bat Coronavirus Emergence Daszak, Peter / Ecohealth Alliance, Inc.	$630,445
NIH 2014 R01 AI	Understanding the Risk of Bat Coronavirus Emergence Daszak, Peter / Ecohealth Alliance, Inc.	$666,442

Publications

Luo, Chu-Ming; Wang, Ning; Yang, Xing-Lou et al. **(2018)** Discovery of Novel Bat Coronaviruses in South China That Use the Same Receptor as Middle East Respiratory Syndrome Coronavirus. J Virol 92:

Luo, Yun; Li, Bei; Jiang, Ren-Di et al. **(2018)** Longitudinal Surveillance of Betacoronaviruses in Fruit Bats in Yunnan Province, China During 2009-2016. Virol Sin 33:87-95

Zhou, Peng; Fan, Hang; Lan, Tian et al. **(2018)** Fatal swine acute diarrhoea syndrome caused by an HKU2-related coronavirus of bat origin. Nature 556:255-258

Wu, Zhiqiang; Lu, Liang; Du, Jiang et al. **(2018)** Comparative analysis of rodent and small mammal viromes to better understand the wildlife origin of emerging infectious diseases. Microbiome 6:178

Wang, Ning; Li, Shi-Yue; Yang, Xing-Lou et al. **(2018)** Serological Evidence of Bat SARS-Related Coronavirus Infection in Humans, China. Virol Sin 33:104-107

Eskew, Evan A; Olival, Kevin J **(2018)** De-urbanization and Zoonotic Disease Risk. Ecohealth 15:707-712

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Hu, Ben; Zeng, Lei-Ping; Yang, Xing-Lou et al. **(2017)** Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus. PLoS Pathog 13:e1006698

Olival, Kevin J; Hosseini, Parviez R; Zambrana-Torrelio, Carlos et al. **(2017)** Host and viral traits predict zoonotic spillover from mammals. Nature 546:646-650

Olival, Kevin J; Willoughby, Anna R **(2017)** Prioritizing the 'Dormant' Flaviviruses. Ecohealth 14:1-2

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Comments

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