From:	Lauer, Michael (NIH/OD) [E]
To:	Jacobs, Anna (NIH/OD) [E]
Cc:	Lauer, Michael (NIH/OD) [E]
Subject:	FW: Oversight Committee letter on WIV
Date:	Thursday, March 18, 2021 10:26:55 AM
Attachments:	WIV US STATE DEPT CABLES in Appendix to GOP-Report-OriginsOfCOVID-19-Global-Pandemic-Including-Roles-of-CCPandWHO.09.20.20.pdf WIV 2021.03.16 - NIH Letter on WIV.pdf

Hi Anna – FYI.

Mike

From: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Date: Thursday, March 18, 2021 at 10:23 AM
To: "Hallett, Adrienne (NIH/OD) [E]" (b) (6), "Lauer, Michael (NIH/OD) [E]" <michael.lauer@nih.gov>
Subject: Re: Oversight Committee letter on WIV

Yup; that is what I spoke to Alan about.

From: "Hallett, Adrienne (NIH/OD) [E]" (b) (6)
Date: Thursday, March 18, 2021 at 10:22 AM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6), "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Subject: Oversight Committee letter on WIV

The attached letter just came in.

Important Context: (b) (5)

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MRN:	18 BEIJING 138
Date/DTG:	Jan 19, 2018 / 190739Z JAN 18
From:	AMEMBASSY BEIJING
Action:	WASHDC, SECSTATE *ROUTINE*
E.O.:	13526
TAGS:	SHLH, ETRD, ECON, PGOV, CN
Captions:	SENSITIVE
Reference:	17 WUHAN 48
Subject:	China Opens First Bio Safety Level 4 Laboratory

1. (SBU) **Summary and Comment:** The Chinese Academy of Sciences (CAS) has recently established what is reportedly China's first Biosafety Level 4 (BSL-4) laboratory in Wuhan. This state-of-the-art facility is designed for prevention and control research on diseases that require the highest level of biosafety and biosecurity containment. Ultimately, scientists hope the lab will contribute to the development of new antiviral drugs and vaccines, but its current productivity is limited by a shortage of the highly trained technicians and investigators required to safely operate a BSL-4 laboratory and a lack of clarity in related Chinese government policies and guidelines. (b)(5)

(b)(5)

(b)(5) **End Summary and Comment.**

China Investing in Infectious Disease Control

2. (U) Between November 2002 and July 2003, China faced an outbreak of Severe Acute Respiratory Syndrome (SARS), which, according to the World Health Organization, resulting in 8,098 cases and leading to 774 deaths reported in 37 countries. A majority of cases occurred in China, where the fatality rate was 9.6%. This incident convinced China to prioritize international cooperation for infectious disease control. An aspect of this prioritization was China's work with the Jean Merieux BSL-4 Laboratory in Lyon, France, to build China's first high containment laboratory at Wuhan's Institute of Virology (WIV), an institute under the auspices of the Chinese Academy of Sciences (CAS). Construction took 11 years and $44 million USD, and construction on the facility was completed on January 31, 2015. Following

two years of effort, which is not unusual for such facilities, the WIV lab was accredited in February 2017 by the China National Accreditation Service for Conformity Assessment. It occupies four floors and consists of over 32,000 square feet. WIV leadership now considers the lab operational and ready for research on class-four pathogens (P4), among which are the most virulent viruses that pose a high risk of aerosolized person-to-person transmission.

Unclear Guidelines on Virus Access and a Lack of Trained Talent Impede Research

3. (SBU) In addition to accreditation, the lab must also receive permission from the National Health and Family Planning Commission (NHFPC) to initiate research on specific highly contagious pathogens. According to some WIV scientists, it is unclear how NHFPC determines what viruses can or cannot be studied in the new laboratory. To date, WIV has obtained permission for research on three viruses: Ebola virus, Nipah virus, and Xinjiang hemorrhagic fever virus (a strain of Crimean Congo hemorrhagic fever found in China's Xinjiang Province). Despite this permission, however, the Chinese government has not allowed the WIV to import Ebola viruses for study in the BSL-4 lab. Therefore, WIV scientists are frustrated and have pointed out that they won't be able to conduct research project with Ebola viruses at the new BSL-4 lab despite of the permission.

(b)(6)

(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.

(b)(6) noted that the new lab has a serious shortage of appropriately trained technicians and investigators needed to safely operate this high-containment laboratory. University of Texas Medical Branch in Galveston (UTMB), which has one of several well-established BSL-4 labs in the United States (supported by the National Institute of Allergy and Infectious Diseases (NIAID of NIH)), has scientific collaborations with WIV, which may help alleviate this talent gap over time. Reportedly, researchers from GTMB are helping train technicians who work in the WIV BSL-4 lab. Despite this, (b)(6) they would welcome more help from U.S. and international organizations as they establish "gold standard" operating procedures and training courses for the first time in China. As China is building more BSL-4 labs, including one in Harbin Veterinary Research Institute subordinated to the Chinese Academy of Agricultural Sciences (CAAS) for veterinary research use, (b)(6) the training for technicians and investigators working on dangerous pathogens will certainly be in demand.

Despite Limitations, WIV Researchers Produce SARS Discoveries

6. (SBU) The ability of WIV scientists to undertake productive research despite limitations on the use of the new BSL-4 facility is demonstrated by a recent publication on the origins of SARS. Over a five-year study, (b)(6) (and their research team) widely sampled bats in Yunnan province with funding support from NIAID/NIH, USAID, and several Chinese funding agencies. The study results were published in PLoS Pathogens online on Nov. 30, 2017 (1), and it demonstrated that a SARS-like coronaviruses isolated from horseshoe bats in a single cave contain all the building blocks of the pandemic SARS-coronavirus genome that caused the human outbreak. These results strongly suggest that the highly pathogenic SARS-coronavirus originated in this bat population. Most importantly, the researchers also showed that various SARS-like coronaviruses can interact with ACE2, the human receptor identified for SARS-coronavirus. This finding strongly suggests that SARS-like coronaviruses from bats can be transmitted to humans to cause SARS-like disease. From a public health perspective, this makes the continued surveillance of SARS-like coronaviruses in bats and study of the animal-human interface critical to future emerging coronavirus outbreak prediction and prevention. (b)(5) (b)(5) WIV scientists are allowed to study the SARS-like coronaviruses isolated from bats while they are precluded from studying human-disease causing SARS coronavirus in their new BSL-4 lab until permission for such work is granted by the NHFCP.

1. Hu B, Zeng L-P, Yang X-L, Ge X-Y, Zhang W, Li B, 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(11): e1006698. https://doi.org/10.1371/journal.ppat.1006698

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MRN:	18 WUHAN 38
Date/DTG:	Apr 19, 2018 / 190551Z APR 18
From:	AMCONSUL WUHAN
Action:	WASHDC, SECSTATE *ROUTINE*
E.O.:	13526
TAGS:	SHLH, PGOV, CN, PREL, TBIO, KGHI, CDC, EAID, KHIV, IN, JP, TW, TSPL, PINS, SENV
Captions:	SENSITIVE
Reference:	A) 18 BEIJING 138 B) 17 BEIJING 2458 C) 11 MUMBAI 630 D) 17 TOKYO 716 E) 13 SEOUL 790
Subject:	China Virus Institute Welcomes More U.S. Cooperation on Global Health Security

1. (SBU) **Summary with Comment:** China's Wuhan Institute of Virology, a global leader in virus research, is a key partner for the United States in protecting global health security. Its role as operator of the just-launched Biosafety Level 4 (or "P4") lab -- the first such lab in China -- opens up even more opportunities for expert exchange, especially in light of the lab's shortage of trained staff (Ref A). (b)(5)

(b)(5)

(b)(5) **End Summary with Comment.**

2. (U) Wuhan Institute of Virology researchers and staff gave an overview of the lab and current cooperation with the United States to visiting Environment, Science, Technology and Health Counsellor Rick Switzer and Consulate Wuhan Consul General Jamie Fouss in late March. In the last year, the institute has also hosted visits from the National Institutes of Health (NIH), National Science Foundation, and experts from the University of Texas Medical Branch in Galveston. The institute reports to the Chinese Academy of Sciences in Beijing.

P4 Lab is Open and Transparent, Officials Emphasize

3. (SBU) The Wuhan P4 lab, referring to labs with the highest level of safety precautions, became fully operational and began working with live viruses early this year. Institute officials said they believed it is the only operational P4 lab in Asia aside from a U.S. Centers for Disease

Control (CDC)-supported facility in Pune, India (Ref C). China plans to stand up a second P4 lab in Harbin. Institute officials said Japan's biosafety labs are "old" and lack cutting-edge equipment, so they consider Japan's labs to be "P3 Plus" (*Note*: the Japanese government says it has one P4-level lab in the Tokyo suburbs, though its activities are limited, and Japan is building a new P4 lab in Nagasaki, see Ref D. Taiwan operates at least one P4 lab. South Korea was close to opening a P4 lab as of last year, see Ref E. *End.Note.*) Wuhan's lab is located about 20 miles from the city center in Zhengdian district, and the institute plans to gradually consolidate its other training, classroom and lab facilities at that location.

4. (U) Officials described the lab as a "regional node" in the global biosafety system and said it would play an emergency response role in an epidemic or pandemic. The lab's English brochure highlighted a national security role, saying that it "is an effective measure to improve China's availability in safeguarding national bio-safety if [a] possible biological warfare or terrorist attack happens."

5. (SBU) Institute officials said there would be "limited availability" for international and domestic scientists who had gone through the necessary approval process to do research at the lab. They stressed that the lab aimed to be a "worldwide, open platform" for virology. They said they welcomed U.S. Centers for Disease Control (CDC) experts, noting that the Chinese Academy of Sciences was not strong on human disease expertise, having only focused on it in the last 15 years, after the SARS outbreak. A Wuhan-based French consulate official who works on science and technology cooperation with China also emphasized that the lab, which was initiated in 2004 as a France-China joint project, was meant to be "open and transparent" to the global scientific community. "The intent was to set up a lab to international standards, and open to international research," he said. French experts have provided guidance and biosafety training to the lab, which will continue, the French official said. Institute officials said that France provided the lab's design and much of its technology, but that it is entirely China-funded and has been completely China-run since a "handover" ceremony in 2016.

6. (U) In addition to French assistance, experts from the NIH-supported P4 lab at the University of Texas Medical Branch in Galveston have trained Wuhan lab technicians in lab management and maintenance, institute officials said. The Wuhan institute plans to invite scientists from the Galveston lab to do research in Wuhan's lab. One Wuhan Institute of Virology researcher trained for two years at the Galveston lab, and the institute also sent one scientist to U.S. CDC headquarters in Atlanta for six months' work on influenza.

NIH-Supported Research Revises SARS Origin Story

7. (U) NIH was a major funder, along with the Natural Science Foundation of China (NSFC), of SARS research by the Wuhan Institute of Virology's [redacted] This lends weight to the theory that SARS originated in bat populations before jumping first to civet cats (likely via bat feces) and then to humans, [redacted]

(b)(6)
(b)(6) team has provided support in statistical modeling to assess the risk of more coronaviruses like SARS crossing over to human populations.

Ready to Help with the Global Virome Project

8. (U) Institute officials expressed strong interest in the Global Virome Project (GVP), and said Chinese funding for the project would likely come from Chinese Academy of Sciences funding already earmarked for One Belt, One Road-related initiatives. The GVP aims to launch this year as an international collaborative effort to identify within ten years virtually all of the planet's viruses that have pandemic or epidemic potential and the ability to jump to humans. "We hope China will be one of the leading countries to initiate the Global Virome Project," one Wuhan Institute of Virology official said. China attended a GVP unveiling meeting in January in Thailand and is waiting for more details on the initiative. The officials said that the Chinese government funds projects similar to GVP to investigate the background of viruses and bacteria. This essentially constituted China's own Virome Project, officials said, but they noted the program currently has no official name.

9. (SBU) The Wuhan Institute of Virology's (b)(6) is the (b)(6) (b)(6) (b)(6) which is designed to show "proof of concept" and be a forerunner to the Global Virome Project. (b)(6) with the EcoHealth Alliance (a New York City-based NGO that is working with the University of California, Davis to manage the (b)(5) recently planned to visit Wuhan to meet with (b)(6) (b)(6) noted that China has expressed interest in building the GVP database, which would put China in a leadership position. Other countries have confidence in China's ability to build such a database, but are skeptical on whether China could remain transparent as a "gatekeeper" for this information (b)(6) said. (b)(6) expressed frustration with the slow progress so far in launching GVP, noting that the effort lacked funding sources, needed to hire a CEO, and would have to boost its profile at G7, G20 and other high-level international meetings.

U.S.-China Workshop Explores Research Partnerships

10. (U) The Institute also has ongoing collaboration with the U.S. National Science Foundation, including a just-concluded workshop in Shenzhen, involving about 40 scientists from the United States and China, on the topic of the "Ecology and Evolution of Infectious Diseases." Co-sponsored by the Natural Science Foundation of China (NSFC), (b)(6)
(b)(6)
(b)(6) The workshop explored opportunities for U.S.-China research cooperation in areas like using "big data" to predict emerging infectious diseases, climate change's effect on vector-borne diseases, and pathogen transmission between wildlife, domestic animals and humans.

11. (SBU) Some workshop participants also expressed skepticism about the Global Virome Project's (GVP) approach, saying that gaining a predictive understanding of viruses with pandemic potential would require going beyond the GVP's strategy of sample collection, to take an "ecological" approach that considers the virome beyond vertebrate systems to identify

mechanisms driving pathogen evolution. A follow-on workshop will be held in June at the University of Berkeley. NSF and NSFC hope to jointly announce a funding call for collaborative projects later this year.

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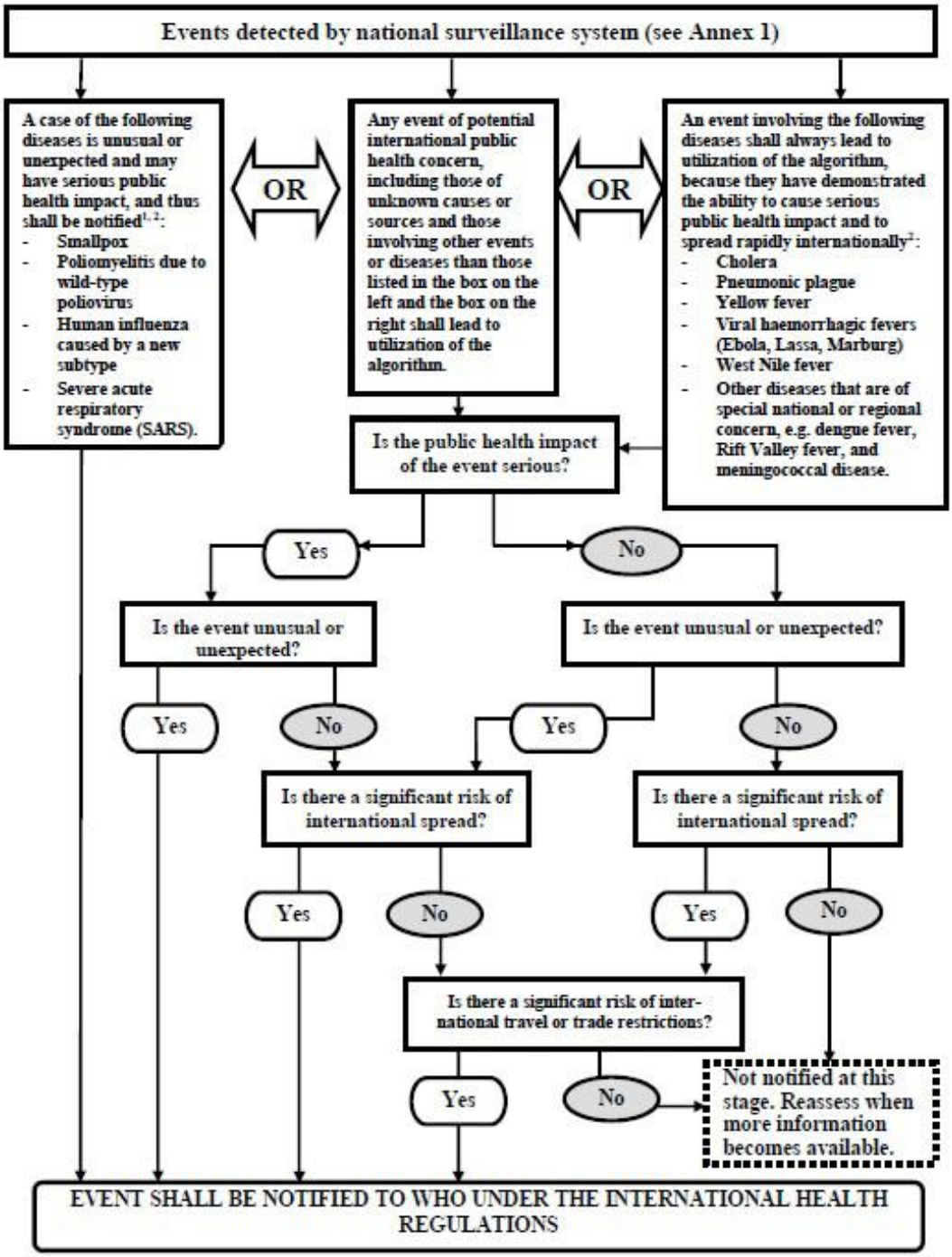
Annex 2 of the 2005 International Health Regulations

ANNEX 2

DECISION INSTRUMENT FOR THE ASSESSMENT AND NOTIFICATION OF EVENTS THAT MAY CONSTITUTE A PUBLIC HEALTH EMERGENCY OF INTERNATIONAL CONCERN



[1] As per WHO case definitions.
[2] The disease list shall be used only for the purposes of these Regulations.

FRANK PALLONE, JR., NEW JERSEY
CHAIRMAN

CATHY McMORRIS RODGERS, WASHINGTON
RANKING MEMBER

ONE HUNDRED SEVENTEENTH CONGRESS

Congress of the United States
House of Representatives
COMMITTEE ON ENERGY AND COMMERCE
2125 RAYBURN HOUSE OFFICE BUILDING
WASHINGTON, DC 20515-6115
Majority (202) 225-2927
Minority (202) 225-3641

March 18, 2021

The Honorable Francis Collins, M.D., Ph.D.
Director
National Institutes of Health
9000 Rockville Pike
Bethesda, MD 20892

Dear Dr. Collins,

We write to request information, assistance, and needed-leadership from the National Institutes of Health (NIH) to advance an independent, scientific investigation into the origins of the COVID-19 pandemic.

The COVID-19 pandemic has been the worst public health crisis in the U.S. in about a hundred years. Over a year has passed since the deadly virus reached our shores and yet, the origin of the virus has yet to be determined. An independent, expert investigation of the origin of COVID-19 is of paramount importance to public health and biosecurity. As noted by Stanford Medical School Professor David Relman:

> A more complete understanding of the origins of COVID-19 clearly serves the interests of every person in every country on this planet. It will limit further recriminations and diminish the likelihood of conflict; it will lead to more effective responses to this pandemic, as well as efforts to anticipate and prevent the next one. It will also advance our discussions about risky science. And it will do something else: Delineating COVID-19's origin story will help elucidate the nature of our very precarious coexistence within the biosphere.[1]

Recently, the World Health Organization (WHO) attempted to investigate the origin of COVID-19. The WHO said that this investigative mission would be guided by the science, be

[1] David A. Relman, *Opinion: To stop the next pandemic, we need to unravel the origins of COVID-19*, PNAS (Nov. 2020), *available at* https://www.pnas.org/content/117/47/29246.

"open-minded," and "not exclude[e] any hypothesis."[2] Unfortunately, China did not provide complete access or independence for the critical WHO mission. On February 13, 2021, National Security Advisor Jake Sullivan issued the following statement:

> We have deep concerns about the way in which the early findings of the COVID-19 investigation were communicated and questions about the process used to reach them. It is imperative that this report be independent, with expert findings free from intervention or alteration by the Chinese government. To better understand this pandemic and prepare for the next one, China must make available its data from the earliest days of the outbreak.[3]

Because of rising tensions between the U.S. and China, the WHO scrapped plans for an interim report.[4] An international group of science experts, including specialists in virology, microbiology, and zoology, asked for a new review.[5]

The NIH, as a premier scientific institution, must lead in order to foster a transparent, independent, and science-based investigation into the origin of the COVID-19 pandemic. Such an effort must meet the WHO's stated goals of an open-minded investigation that does not exclude any plausible hypothesis.[6] In addition, the NIH is well-positioned to gather and provide information through oversight of its grants and other federal awards. Thus, the NIH is in a unique position to investigate the possibility that the pandemic stemmed from a laboratory accident or leak, especially regarding the Wuhan Institute of Virology (WIV).

NIH raised concerns over a possible link between WIV and the COVID-19 outbreak during its review of federal awards to EcoHealth Alliance, a global environmental health nonprofit organization dedicated to protecting wildlife and public health from the emergence of disease. Of the $13.7 million in federal awards that NIH authorized for EcoHealth Alliance, 17

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[2] Smriti Mallapaty, *Where did COVID come from? WHO investigation begins but faces challenges*, NATURE (Nov. 11, 2020), *available at* https://www nature.com/articles/d41586-020-03165-9.

[3] The White House, Statement of National Security Advisor Jake Sullivan (Feb. 13, 2021), *available at* https://www.whitehouse.gov/briefing-room/statements-releases/2021/02/13/statement-by-national-security-advisor-jake-sullivan/.

[4] Betsy McKay, Drew Hinshaw and Jeremy Page, *WHO Investigators to Scrap Plans for Interim Report on Probe of Covid-19 Origins*, THE WALL STREET JOURNAL (Mar. 4, 2021), *available at* https://www.wsj.com/articles/who-investigators-to-scrap-interim-report-on-probe-of-covid-19-origins-11614865067?mod=latest_headlines

[5] Jaime Metzl, et al, *Call for a Full and Unrestricted International Forensic Investigation into the Origins of COVID-19* (March 4, 2021), *available at* https://s.wsj net/public/resources/documents/COVID%20OPEN%20LETTER%20FINAL%20030421%20(1).pdf. The co-organizer of the letter and a WHO advisor on human genome editing, Jaime Metzl, PhD, said there is an eighty-five percent chance the pandemic started with an accidental leak from the WIV or Wuhan CDC laboratory, *available at* https://jamiemetzl.com/origins-of-sars-cov-2/. ("I have no definitive way of proving this thesis but the evidence is, in my view, extremely convincing. If forced to place odds on the confidence of my hypothesis, I would say there's an 85% chance the pandemic started with an accidental leak from the Wuhan Institute of Virology or Wuhan CDC and a 15% chance it began in some other way (in fairness, here is an article making the case for a zoonotic jump "in the wild"). If China keeps preventing a full and unrestricted international forensic investigation into the origins of the pandemic, I believe it is fair to deny Beijing the benefit of the doubt.")

[6] Washington Post Editorial Board, *We're still missing the origin story of this pandemic. China is sitting on the answers*, THE WASHINGTON POST (Feb. 5, 2021), *available at* https://www.washingtonpost.com/opinions/2021/02/05/coronavirus-origins-mystery-china/?arc404=true.

projects sponsored by the National Institute of Allergy and Infectious Disease (NIAID) have provided over $7.9 million in federal awards for research of viral emergence from bats in Southeast Asia.[7] EcoHealth Alliance passed some of its funding to the WIV, and in 2020, NIH made efforts to obtain information from EcoHealth Alliance about WIV related to concerns about the origins of COVID-19. In April 2020, NIH wrote to EcoHealth Alliance and Columbia University about an NIH-funded project entitled, "Understanding the Risk of Bat Coronavirus Emergency:"

> It is our understanding that one of the sub-recipients of the grant funds is the Wuhan Institute of Virology ('WIV'). It is our understanding that WIV studies the interaction between corona viruses and bats. The scientific community believes that the coronavirus causing COVID-19 jumped from bats to humans likely in Wuhan where the COVID-19 pandemic began. There are now allegations that the current crisis was precipitated by the release from WIV of the coronavirus responsible for COVID-19. Given these concerns, we are pursuing suspension of WIV from participation in Federal programs. It is in the public interest that NIH ensure that a sub-recipient has taken all appropriate precautions to prevent the release of pathogens that it is studying. This suspension of the sub-recipient does not affect the remainder of your grant assuming that no grant funds are provided to WIV following receipt of this email during the period of suspension.[8]

In January 2021, the U.S. Department of State issued a fact sheet about the activity at the WIV.[9] Among other revelations, it reported the following:

- The U.S. government has reason to believe that several researchers inside the WIV became sick in autumn 2019, before the first identified case of the outbreak, with symptoms consistent with both COVID-19 and common seasonal illnesses. This raises questions about the credibility of WIV senior researcher Shi Zhengli's public claim that there was "zero infection" among the WIV's staff and students of SARS-CoV-2 or SARS-related viruses.[10]

- Starting in at least 2016, WIV researchers conducted experiments involving RaTG13, the bat coronavirus identified by the WIV in January 2020 as the closest sample to SARS-CoV-2 (96.2 percent similar).[11] There was no indication that this research was suspended at any time prior to the COVID-19 outbreak.

- The WIV has a published record of conducting "gain-of-function" research to engineer chimeric viruses.[12] But the WIV has not been transparent or consistent about its record of

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[7] NIH RePORTER, *Research Portfolio Online Reporting Tools* (queried Mar. 4, 2021), *available at* https://reporter.nih.gov/search/qlYUeI9DIk2JfWUdCcWxcA/projects/charts.
[8] Mark Moore, *NIH investigating Wuhan lab at center of coronavirus pandemic*, NEW YORK POST (Apr. 28, 2020), *available at* https://nypost.com/2020/04/28/nih-investigating-wuhan-lab-at-center-of-coronavirus-pandemic/.
[9] U.S. Department of State, *Fact Sheet: Activity at the Wuhan Institute of Virology*, Office of the Spokesperson (Jan. 15, 2021), *available at* https://2017-2021.state.gov/fact-sheet-activity-at-the-wuhan-institute-of-virology//index html.
[10] *Id.*
[11] *Id.*
[12] *Id.*

studying viruses similar to the COVID-19 virus, including "RaTG13," which was sampled from a cave in Yunnan Province in 2013 after several miners died of SARS-like illness.[13]

- WHO investigators must have access to the records of the WIV's work on bat and other coronaviruses before the COVID-19 outbreak. As part of a thorough inquiry, they must have a full accounting of why the WIV altered and then removed online records of its work with RaTG13 and other viruses.[14]

- Despite the WIV presenting itself as a civilian institution, the U.S. has determined that the WIV has collaborated on projects with China's military.[15] The WIV has engaged in classified research, including laboratory animal experiments, on behalf of the Chinese military since at least 2017.[16]

- The U.S. and other donors who funded or collaborated on civilian research at the WIV have a right and obligation to determine whether any of our research funding was diverted to secret Chinese military projects at the WIV.[17]

Notably, the State Department's former lead investigator who oversaw the Task Force into the COVID-19 virus origin stated recently that he not only believes the virus escaped from the WIV, but that it may have been the result of research that the Chinese military, or People's Liberation Army, was doing on a bioweapon.[18]

Accordingly, it is imperative to determine not only where SARS-CoV-2 originated, but also how and if NIH's funding and research to projects at the WIV could have contributed to SARS CoV-2. To assist our requests and inquiry, please provide the following by April 19, 2021:

1. An assessment from a classified U.S. Defense Intelligence Agency (DIA) report included the possibility that the origins of SARS CoV-2 could have emerged accidentally from a laboratory in Wuhan, China due to unsafe laboratory practices.[19] The DIA report cited U.S. government and Chinese researchers who found "about 33 percent of the original 41 identified cases did not have direct exposure" to the market.[20] That, along with what is known of the WIV's work in past few years, raised reasonable suspicion that the

[13] *Id.*
[14] *Id.*
[15] *Id.*
[16] *Id.*
[17] *Id.*

[18] Jennifer Griffin, Former top State Dept. investigator says COVID-19 outbreak may have resulted from bioweapons research accident, Fox News (March 13, 2021), *available at* https://www.foxnews.com/world/top-state-official-coronavirus-bioweapon-accident

[19] Fred Guterl, Naveed Jamali and Tom O'Connor, *The Controversial Experiments ad Wuhan Lab Suspected of Starting the Coronavirus Pandemic*, NEWSWEEK (Apr. 27, 2020), *available at* https://www.newsweek.com/controversial-wuhan-lab-experiments-that-may-have-started-coronavirus-pandemic-1500503.
[20] *Id.*

pandemic may have been caused by a lab error, not a wet market.[21] Further, a WHO inspector on the recent mission noted that "we know not all of those first 174 early COVID-19 cases visited the market, including the man diagnosed in December 2019 with the earliest onset date."[22] What information does the NIH have on the earliest COVID-19 cases?

2. According to an editorial on February 23, 2021, in *The Wall Street Journal* by former Secretary of State Mike Pompeo and Miles Yu, "[China's] army of scientists claim to have discovered almost 2,000 new viruses in a little over a decade."[23] How many of these discovered viruses does the NIH have information on and were any of these viruses discovered at the WIV?

3. According to *The Wall Street Journal* editorial mentioned in the previous question, some have alleged that the WIV's virus-carrying animals were sold as pets and may even show up at local wet markets.[24] Is the NIH aware of these allegations? If so, please provide any information the NIH has related to these allegations.

4. Please provide all information that NIH has about laboratory accidents and/or biosafety practices at the WIV since January 1, 2015.

5. Please provide all information that NIH has from NIH staff, grantees, sub-grantees, contractors, or subcontractors about communications and events at the WIV from August 2019 to the present.

6. Please provide all information that NIH has from NIH staff, grantees, sub-grantees, contractors, or subcontractors about their communications with China-based NIH, Chinese National Science Foundation, CDC, and China CDC about events at the WIV from August 2019 to the present.

<u>State Department Cables</u>

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[21] *Id.*

[22] Dominic Dwyer, I was the Australian doctor on the WHO's COVID-19 mission to China. Here's what we found about the origins of the coronavirus, THE CONVERSATION (Feb. 21, 2021), *available at*https://www.theguardian.com/commentisfree/2021/feb/22/i-was-on-the-whos-covid-mission-to-china-heres-what-we-found. *See also* Jeremy Page and Drew Hinshaw, *China Refuses to Give WHO Raw Data on Early Covid-19 Cases*, THE WALL STREET JOURNAL (Feb. 12, 2021), *available at* https://www.wsj.com/articles/china-refuses-to-give-who-raw-data-on-early-covid-19-cases-11613150580#:~:text=BEIJING%E2%80%94Chinese%20authorities%20refused%20to,over%20the%20lack%20of%20detail. ("Chinese authorities refused to provide World Health Organization investigators with raw, personalized data on early Covid-19 cases that could help them determine how and when the coronavirus first began to spread in China, according to WHO investigators who described heated exchanges over the lack of detail. The Chinese authorities turned down requests to provide such data on 174 cases of Covid-19 that they have identified from the early phase of the outbreak in the Chinese city of Wuhan in December 2019. Investigators are part of a WHO team that this week completed a monthlong mission in China aimed at determining the origins of the pandemic.")

[23] *Id.*

[24] Mike Pompeo and Miles Yu, *NIH Presses U.S. Nonprofit for Information on Wuhan Virology Lab*, THE WALL STREET JOURNAL (Feb. 23, 2021), available at https://www.wsj.com/articles/chinas-reckless-labs-put-the-world-at-risk-11614102828.

7. What information does NIH have about the WIV's responses to the 2018 U.S. Department of State cables (attached to this letter) regarding safety concerns?

8. The April 2018 cable from the U.S. Department of State stated that the WIV planned to invite University of Texas Medical Branch Galveston (UTMBG) researchers to do research in Wuhan's labs. Please provide any information NIH received that indicates whether the WIV invited UTMBG researchers, and whether UTMBG researchers conducted any research in Wuhan's labs.

    a. If there was such research, please provide information and any documents related to this research.

9. Why was it pertinent to the NIH investigation that the "nonprofit [EcoHealth Alliance] must provide the "WIV's responses to the 2018 Department of State cables regarding safety concerns"?[25]

    a. Did EcoHealth Alliance provide this information? If so, how did NIH use the information to further its investigation?

<u>EcoHealth Alliance, Columbia University Health Sciences</u>

10. Was the 2019 NIH federal award to EcoHealth Alliance reviewed and approved by the HHS Potential Pandemic Pathogen Care and Oversight (P3CO) committee?[26]

    a. If so, please provide the documentation with the committee's decision.

    b. Please also provide the names of the individuals who were members of the committee at the time.

11. Please provide all correspondence and communications between NIH and EcoHealth Alliance, since January 1, 2020, related to federal funding involving the WIV. The documentation should include, but not be limited to, correspondence between NIH and EcoHealth Alliance dated sometime in April 2020, on July 8, 2020, and sometime in August 2020.

12. In April 2020, NIH suspended a 2019 federal award to EcoHealth Alliance, in part, because NIH did not believe the work aligned with "program goals and agency priorities."[27] Please specify the work that was done by the EcoHealth Alliance that did

[25] Meredith Wadman, *NIH imposes 'outrageous' conditions on resuming coronavirus grant targeted by Trump*, SCIENCEMAG (Aug. 19, 2020), *available at* https://www.sciencemag.org/news/2020/08/nih-imposes-outrageous-conditions-resuming-coronavirus-grant-targeted-trump.
[26] National Institutes of Health, *Notice Announcing the Removal of the Funding Pause for Gain-of-Function Research Project* (Dec. 19, 2017), *available at* https://grants nih.gov/grants/guide/notice-files/NOT-OD-17-071.html.
[27] *Id.*

not align with the agency's program goals and priorities, and when that work was conducted.

a. Was an evaluation of EcoHealth Alliance's work and whether it aligned with the agency's program goals and priorities conducted by the NIH before the award was issued? If yes, please provide any related documentation. If not, why not?

13. In April 2020 correspondence with EcoHealth Alliance, NIH wrote that it "received reports that the Wuhan Institute of Virology…has been conducting research at its facilities in China that pose serious bio-safety concerns."[28] What are the sources for those reports to NIH and what were the specific allegations reported?

14. Why did the NIH request that EcoHealth Alliance provide a sample of the pandemic coronavirus that the WIV used to determine its genetic sequence for SARS CoV-2?[29]

    a. Why is this information important to NIH's investigation?

    b. Has NIH obtained the sample and if so, what evaluations have been done, and for what purpose?

    c. If NIH has not yet obtained the sample, what are the planned studies and evaluations NIH will conduct with the sample when it is obtained?

15. What is the nature of NIH's concerns about purported restrictions at the WIV including "diminished cell-phone traffic in October 2019, and the evidence that there may have been roadblocks surrounding the facility from October 14-19, 2019[,]" about the WIV lab or virus origin?[30]

    a. What is the basis of information to NIH about the purported restrictions at the WIV?

    b. What are the other purported restrictions at the WIV in October 2019?

16. After terminating EcoHealth Alliance's 2019 project entitled "Understanding the Risk of Bat Coronavirus Emergence," the NIH later offered to reinstate the EcoHealth Alliance funding in July 2020 if EcoHealth Alliance agreed to meet certain conditions.[31]

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[28] Betsy McKay, *NIH Presses U.S. Nonprofit for Information on Wuhan Virology Lab*, THE WALL STREET JOURNAL (Aug. 19. 2020), *available at* https://www.wsj.com/articles/nih-presses-u-s-nonprofit-for-information-on-wuhan-virology-lab-11597829400.
[29] Meredith Wadman, *NIH imposes 'outrageous' conditions on resuming coronavirus grant targeted by Trump*, SCIENCEMAG (Aug. 19, 2020), *available at* https://www.sciencemag.org/news/2020/08/nih-imposes-outrageous-conditions-resuming-coronavirus-grant-targeted-trump.
[30] *Id.*
[31] Betsy McKay, *NIH Presses U.S. Nonprofit for Information on Wuhan Virology Lab*, THE WALL STREET JOURNAL (Aug. 19. 2020), *available at* https://www.wsj.com/articles/nih-presses-u-s-nonprofit-for-information-on-wuhan-virology-lab-11597829400.

a. Please provide all of the information presented to NIH from EcoHealth Alliance in response to NIH's conditions for reinstatement.

b. What actions did NIH take based upon the information received? How has the information been used in NIH's investigation?

c. One condition for the federal award reinstatement was for EcoHealth Alliance to arrange for an outside inspection of the WIV and its records, "with specific attention to addressing the question of whether WIV staff had SARS-CoV-2their possession prior to December 2019."[32] Why is it pertinent to the NIH's investigation if staff at WIV had SARS-CoV-2 in their possession prior to December 2019? What is the potential significance if the staff did have the virus in their possession prior to December 2019?

d. What information does NIH have that was used for the basis of requesting that the EcoHealth Alliance "must 'explain the apparent disappearance' of a scientist who worked in the Wuhan lab," and on social media was rumored to be "patient zero" of the pandemic?[33]

i. What is the potential significance about the whereabouts of this scientist and the photo being removed from the website?

17. Please provide all correspondence and communications between NIH and Columbia University related to federal funding involving the WIV, including email correspondence in April 2020 between Dr. Michael Lauer, Deputy Director of extramural research, and Naomi Schrag of Columbia University.

a. In an April 2020 email, Dr. Lauer advised Naomi Schrag of Columbia University that it would be helpful for NIH "to know about all China-based participants in this work since the Type 1 grant started in 2014 - who they were and how much money they received."[34] Why did NIH request that Columbia University provide information about all of the China-based participants?

i. What is the pertinence of the timeframe starting in 2014 for the requested information?

ii. Did Columbia University provide the NIH with the requested information about all of the China-based participants from all grantees since 2014? If so, please provide the information1. If not, why not?

<u>Federal Funding Records</u>

[32] *Id.*
[33] *Id.*
[34] Meredith Wadman and Jon Cohen, *NIH's axing of bat coronavirus grant a 'horrible precedent' and might break rules, critics say*, SCIENCEMAG (Apr. 30, 2020), *available at* https://www.sciencemag.org/news/2020/04/nih-s-axing-bat-coronavirus-grant-horrible-precedent-and-might-break-rules-critics-say.

18. Please provide ledgers or any accounting for dispersion of all NIH federal funding awards that EcoHealth Alliance has sent to the WIV, including through contracts, grants, donations, cooperative agreements, staffing, or any other support or means. In addition, please provide the results and outcomes from the funding and support.[35]

19. What is the total amount of NIH federal funding per year from 2017 through 2021 that has directly or indirectly supported the WIV scientists or research through grant recipients, including to EcoHealth Alliance; Wildlife Trust, Inc.; Columbia University Health Sciences; Trustees of Columbia University; University of North Carolina Chapel Hill; Vanderbilt University; University of Virginia; and Oregon Health and Science University?[36]

20. According to a report in *The Washington Post* on April 14, 2020, the WIV issued a news release in English about the final visit from U.S. Embassy scientist diplomats in Beijing, which occurred on March 27, 2018.[37] Does the NIH have a copy of this news release? If so, please provide a copy.

21. For NIH award recipients that have provided support to the WIV since January 1, 2012, please provide annual reports, trip reports related to the WIV, documentation of any survey or field trips by the WIV, and interim data summaries from the WIV.

22. Please provide copies of all grantee annual reports, progress reports, projects, studies, and observations since 2014 where foreign sites for all Type 1 and Type 2 awards have been documented as involving the WIV.

23. Please provide copies of all grantee annual reports, progress reports, projects, studies, and observations since 2014 for NIH domestic grantee awards with a foreign component involving the WIV.

24. Please provide the name(s) of the NIH program manager(s) or officer(s) responsible for overseeing the grants to EcoHealth Alliance and time period(s) of responsibility.

25. Please provide the name(s) of the NIH Scientific Review Officers responsible for reviewing and approving any NIH financial awards to EcoHealth Alliance and any other funding recipients that supported the WIV.

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[35] Betsy McKay, *NIH Presses U.S. Nonprofit for Information on Wuhan Virology Lab*, THE WALL STREET JOURNAL (Aug. 19. 2020), *available at* https://www.wsj.com/articles/nih-presses-u-s-nonprofit-for-information-on-wuhan-virology-lab-11597829400.

[36] National Institutes of Health, Research Portfolio online Reporting Tools, NIH RePorter *available at* https://report nih.gov/ (last accessed March 6, 2020).

[37] Josh Rogin, *Opinion: State Department cables warned of safety issues at Wuhan lab studying bat coronaviruses*, THE WASHINGTON POST (Apr. 14, 2020), *available at* https://www.washingtonpost.com/opinions/2020/04/14/state-department-cables-warned-safety-issues-wuhan-lab-studying-bat-coronaviruses/.

26. According to an editorial in *The Wall Street Journal*, the WIV housed tens of thousands of bat samples and laboratory animals in 2019.[38] Please provide any information the NIH has on the number of bat samples and animals at the WIV.

    a. Did any NIH scientists who are fluent in Mandarin review the Chinese scientific literature on the WIV research related to coronaviruses that is dated before February 1, 2020?

27. Does the NIH have the unpublished sequences of bat coronaviruses that were maintained in the WIV database before December 30, 2019, or before the database was removed from the internet?[39] Does NIH have the full sequences of the eight viruses sampled in the Yunnan province on an EcoHealth Alliance bat-virus sampling trip in 2015?

    a. Please provide NIH's analysis if the sequences have been analyzed.

    b. If NIH does not have the sequences, can NIH get this information from the EcoHealth Alliance or from other NIH-funded sources?

28. Please provide the original version of "Origin and cross-species transmission of bat coronaviruses in China" that was submitted to *Nature* by EcoHealth Alliance on October 6, 2019, published August 25, 2020, and funded in part by NIAID (award number R01AI110964).[40] If NIH does not have the October 6, 2019 report, can NIH obtain it from EcoHealth Alliance for this response? If so, please provide the report.

29. Have NIH, EcoHealth Alliance, or other NIH award recipient(s) been denied permission or access to results of any WIV research, which indirectly received financial support from NIH awards? If so, please provide the date(s), individuals involved, and circumstances of each denial.

We request that the NIH provide the requested documents and information in a coordinated response from all stakeholders and the appropriate divisions within NIH, including but not limited to subject matter experts from NIH's Division of Security and Emergency Response, the Office of Management Assessment, the Center for Scientific Review, the National Institute of Allergy and Infectious Diseases, and the Office of Extramural Research. After the requested information has been provided, we ask that the NIH provide a briefing to the Minority Committee staff to discuss the information that the NIH has related to the origins of SARS-CoV-2, including any potential links to the WIV. Finally, we request that you appoint an NIH working group representing an appropriate diversity of scientific disciplines to collect data and

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[38] Mike Pompeo and Miles Yu, *NIH Presses U.S. Nonprofit for Information on Wuhan Virology Lab*, THE WALL STREET JOURNAL (Feb. 23, 2021), *available at* https://www.wsj.com/articles/chinas-reckless-labs-put-the-world-at-risk-11614102828.

[39] Washington Post Editorial Board, *We're still missing the origin story of this pandemic. China is sitting on the answers*, THE WASHINGTON POST (Feb. 5, 2021), *available at* https://www.washingtonpost.com/opinions/2021/02/05/coronavirus-origins-mystery-china/?arc404=true.

[40] Latinne, A., Hu, B., Olival, K.J. et al,. *Origin and cross-species transmission of bat coronaviruses in China*, Nature (Aug. 25, 2020), *available at* https://www.nature.com/articles/s41467-020-17687-3#Ack1.

information related to COVID-19 origins (including the WIV), and that the NIH working group coordinate and consult with foreign scientific agencies involved in similar work.

Your assistance with this request is greatly appreciated. If you have any questions, please contact Alan Slobodin or Diane Cutler of the Minority Committee staff.

Sincerely,

Cathy McMorris Rodgers
Republican Leader
Committee on Energy and Commerce

Brett Guthrie
Republican Leader
Subcommittee on Health

H. Morgan Griffith
Republican Leader
Subcommittee on Oversight and Investigations

Attachment

Cc: The Honorable Frank Pallone, Chairman
The Honorable Diana DeGette, Chair, Subcommittee on Oversight and Investigations
The Honorable Anna Eshoo, Chair, Subcommittee on Health

From: Lauer, Michael (NIH/OD) [E]
To: Black, Jodi (NIH/OD) [E]
Cc: Lauer, Michael (NIH/OD) [E]
Subject: FW: request for a call...
Date: Thursday, April 16, 2020 7:57:51 AM
Attachments: Re Wuhan lab research .msg
RE Wuhan lab research .msg
RE Wuhan lab research .msg
Re Wuhan lab research .msg

Good morning Jodi – we discussed this grant at 0730 meeting. (b) (5)

Happy to talk.

Thanks, Mike

From: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Date: Wednesday, April 15, 2020 at 5:14 PM
To: "Black, Jodi (NIH/OD) [E]" (b) (6), "Bulls, Michelle G. (NIH/OD) [E]" (b) (6)
Cc: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Subject: Re: request for a call...

FYI – some email exchanges from earlier today.

Thanks, Mike

From: "Black, Jodi (NIH/OD) [E]" (b) (6)
Date: Wednesday, April 15, 2020 at 4:07 PM
To: "Bulls, Michelle G. (NIH/OD) [E]" (b) (6)
Cc: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Subject: Re: request for a call...

Ok thanks for working on this with Emily.

Best,
Jodi

Jodi B. Black, PhD, MMSc
Deputy Director
Office of Extramural Research, NIH

From: Michelle Bulls (b) (6)
Date: Wednesday, April 15, 2020 at 3:49 PM
To: Jodi OER (b) (6)

Cc: Mike Lauer (b) (6), Michelle Bulls (b) (6)
Subject: FW: request for a call...

FYI. Urgent.

(b) (5)

(b) (5) Waiting to hear back from Emily and will set up time to talk to Jodi tomorrow.

Thanks,
Michelle

From: Linde, Emily (NIH/NIAID) [E] (b) (6)
Sent: Wednesday, April 15, 2020 12:03 PM
To: Bulls, Michelle G. (NIH/OD) [E] (b) (6); Ta, Kristin (NIH/OD) [E] (b) (6); Tarwater, Robert (NIH/OD) [E] (b) (6); Dean, Diane (NIH/OD) [E] (b) (6)
Subject: request for a call...

Hello,

(b) (5)

Can we have a call to discuss (b) (5)

Many thanks,

Emily

Emily Linde

Director, Grants Management Program

NIAID, NIH, DHHS

Telephone Number: (b) (6)

Email Address: (b) (6)

From: Lauer, Michael (NIH/OD) [E]
To: Tabak, Lawrence (NIH/OD) [E]
Cc: Schwetz, Tara (NIH/OD) [E]; Wolinetz, Carrie (NIH/OD) [E]; Lauer, Michael (NIH/OD) [E]
Subject: Re: Wuhan lab research
Date: Wednesday, April 15, 2020 7:04:15 AM
Attachments: FACTS Snapshot for 2-R01-AI110964-06 DASZAK, PETER QVR.pdf
NoA R01AI110964-06.pdf
NoA R01AI110964-01.pdf

(b) (5)

[redacted]

(b) (5)

RESEARCH
Department of Health and Human Services
National Institutes of Health

Federal Award Date: 08/05/2019

NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Grant Number: 2R01AI110964-06 REVISED
FAIN: R01AI110964

Principal Investigator(s):
PETER DASZAK, PHD

Project Title: Understanding the Risk of Bat Coronavirus Emergence

Dr. Daszak, Peter
PD/PI
460 West 34th Street
Suite 1701
New York, NY 100012320

Award e-mailed to: (b) (6)

Period Of Performance:
Budget Period: 07/24/2019 – 06/30/2020
Project Period: 06/01/2014 – 06/30/2024

Dear Business Official:

The National Institutes of Health hereby revises this award to reflect a decrease in the amount of $71,770 (see "Award Calculation" in Section I and "Terms and Conditions" in Section III) to ECOHEALTH ALLIANCE, INC. in support of the above referenced project. This award is pursuant to the authority of 42 USC 241 42 CFR 52 and is subject to the requirements of this statute and regulation and of other referenced, incorporated or attached terms and conditions.

Acceptance of this award including the "Terms and Conditions" is acknowledged by the grantee when funds are drawn down or otherwise obtained from the grant payment system.

Each publication, press release, or other document about research supported by an NIH award must include an acknowledgment of NIH award support and a disclaimer such as "Research reported in this publication was supported by the National Institute Of Allergy And Infectious Diseases of the National Institutes of Health under Award Number R01AI110964. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health." Prior to issuing a press release concerning the outcome of this research, please notify the NIH awarding IC in advance to allow for coordination.

Award recipients must promote objectivity in research by establishing standards that provide a reasonable expectation that the design, conduct and reporting of research funded under NIH awards will be free from bias resulting from an Investigator's Financial Conflict of Interest (FCOI), in accordance with the 2011 revised regulation at 42 CFR Part 50 Subpart F. The Institution shall submit all FCOI reports to the NIH through the eRA Commons FCOI Module. The regulation does not apply to Phase I Small Business Innovative Research (SBIR) and Small Business Technology Transfer (STTR) awards. Consult the NIH website http://grants.nih.gov/grants/policy/coi/ for a link to the regulation and additional important information.

If you have any questions about this award, please contact the individual(s) referenced in Section IV.

Sincerely yours,

Tseday G Girma
Grants Management Officer
NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Additional information follows

SECTION I – AWARD DATA – 2R01AI110964-06 REVISED

Award Calculation (U.S. Dollars)

Salaries and Wages	$170,123
Fringe Benefits	$53,590
Personnel Costs (Subtotal)	$223,713
Consultant Services	$49,750
Materials & Supplies	$20,850
Travel	$15,027
Subawards/Consortium/Contractual Costs	$229,651
Federal Direct Costs	$538,991
Federal F&A Costs	$122,989
Approved Budget	$661,980
Total Amount of Federal Funds Obligated (Federal Share)	$661,980
TOTAL FEDERAL AWARD AMOUNT	$661,980
AMOUNT OF THIS ACTION (FEDERAL SHARE)	($-71,770)

SUMMARY TOTALS FOR ALL YEARS		
YR	**THIS AWARD**	**CUMULATIVE TOTALS**
6	$661,980	$661,980
7	$637,980	$637,980
8	$637,980	$637,980
9	$637,980	$637,980
10	$637,980	$637,980

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

Fiscal Information:

CFDA Name:	Allergy and Infectious Diseases Research
CFDA Number:	93.855
EIN:	1311726494A1
Document Number:	RAI110964B
PMS Account Type:	P (Subaccount)
Fiscal Year:	2019

IC	CAN	2019	2020	2021	2022	2023
AI	8472364	$661,980	$637,980	$637,980	$637,980	$637,980

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

NIH Administrative Data:
PCC: M51C B / **OC**: 414B / **Released**: (b) (6) 08/02/2019
Award Processed: 08/05/2019 12:01:51 AM

SECTION II – PAYMENT/HOTLINE INFORMATION – 2R01AI110964-06 REVISED

For payment and HHS Office of Inspector General Hotline information, see the NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm

SECTION III – TERMS AND CONDITIONS – 2R01AI110964-06 REVISED

This award is based on the application submitted to, and as approved by, NIH on the above-titled project and is subject to the terms and conditions incorporated either directly or by reference in the following:

a. The grant program legislation and program regulation cited in this Notice of Award.
b. Conditions on activities and expenditure of funds in other statutory requirements, such as those included in appropriations acts.

c. 45 CFR Part 75.
d. National Policy Requirements and all other requirements described in the NIH Grants Policy Statement, including addenda in effect as of the beginning date of the budget period.
e. Federal Award Performance Goals: As required by the periodic report in the RPPR or in the final progress report when applicable.
f. This award notice, INCLUDING THE TERMS AND CONDITIONS CITED BELOW.

(See NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm for certain references cited above.)

Research and Development (R&D): All awards issued by the National Institutes of Health (NIH) meet the definition of "Research and Development" at 45 CFR Part§ 75.2**.** As such, auditees should identify NIH awards as part of the R&D cluster on the Schedule of Expenditures of Federal Awards (SEFA). The auditor should test NIH awards for compliance as instructed in Part V, Clusters of Programs. NIH recognizes that some awards may have another classification for purposes of indirect costs. The auditor is not required to report the disconnect (i.e., the award is classified as R&D for Federal Audit Requirement purposes but non-research for indirect cost rate purposes), unless the auditee is charging indirect costs at a rate other than the rate(s) specified in the award document(s).

An unobligated balance may be carried over into the next budget period without Grants Management Officer prior approval.

This grant is subject to Streamlined Noncompeting Award Procedures (SNAP).

This award is subject to the requirements of 2 CFR Part 25 for institutions to receive a Dun & Bradstreet Universal Numbering System (DUNS) number and maintain an active registration in the System for Award Management (SAM). Should a consortium/subaward be issued under this award, a DUNS requirement must be included. See http://grants.nih.gov/grants/policy/awardconditions.htm for the full NIH award term implementing this requirement and other additional information.

This award has been assigned the Federal Award Identification Number (FAIN) R01AI110964. Recipients must document the assigned FAIN on each consortium/subaward issued under this award.

Based on the project period start date of this project, this award is likely subject to the Transparency Act subaward and executive compensation reporting requirement of 2 CFR Part 170. There are conditions that may exclude this award; see http://grants.nih.gov/grants/policy/awardconditions.htm for additional award applicability information.

In accordance with P.L. 110-161, compliance with the NIH Public Access Policy is now mandatory. For more information, see NOT-OD-08-033 and the Public Access website: http://publicaccess.nih.gov/.

In accordance with the regulatory requirements provided at 45 CFR 75.113 and Appendix XII to 45 CFR Part 75, recipients that have currently active Federal grants, cooperative agreements, and procurement contracts with cumulative total value greater than $10,000,000 must report and maintain information in the System for Award Management (SAM) about civil, criminal, and administrative proceedings in connection with the award or performance of a Federal award that reached final disposition within the most recent five-year period. The recipient must also make semiannual disclosures regarding such proceedings. Proceedings information will be made publicly available in the designated integrity and performance system (currently the Federal Awardee Performance and Integrity Information System (FAPIIS)). Full reporting requirements and procedures are found in Appendix XII to 45 CFR Part 75. This term does not apply to NIH fellowships.

Treatment of Program Income:
Additional Costs

SECTION IV – AI Special Terms and Conditions – 2R01AI110964-06 REVISED

Clinical Trial Indicator: No
This award does not support any NIH-defined Clinical Trials. See the NIH Grants Policy Statement Section 1.2 for NIH definition of Clinical Trial.

REVISED AWARD: This award is revised to adjust the budget in accordance with the letter from Aleksei Chmura/ECOHealth Alliance.

Supersedes previous Notice of Award dated **07/24/2019**.

****
This Notice of Award (NoA) includes funds for activity with **The University of North Carolina at Chapel Hill** in the amount of **$77,750** (**$50,000** direct costs + **$27,750**F&A costs).

This Notice of Award (NoA) includes funds for activity with **Wuhan Institute of Virology** in the amount of **$76,301** (**$70,649** direct costs + **$5,652** F&A costs).

This Notice of Award (NoA) includes funds for activity with **Institute of Pathogen Biology** in the amount of **$75,600** (**$70,000** direct costs + **$5,600** F&A costs).

****
The Research Performance Progress Report (RPPR), Section G.9 (Foreign component), includes reporting requirements for all research performed outside of the United States. Research conducted at the following site(s) must be reported in your RPPR:

Wuhan Institute of Virology, CHINA

Institute of Pathogen Biology, CHINA

East China Normal University, CHINA

Duke-NUS Medical School, SINGAPORE

****
This award reflects current Federal policies regarding Facilities & Administrative (F&A) Costs for foreign grantees including foreign sub-awardees, and domestic awards with foreign sub-awardees. Please see: Chapter 16 Grants to Foreign Organizations, International Organizations, and Domestic Grants with Foreign Components, Section 16.6 “Allowable and Unallowable Cost” of the NIH Grants Policy.

****
This award may include collaborations with and/or between foreign organizations. Please be advised that short term travel visa expenses are an allowable expense on this grant, if justified as critical and necessary for the conduct of the project.

****
The budget period anniversary start date for future year(s) will be **July** 1.

****
Dissemination of study data will be in accord with the Recipient’s accepted genomic data sharing plan as stated in the page(s) **203** of the application. Failure to adhere to the sharing plan as mutually agreed upon by the Recipient and the NIAID may result in Enforcement Actions as described in the NIH Grants Policy Statement.

****
This award is subject to the Clinical Terms of Award referenced in the NIH Guide for Grants and Contracts, July 8, 2002, NOT AI-02-032. These terms and conditions are hereby incorporated by

reference, and can be accessed via the following World Wide Web address: https://www.niaid.nih.gov/grants-contracts/niaid-clinical-terms-award All submissions required by the NIAID Clinical Terms of Award must be forwarded electronically or by mail to the responsible NIAID Program Official identified on this Notice of Award.

****

Awardees who conduct research involving Select Agents (see 42 CFR 73 for the Select Agent list; and 7 CFR 331 and 9 CFR 121 for the relevant animal and plant pathogens at http://www.selectagents.gov/Regulations.html) must complete registration with CDC (or APHIS, depending on the agent) before using NIH funds. No funds can be used for research involving Select Agents if the final registration certificate is denied.

Prior to conducting a restricted experiment with a Select Agent or Toxin, awardees must notify the NIAID and must request and receive approval from CDC or APHIS.

****

Select Agents:
Awardee of a project that at any time involves a restricted experiment with a select agent, is responsible for notifying and receiving prior approval from the NIAID. Please be advised that changes in the use of a Select Agent will be considered a change in scope and require NIH awarding office prior approval. The approval is necessary for new select agent experiments as well as changes in on-going experiments that would require change in the biosafety plan and/or biosafety containment level. An approval to conduct a restricted experiment granted to an individual cannot be assumed an approval to other individuals who conduct the same restricted experiment as defined in the Select Agents Regulation 42 CFR Part 73, Section 13.b (http://www.selectagents.gov/Regulations.html).

Highly Pathogenic Agent:
NIAID defines a Highly Pathogenic Agent as an infectious Agent or Toxin that may warrant a biocontainment safety level of BSL3 or higher according to the current edition of the CDC/NIH Biosafety in Microbiological and Biomedical Laboratories (BMBL) (http://www.cdc.gov/OD/ohs/biosfty/bmbl5/bmbl5toc.htm). Research funded under this grant must adhere to the BMBL, including using the BMBL-recommended biocontainment level at a minimum. If your Institutional Biosafety Committee (or equivalent body) or designated institutional biosafety official recommend a higher biocontainment level, the highest recommended containment level must be used.
When submitting future Progress Reports indicate at the beginning of the report:

If no research with a Highly Pathogenic Agent or Select Agent has been performed or is planned to be performed under this grant.

If your IBC or equivalent body or official has determined, for example, by conducting a risk assessment, that the work being planned or performed under this grant may be conducted at a biocontainment safety level that is lower than BSL3.

If the work involves Select Agents and/or Highly Pathogenic Agents, also address the following points:

Any changes in the use of the Agent(s) or Toxin(s) including its restricted experiments that have resulted in a change in the required biocontainment level, and any resultant change in location, if applicable, as determined by your IBC or equivalent body or official.

If work with a new or additional Agent(s)/Toxin(s) is proposed in the upcoming project period, provide:

- A list of the new and/or additional Agent(s) that will be studied;
- A description of the work that will be done with the Agent(s), and whether or not the work is a restricted experiment;
- The title and location for each biocontainment resource/facility, including the name of the organization that operates the facility, and the biocontainment level at which the work will be conducted, with documentation of approval by your IBC or equivalent body or official. It is important to note if the work is being done in a new location.

STAFF CONTACTS

The Grants Management Specialist is responsible for the negotiation, award and administration of this project and for interpretation of Grants Administration policies and provisions. The Program Official is responsible for the scientific, programmatic and technical aspects of this project. These individuals work together in overall project administration. Prior approval requests (signed by an Authorized Organizational Representative) should be submitted in writing to the Grants Management Specialist. Requests may be made via e-mail.

Grants Management Specialist: Tseday G Girma
Email: (b) (6) **Phone**: (b) (6) **Fax**: 301-493-0597

Program Official: Erik J. Stemmy
Email: (b) (6) **Phone**: (b) (6)

SPREADSHEET SUMMARY
GRANT NUMBER: 2R01AI110964-06 REVISED

INSTITUTION: ECOHEALTH ALLIANCE, INC.

Budget	Year 6	Year 7	Year 8	Year 9	Year 10
Salaries and Wages	$170,123	$170,123	$170,123	$170,123	$170,123
Fringe Benefits	$53,590	$53,590	$53,590	$53,590	$53,590
Personnel Costs (Subtotal)	$223,713	$223,713	$223,713	$223,713	$223,713
Consultant Services	$49,750	$49,750	$49,750	$49,750	$49,750
Materials & Supplies	$20,850	$14,850	$14,850	$14,850	$14,850
Travel	$15,027	$15,027	$15,027	$15,027	$15,027
Subawards/Consortium/Contractual Costs	$229,651	$229,651	$229,651	$229,651	$229,651
Publication Costs		$6,000	$6,000	$6,000	$6,000
TOTAL FEDERAL DC	$538,991	$538,991	$538,991	$538,991	$538,991
TOTAL FEDERAL F&A	$122,989	$98,989	$98,989	$98,989	$98,989
TOTAL COST	$661,980	$637,980	$637,980	$637,980	$637,980

Facilities and Administrative Costs	Year 6	Year 7	Year 8	Year 9	Year 10
F&A Cost Rate 1	32%	32%	32%	32%	32%
F&A Cost Base 1	$384,340	$309,340	$309,340	$309,340	$309,340
F&A Costs 1	$122,989	$98,989	$98,989	$98,989	$98,989

Notice of Award

RESEARCH **Issue Date:** 05/27/2014

Department of Health and Human Services
National Institutes of Health
NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Grant Number: 1R01AI110964-01
FAIN: R01AI110964

Principal Investigator(s):
PETER DASZAK, PHD

Project Title: Understanding the Risk of Bat Coronavirus Emergence

Aleksei
President
460 West 34th Street
17th Floor
New York, NY 100012317

Award e-mailed to: (b) (6)

Budget Period: 06/01/2014 – 05/31/2015
Project Period: 06/01/2014 – 05/31/2019

Dear Business Official:

The National Institutes of Health hereby awards a grant in the amount of $666,442 (see "Award Calculation" in Section I and "Terms and Conditions" in Section III) to ECOHEALTH ALLIANCE, INC. in support of the above referenced project. This award is pursuant to the authority of 42 USC 241 42 CFR 52 and is subject to the requirements of this statute and regulation and of other referenced, incorporated or attached terms and conditions.

Acceptance of this award including the "Terms and Conditions" is acknowledged by the grantee when funds are drawn down or otherwise obtained from the grant payment system.

Each publication, press release, or other document about research supported by an NIH award must include an acknowledgment of NIH award support and a disclaimer such as "Research reported in this publication was supported by the National Institute Of Allergy And Infectious Diseases of the National Institutes of Health under Award Number R01AI110964. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health." Prior to issuing a press release concerning the outcome of this research, please notify the NIH awarding IC in advance to allow for coordination.

Award recipients must promote objectivity in research by establishing standards that provide a reasonable expectation that the design, conduct and reporting of research funded under NIH awards will be free from bias resulting from an Investigator's Financial Conflict of Interest (FCOI), in accordance with the 2011 revised regulation at 42 CFR Part 50 Subpart F. The Institution shall submit all FCOI reports to the NIH through the eRA Commons FCOI Module. The regulation does not apply to Phase I Small Business Innovative Research (SBIR) and Small Business Technology Transfer (STTR) awards. Consult the NIH website http://grants.nih.gov/grants/policy/coi/ for a link to the regulation and additional important information.

If you have any questions about this award, please contact the individual(s) referenced in Section IV.

Sincerely yours,

Laura A. Pone
Grants Management Officer
NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Additional information follows

SECTION I – AWARD DATA – 1R01AI110964-01

Award Calculation (U.S. Dollars)

Salaries and Wages	$167,708
Fringe Benefits	$54,168
Supplies	$21,400
Travel Costs	$35,918
Other Costs	$10,000
Consortium/Contractual Cost	$227,663
Federal Direct Costs	$516,857
Federal F&A Costs	$149,585
Approved Budget	$666,442
Federal Share	$666,442
TOTAL FEDERAL AWARD AMOUNT	$666,442
AMOUNT OF THIS ACTION (FEDERAL SHARE)	$666,442

SUMMARY TOTALS FOR ALL YEARS		
YR	**THIS AWARD**	**CUMULATIVE TOTALS**
1	$666,442	$666,442
2	$630,445	$630,445
3	$611,090	$611,090
4	$597,112	$597,112
5	$581,646	$581,646

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

Fiscal Information:

CFDA Number:	93.855
EIN:	1311726494A1
Document Number:	RAI110964A
PMS Account Type:	P (Subaccount)
Fiscal Year:	2014

IC	CAN	2014	2015	2016	2017	2018
AI	8472350	$666,442	$630,445	$611,090	$597,112	$581,646

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

NIH Administrative Data:
PCC: M51C / **OC**: 414A / **Released**: (b) (6) 05/20/2014
Award Processed: 05/08/2014 01:52:21 PM

SECTION II – PAYMENT/HOTLINE INFORMATION – 1R01AI110964-01

For payment and HHS Office of Inspector General Hotline information, see the NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm

SECTION III – TERMS AND CONDITIONS – 1R01AI110964-01

This award is based on the application submitted to, and as approved by, NIH on the above-titled project and is subject to the terms and conditions incorporated either directly or by reference in the following:

a. The grant program legislation and program regulation cited in this Notice of Award.

b. Conditions on activities and expenditure of funds in other statutory requirements, such as those included in appropriations acts.
c. 45 CFR Part 74 or 45 CFR Part 92 as applicable.
d. The NIH Grants Policy Statement, including addenda in effect as of the beginning date of the budget period.
e. This award notice, INCLUDING THE TERMS AND CONDITIONS CITED BELOW.

(See NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm for certain references cited above.)

An unobligated balance may be carried over into the next budget period without Grants Management Officer prior approval.

This grant is subject to Streamlined Noncompeting Award Procedures (SNAP).

This award is subject to the requirements of 2 CFR Part 25 for institutions to receive a Dun & Bradstreet Universal Numbering System (DUNS) number and maintain an active registration in the Central Contractor Registration. Should a consortium/subaward be issued under this award, a DUNS requirement must be included. See http://grants.nih.gov/grants/policy/awardconditions.htm for the full NIH award term implementing this requirement and other additional information.

This award has been assigned the Federal Award Identification Number (FAIN) R01AI110964. Recipients must document the assigned FAIN on each consortium/subaward issued under this award.

Based on the project period start date of this project, this award is likely subject to the Transparency Act subaward and executive compensation reporting requirement of 2 CFR Part 170. There are conditions that may exclude this award; see http://grants.nih.gov/grants/policy/awardconditions.htm for additional award applicability information.

In accordance with P.L. 110-161, compliance with the NIH Public Access Policy is now mandatory. For more information, see NOT-OD-08-033 and the Public Access website: http://publicaccess.nih.gov/.

Treatment of Program Income:
Additional Costs

SECTION IV – AI Special Terms and Conditions – 1R01AI110964-01

THIS AWARD CONTAINS GRANT SPECIFIC RESTRICTIONS. THESE RESTRICTIONS MAY ONLY BE LIFTED BY A REVISED NOTICE OF AWARD.

RESTRICTION: This award is issued with the knowledge that subjects may be involved within the period of support, but definite plans were not set forth in the application as per 45 CFR 46.118. No human subjects may be involved in any project supported by this award until all requirements for Human Subjects research as identified in the PHS398/SF424 Instructions have been provided to and approved by NIH.

RESTRICTION: The present award is being made without a currently valid certification of IRB approval for this project with the following restriction: Only activities that are clearly severable and independent from activities that involve human subjects may be conducted pending the NIAID's acceptance of the certification of IRB review and approval.

No funds may be drawn down from the payment system and no obligations may be made against Federal funds for any research involving human subjects prior to the NIAID's notification to the grantee that the identified issues have been resolved and this restriction removed.

~~~~~~~~~
This award includes funds for subcontract/consortium activity with Wuhan Institute of Virology, CHINA and is budgeted as follows:

	-Yr 1	-Yr 2	-Yr 3	-Yr 4	-Yr 5
Total Direct Costs	$123,699	$128,718	$147,335	$147,335	$147,335
F&A Costs @ 8%(MTDC)	$9,896	$10,297	$11,787	$11,787	$11,787
TOTAL COSTS	$133,595	$139,015	$159,122	$159,122	$159,122

Consortiums are to be established and administered as described in the NIH Grants Policy Statement. This written agreement with the consortium must address the negotiated arrangements for meeting the scientific, administrative, financial, and reporting requirements for this grant.
~~~~~~~~~
This award includes funds for subcontract/consortium activity with East China Normal University, CHINA and is budgeted as follows:

	-Yr 1	-Yr 2	-Yr 3	-Yr 4	-Yr 5
Total Direct Costs	$87,100	$67,300	$50,108	$39,167	$14,850
F&A Costs @ 8%(MTDC)	$6,968	$5,384	$4,009	$3,133	$2,404
TOTAL COSTS	$94,068	$72,684	$54,117	$42,300	$32,454

Consortiums are to be established and administered as described in the NIH Grants Policy Statement. This written agreement with the consortium must address the negotiated arrangements for meeting the scientific, administrative, financial, and reporting requirements for this grant.
~~~~~~~~~
Select Agents:
Awardee of a project that at any time involves a restricted experiment with a select agent, is responsible for notifying and receiving prior approval from the NIAID. Please be advised that changes in the use of a Select Agent will be considered a change in scope and require NIH awarding office prior approval. The approval is necessary for new select agent experiments as well as changes in on-going experiments that would require change in the biosafety plan and/or biosafety containment level. An approval to conduct a restricted experiment granted to an individual cannot be assumed an approval to other individuals who conduct the same restricted experiment as defined in the Select Agents Regulation 42 CFR Part 73, Section 13.b (http://www.selectagents.gov/Regulations.html).

Highly Pathogenic Agent:
NIAID defines a Highly Pathogenic Agent as an infectious Agent or Toxin that may warrant a biocontainment safety level of BSL3 or higher according to the current edition of the CDC/NIH Biosafety in Microbiological and Biomedical Laboratories (BMBL) (http://www.cdc.gov/OD/ohs/biosfty/bmbl5/bmbl5toc.htm). Research funded under this grant must adhere to the BMBL, including using the BMBL-recommended biocontainment level at a minimum. If your Institutional Biosafety Committee (or equivalent body) or designated institutional biosafety official recommend a higher biocontainment level, the highest recommended containment level must be used.
When submitting future Progress Reports indicate at the beginning of the report:

If no research with a Highly Pathogenic Agent or Select Agent has been performed or is planned to be performed under this grant.

If your IBC or equivalent body or official has determined, for example, by conducting a risk assessment, that the work being planned or performed under this grant may be conducted at a biocontainment safety level that is lower than BSL3.

If the work involves Select Agents and/or Highly Pathogenic Agents, also address the following points:

Any changes in the use of the Agent(s) or Toxin(s) including its restricted experiments that have resulted in a change in the required biocontainment level, and any resultant change in location, if applicable, as determined by your IBC or equivalent body or official.
~~~~~~~~~

If work with a new or additional Agent(s)/Toxin(s) is proposed in the upcoming project period, provide:

o A list of the new and/or additional Agent(s) that will be studied;
o A description of the work that will be done with the Agent(s), and whether or not the work is a restricted experiment;
o The title and location for each biocontainment resource/facility, including the name of the organization that operates the facility, and the biocontainment level at which the work will be conducted, with documentation of approval by your IBC or equivalent body or official. It is important to note if the work is being done in a new location.

STAFF CONTACTS

The Grants Management Specialist is responsible for the negotiation, award and administration of this project and for interpretation of Grants Administration policies and provisions. The Program Official is responsible for the scientific, programmatic and technical aspects of this project. These individuals work together in overall project administration. Prior approval requests (signed by an Authorized Organizational Representative) should be submitted in writing to the Grants Management Specialist. Requests may be made via e-mail.

Grants Management Specialist: Laura A. Pone
Email: (b) (6) **Phone**: (b) (6) **Fax**: 301-493-0597

Program Official: Erik J. Stemmy
Email: (b) (6) **Phone**: (b) (6)

SPREADSHEET SUMMARY
GRANT NUMBER: 1R01AI110964-01

INSTITUTION: ECOHEALTH ALLIANCE, INC.

Budget	Year 1	Year 2	Year 3	Year 4	Year 5
Salaries and Wages	$167,708	$167,708	$167,708	$167,708	$167,708
Fringe Benefits	$54,168	$54,168	$54,168	$54,168	$54,168
Supplies	$21,400	$19,250	$7,250	$7,000	$3,500
Travel Costs	$35,918	$35,918	$35,918	$35,918	$35,918
Other Costs	$10,000	$13,550	$11,050	$9,800	$9,400
Consortium/Contractual Cost	$227,663	$211,699	$213,239	$201,422	$191,576
TOTAL FEDERAL DC	$516,857	$502,293	$489,333	$476,016	$462,270
TOTAL FEDERAL F&A	$149,585	$128,152	$121,757	$121,096	$119,376
TOTAL COST	$666,442	$630,445	$611,090	$597,112	$581,646

Facilities and Administrative Costs	Year 1	Year 2	Year 3	Year 4	Year 5
F&A Cost Rate 1	44.1%	44.1%	44.1%	44.1%	44.1%
F&A Cost Base 1	$339,194	$290,594	$276,094	$274,594	$270,694
F&A Costs 1	$149,585	$128,152	$121,757	$121,096	$119,376

From: Lauer, Michael (NIH/OD) [E]
To: (b) (6); Naomi Schrag
Cc: Black, Jodi (NIH/OD) [E]
Subject: Please read and acknowledge receipt -- Actions needed regarding 2R01AI110964-06
Date: Sunday, April 19, 2020 10:59:54 AM
Attachments: EcoHealth Alliance re AI grant 4 19 20.pdf

Dear Dr. Olival and Ms. Schrag

Please see attached.

Many thanks, Mike

Michael S Lauer, MD
NIH Deputy Director for Extramural Research
1 Center Drive, Building 1, Room 144
Bethesda, MD 20892
Phone: (b) (6)
Email: (b) (6)

Date: April 19, 2020

From: Michael S Lauer, MD
NIH Deputy Director for Extramural Research

To: Kevin Olival, PhD
Vice-President for Research
EcoHealth Alliance
(b) (6)

Naomi Schrag, JD
Vice-President for Research Compliance, Training, and Policy
Columbia University
(b) (6)

Subject: Project Number 2R01AI110964-06

Dear Dr. Olival and Ms. Schrag:

EcoHealth Alliance, Inc. is the recipient, as grantee, of an NIH grant entitled "Understanding the Risk of Bat Coronavirus Emergence." It is our understanding that one of the sub-recipients of the grant funds is the Wuhan Institute of Virology ("WIV"). It is our understanding that WIV studies the interaction between corona viruses and bats. The scientific community believes that the coronavirus causing COVID-19 jumped from bats to humans likely in Wuhan where the COVID-19 pandemic began. There are now allegations that the current crisis was precipitated by the release from WIV of the coronavirus responsible for COVID-19. Given these concerns, we are pursuing suspension of WIV from participation in Federal programs.

While we review these allegations during the period of suspension, you are instructed to cease providing any funds from the above noted grant to the WIV. This temporary action is authorized by 45 C.F.R. § 75.371(d) ("Initiate suspension or debarment proceedings as authorized under 2 C.F.R. part 180"). The incorporated OMB provision provides that the funding agency may, through suspension, immediately and temporarily exclude from Federal programs persons who are not presently responsible where "immediate action is necessary to protect the public interest." 2 C.F.R. § 180.700(c). It is in the public interest that NIH ensure that a sub-recipient has taken all appropriate precautions to prevent the release of pathogens that it is studying. This suspension of the sub-recipient does not affect the remainder of your grant assuming that no grant funds are provided to WIV following receipt of this email during the period of suspension.

From:	Lauer, Michael (NIH/OD) [E]
To:	Tabak, Lawrence (NIH/OD) [E]
Cc:	Lauer, Michael (NIH/OD) [E]
Subject:	Re: Draft response for review -- FW: Request for information: Senate Qs - Wuhan Institute of Virology
Date:	Wednesday, April 15, 2020 7:23:10 AM
Attachments:	NoA R01AI110964-06.pdf NoA R01AI110964-01.pdf FACTS Snapshot for 2-R01-AI110964-06 DASZAK, PETER QVR.pdf

Hi Larry – on the Type 1 total is 749,976. On the Type 2, looks like the total is 76,301 (so far). Thus total is 749,976+76,301=826,277.

It's a subcontract going through New York.

Mike

From: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Date: Wednesday, April 15, 2020 at 7:12 AM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Subject: Re: Draft response for review -- FW: Request for information: Senate Qs - Wuhan Institute of Virology

Mike – sorry – what is the total amount Wuhan has received since 2014?

Does the money go to NY and they send to Wuhan or do we send to Wuhan directly.

Thanks
Larry

From: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Date: Wednesday, April 15, 2020 at 7:11 AM
To: "Tabak, Lawrence (NIH/OD) [E]" (b) (6), "Erbelding, Emily (NIH/NIAID) [E]" (b) (6)
Cc: "Marston, Hilary (NIH/NIAID) [E]" (b) (6), "Lauer, Michael (NIH/OD) [E]" (b) (6)
Subject: Re: Draft response for review -- FW: Request for information: Senate Qs - Wuhan Institute of Virology

Thanks – just sent you budget details.

Mike

From: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Date: Tuesday, April 14, 2020 at 10:12 PM
To: "Erbelding, Emily (NIH/NIAID) [E]" (b) (6)
Cc: "Marston, Hilary (NIH/NIAID) [E]" (b) (6), "Lauer, Michael (NIH/OD) [E]" (b) (6)
Subject: Re: Draft response for review -- FW: Request for information: Senate Qs - Wuhan Institute of Virology

Thanks Emily.
Looping in Mike Lauer,
Larry

From: "Erbelding, Emily (NIH/NIAID) [E]" (b) (6)
Date: Tuesday, April 14, 2020 at 10:11 PM
To: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Cc: "Marston, Hilary (NIH/NIAID) [E]" (b) (6)
Subject: Fwd: Draft response for review -- FW: Request for information: Senate Qs - Wuhan Institute of Virology

I am forwarding draft response below to inquiry from Rubio et al earlier.

PI is Peter Dazsak, Eco Health alliance in NYC. Wuhan subcontract is approximately 74k per year. I will try to find more accurate subcontract numbers.

Sent from my iPad

Begin forwarded message:

> **From:** "Abbey, Lillian (NIH/NIAID) [E]" (b) (6)
> **Date:** April 14, 2020 at 4:24:34 PM EDT
> **To:** "Cassetti, Cristina (NIH/NIAID) [E]" (b) (6), "Erbelding, Emily (NIH/NIAID) [E]" (b) (6)
> **Cc:** "Ford, Andrew (NIH/NIAID) [E]" (b) (6), "Bateman, Karen (NIH/NIAID) [E]" (b) (6), "Werner, Alyssa (NIH/NIAID) [E]" (b) (6), "Mulach, Barbara (NIH/NIAID) [E]" (b) (6)
> **Subject: Draft response for review -- FW: Request for information: Senate Qs - Wuhan Institute of Virology**
>
> Dear Cristina and Emily,
> Incorporated below in red font is a draft response Andrew developed based on his discussion with Erik. (b) (5) Also, Andrew provided the attached publication from mid-March, noting that we may want to share it with the OD.
>
> DRAFT RESPONSE:
>
> | | | | |
> |---|---|---|---|
> | **Project Number:** | 2R01AI110964-06 | **Contact PI / Project Leader:** | DASZAK, PETER |
> | **Title:** | UNDERSTANDING THE RISK OF BAT CORONAVIRUS EMERGENCE | **Awardee Organization:** | ECOHEALTH ALLIANCE, INC. |
>
> https://projectreporter.nih.gov/project_info_description.cfm?

aid=9819304&icde=49588715&ddparam=&ddvalue=&ddsub=&cr=1&csb=default&cs=ASC&pball=

1. What are the goals of the main grant:
   (b) (5)
2. What are the specific activities supported by the sub to the Wuhan lab and the total costs associated with these activities. Please verify if the creation of recombinant bat in Wuhan is included in their research activities.
   (b) (5)

Total award information is available in Reporter at link above but budget information about subcontracts is not publicly available as these awards are administered by the grantee institution.

From: Crawford, Chase (NIH/NIAID) [E] (b) (6)
Sent: Monday, April 13, 2020 5:41 PM
To: NIAID BUGS (b) (6)
Cc: Auchincloss, Hugh (NIH/NIAID) [E] (b) (6); Harper, Jill (NIH/NIAID) [E] (b) (6); NIAID OCGR Leg (b) (6)
Subject: Request for information: Senate Qs - Wuhan Institute of Virology

Hi BUGS,

Staff to Senator Marco Rubio (R-FL) has forwarded an email to Building 1 from the White Coat Waste Project (see bottom of email chain). The forwarded message links to recent articles in The Daily Mail and the Washington Examiner on NIH support for previous coronavirus studies involving the Wuhan Institute of Virology. Building 1 has asked if NIAID has any information related to this research that we can share with staff to Senators Rubio and Mike Braun (R-IN).

To help us better understand this congressional request, is there any background information that you can provide on the activities discussed in the articles referenced

below?

Thanks,
Chase
(b) (6)

From: LaMontagne, Karen (NIH/OD) [E] (b) (6)
Sent: Monday, April 13, 2020 4:23 PM
To: NIAID OCGR Leg (b) (6)
Subject: Senate Qs - Wuhan Institute of Virology

Hi, NIAID,

Separately, we have heard from the offices of Senators Rubio and Braun about these linked articles:

White Coat Waste
Daily Mail
Washington Examiner

Both offices have asked if there's any information we can share with them related to this matter. Thanks in advance for anything you can provide.

Karen

From: Michelle Mitchell (b) (6)
Date: Monday, April 13, 2020 at 3:42 PM
To: Karen LaMontagne (b) (6)
Subject: Sen. Rubio question - NIH funding Wuhan virus lab

Hey Karen,

Sen. Rubio's staff, Ansley Rhyne, forwarded the email below that she received regarding NIH funding for the Wuhan Institute of Virology. Her boss, along with Rep. Gaetz are working on a letter to ensure no taxpayer dollars are sent to that Institute.

Ansley requested our input. Would you ask NIAID for any information on this issue that we could be shared with Ansley?

Thank you.

MM

From: Justin Goodman <justin@whitecoatwaste.org>

Sent: Monday, April 13, 2020 2:36 PM
To:
Subject: Laura- NIH funding Wuhan virus lab

I hope you had a nice weekend and are staying safe and healthy. I wanted to make sure you saw that our taxpayer watchdog group just exposed that **the National Institutes of Health (NIH) has been sending tax dollars to the controversial Wuhan Institute of Virology for years, including for dangerous lab experiments on coronavirus-infected bats captured from caves.** The Daily Mail, Washington Examiner, Drudge and others ran stories about the troubling find over the weekend.

We're working with Rep. Matt Gaetz (R-FL) and others on a sign-on letter about this and would love to work with you and Senator Rubio as well to ensure no more tax dollars are shipped to the Wuhan Institute of Virology.

I'd be happy to send over more info if you're interested and answer any questions you may have.

Thanks for looking,

Justin

_____
Justin Goodman, M.A.
Vice President, Advocacy and Public Policy
White Coat Waste Project

*Taxpayers shouldn't be forced to pay $20 billion+ for **wasteful** government animal experiments.*

PO Box 26029
Washington, DC 20001
Phone: 860.882.2492
Donate | Blog | Web | Twitter | Facebook

RESEARCH
Department of Health and Human Services
National Institutes of Health

Federal Award Date: 08/05/2019

NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Grant Number: 2R01AI110964-06 REVISED
FAIN: R01AI110964

Principal Investigator(s):
PETER DASZAK, PHD

Project Title: Understanding the Risk of Bat Coronavirus Emergence

Dr. Daszak, Peter
PD/PI
460 West 34th Street
Suite 1701
New York, NY 100012320

Award e-mailed to: (b) (6)

Period Of Performance:
Budget Period: 07/24/2019 – 06/30/2020
Project Period: 06/01/2014 – 06/30/2024

Dear Business Official:

The National Institutes of Health hereby revises this award to reflect a decrease in the amount of $71,770 (see "Award Calculation" in Section I and "Terms and Conditions" in Section III) to ECOHEALTH ALLIANCE, INC. in support of the above referenced project. This award is pursuant to the authority of 42 USC 241 42 CFR 52 and is subject to the requirements of this statute and regulation and of other referenced, incorporated or attached terms and conditions.

Acceptance of this award including the "Terms and Conditions" is acknowledged by the grantee when funds are drawn down or otherwise obtained from the grant payment system.

Each publication, press release, or other document about research supported by an NIH award must include an acknowledgment of NIH award support and a disclaimer such as "Research reported in this publication was supported by the National Institute Of Allergy And Infectious Diseases of the National Institutes of Health under Award Number R01AI110964. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health." Prior to issuing a press release concerning the outcome of this research, please notify the NIH awarding IC in advance to allow for coordination.

Award recipients must promote objectivity in research by establishing standards that provide a reasonable expectation that the design, conduct and reporting of research funded under NIH awards will be free from bias resulting from an Investigator's Financial Conflict of Interest (FCOI), in accordance with the 2011 revised regulation at 42 CFR Part 50 Subpart F. The Institution shall submit all FCOI reports to the NIH through the eRA Commons FCOI Module. The regulation does not apply to Phase I Small Business Innovative Research (SBIR) and Small Business Technology Transfer (STTR) awards. Consult the NIH website http://grants.nih.gov/grants/policy/coi/ for a link to the regulation and additional important information.

If you have any questions about this award, please contact the individual(s) referenced in Section IV.

Sincerely yours,

Tseday G Girma
Grants Management Officer
NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Additional information follows

SECTION I – AWARD DATA – 2R01AI110964-06 REVISED

Award Calculation (U.S. Dollars)

Salaries and Wages	$170,123
Fringe Benefits	$53,590
Personnel Costs (Subtotal)	$223,713
Consultant Services	$49,750
Materials & Supplies	$20,850
Travel	$15,027
Subawards/Consortium/Contractual Costs	$229,651
Federal Direct Costs	$538,991
Federal F&A Costs	$122,989
Approved Budget	$661,980
Total Amount of Federal Funds Obligated (Federal Share)	$661,980
TOTAL FEDERAL AWARD AMOUNT	$661,980
AMOUNT OF THIS ACTION (FEDERAL SHARE)	($-71,770)

SUMMARY TOTALS FOR ALL YEARS		
YR	**THIS AWARD**	**CUMULATIVE TOTALS**
6	$661,980	$661,980
7	$637,980	$637,980
8	$637,980	$637,980
9	$637,980	$637,980
10	$637,980	$637,980

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

Fiscal Information:

CFDA Name:	Allergy and Infectious Diseases Research
CFDA Number:	93.855
EIN:	1311726494A1
Document Number:	RAI110964B
PMS Account Type:	P (Subaccount)
Fiscal Year:	2019

IC	CAN	2019	2020	2021	2022	2023
AI	8472364	$661,980	$637,980	$637,980	$637,980	$637,980

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

NIH Administrative Data:
PCC: M51C B / **OC**: 414B / **Released**: (b) (6) 08/02/2019
Award Processed: 08/05/2019 12:01:51 AM

SECTION II – PAYMENT/HOTLINE INFORMATION – 2R01AI110964-06 REVISED

For payment and HHS Office of Inspector General Hotline information, see the NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm

SECTION III – TERMS AND CONDITIONS – 2R01AI110964-06 REVISED

This award is based on the application submitted to, and as approved by, NIH on the above-titled project and is subject to the terms and conditions incorporated either directly or by reference in the following:

a. The grant program legislation and program regulation cited in this Notice of Award.
b. Conditions on activities and expenditure of funds in other statutory requirements, such as those included in appropriations acts.

c. 45 CFR Part 75.
d. National Policy Requirements and all other requirements described in the NIH Grants Policy Statement, including addenda in effect as of the beginning date of the budget period.
e. Federal Award Performance Goals: As required by the periodic report in the RPPR or in the final progress report when applicable.
f. This award notice, INCLUDING THE TERMS AND CONDITIONS CITED BELOW.

(See NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm for certain references cited above.)

Research and Development (R&D): All awards issued by the National Institutes of Health (NIH) meet the definition of "Research and Development" at 45 CFR Part§ 75.2**.** As such, auditees should identify NIH awards as part of the R&D cluster on the Schedule of Expenditures of Federal Awards (SEFA). The auditor should test NIH awards for compliance as instructed in Part V, Clusters of Programs. NIH recognizes that some awards may have another classification for purposes of indirect costs. The auditor is not required to report the disconnect (i.e., the award is classified as R&D for Federal Audit Requirement purposes but non-research for indirect cost rate purposes), unless the auditee is charging indirect costs at a rate other than the rate(s) specified in the award document(s).

An unobligated balance may be carried over into the next budget period without Grants Management Officer prior approval.

This grant is subject to Streamlined Noncompeting Award Procedures (SNAP).

This award is subject to the requirements of 2 CFR Part 25 for institutions to receive a Dun & Bradstreet Universal Numbering System (DUNS) number and maintain an active registration in the System for Award Management (SAM). Should a consortium/subaward be issued under this award, a DUNS requirement must be included. See http://grants.nih.gov/grants/policy/awardconditions.htm for the full NIH award term implementing this requirement and other additional information.

This award has been assigned the Federal Award Identification Number (FAIN) R01AI110964. Recipients must document the assigned FAIN on each consortium/subaward issued under this award.

Based on the project period start date of this project, this award is likely subject to the Transparency Act subaward and executive compensation reporting requirement of 2 CFR Part 170. There are conditions that may exclude this award; see http://grants.nih.gov/grants/policy/awardconditions.htm for additional award applicability information.

In accordance with P.L. 110-161, compliance with the NIH Public Access Policy is now mandatory. For more information, see NOT-OD-08-033 and the Public Access website: http://publicaccess.nih.gov/.

In accordance with the regulatory requirements provided at 45 CFR 75.113 and Appendix XII to 45 CFR Part 75, recipients that have currently active Federal grants, cooperative agreements, and procurement contracts with cumulative total value greater than $10,000,000 must report and maintain information in the System for Award Management (SAM) about civil, criminal, and administrative proceedings in connection with the award or performance of a Federal award that reached final disposition within the most recent five-year period. The recipient must also make semiannual disclosures regarding such proceedings. Proceedings information will be made publicly available in the designated integrity and performance system (currently the Federal Awardee Performance and Integrity Information System (FAPIIS)). Full reporting requirements and procedures are found in Appendix XII to 45 CFR Part 75. This term does not apply to NIH fellowships.

Treatment of Program Income:
Additional Costs

SECTION IV – AI Special Terms and Conditions – 2R01AI110964-06 REVISED

Clinical Trial Indicator: No
This award does not support any NIH-defined Clinical Trials. See the NIH Grants Policy Statement Section 1.2 for NIH definition of Clinical Trial.

REVISED AWARD: This award is revised to adjust the budget in accordance with the letter from Aleksei Chmura/ECOHealth Alliance.

Supersedes previous Notice of Award dated **07/24/2019**.

****
This Notice of Award (NoA) includes funds for activity with **The University of North Carolina at Chapel Hill** in the amount of **$77,750** (**$50,000** direct costs + **$27,750**F&A costs).

This Notice of Award (NoA) includes funds for activity with **Wuhan Institute of Virology** in the amount of **$76,301** (**$70,649** direct costs + **$5,652** F&A costs).

This Notice of Award (NoA) includes funds for activity with **Institute of Pathogen Biology** in the amount of **$75,600** (**$70,000** direct costs + **$5,600** F&A costs).

****
The Research Performance Progress Report (RPPR), Section G.9 (Foreign component), includes reporting requirements for all research performed outside of the United States. Research conducted at the following site(s) must be reported in your RPPR:

Wuhan Institute of Virology, CHINA

Institute of Pathogen Biology, CHINA

East China Normal University, CHINA

Duke-NUS Medical School, SINGAPORE

****
This award reflects current Federal policies regarding Facilities & Administrative (F&A) Costs for foreign grantees including foreign sub-awardees, and domestic awards with foreign sub-awardees. Please see: Chapter 16 Grants to Foreign Organizations, International Organizations, and Domestic Grants with Foreign Components, Section 16.6 “Allowable and Unallowable Cost” of the NIH Grants Policy.

****
This award may include collaborations with and/or between foreign organizations. Please be advised that short term travel visa expenses are an allowable expense on this grant, if justified as critical and necessary for the conduct of the project.

****
The budget period anniversary start date for future year(s) will be **July** 1.

****
Dissemination of study data will be in accord with the Recipient’s accepted genomic data sharing plan as stated in the page(s) **203** of the application. Failure to adhere to the sharing plan as mutually agreed upon by the Recipient and the NIAID may result in Enforcement Actions as described in the NIH Grants Policy Statement.

****
This award is subject to the Clinical Terms of Award referenced in the NIH Guide for Grants and Contracts, July 8, 2002, NOT AI-02-032. These terms and conditions are hereby incorporated by

reference, and can be accessed via the following World Wide Web address: https://www.niaid.nih.gov/grants-contracts/niaid-clinical-terms-award All submissions required by the NIAID Clinical Terms of Award must be forwarded electronically or by mail to the responsible NIAID Program Official identified on this Notice of Award.

****

Awardees who conduct research involving Select Agents (see 42 CFR 73 for the Select Agent list; and 7 CFR 331 and 9 CFR 121 for the relevant animal and plant pathogens at http://www.selectagents.gov/Regulations.html) must complete registration with CDC (or APHIS, depending on the agent) before using NIH funds. No funds can be used for research involving Select Agents if the final registration certificate is denied.

Prior to conducting a restricted experiment with a Select Agent or Toxin, awardees must notify the NIAID and must request and receive approval from CDC or APHIS.

****

Select Agents:
Awardee of a project that at any time involves a restricted experiment with a select agent, is responsible for notifying and receiving prior approval from the NIAID. Please be advised that changes in the use of a Select Agent will be considered a change in scope and require NIH awarding office prior approval. The approval is necessary for new select agent experiments as well as changes in on-going experiments that would require change in the biosafety plan and/or biosafety containment level. An approval to conduct a restricted experiment granted to an individual cannot be assumed an approval to other individuals who conduct the same restricted experiment as defined in the Select Agents Regulation 42 CFR Part 73, Section 13.b (http://www.selectagents.gov/Regulations.html).

Highly Pathogenic Agent:
NIAID defines a Highly Pathogenic Agent as an infectious Agent or Toxin that may warrant a biocontainment safety level of BSL3 or higher according to the current edition of the CDC/NIH Biosafety in Microbiological and Biomedical Laboratories (BMBL) (http://www.cdc.gov/OD/ohs/biosfty/bmbl5/bmbl5toc.htm). Research funded under this grant must adhere to the BMBL, including using the BMBL-recommended biocontainment level at a minimum. If your Institutional Biosafety Committee (or equivalent body) or designated institutional biosafety official recommend a higher biocontainment level, the highest recommended containment level must be used.
When submitting future Progress Reports indicate at the beginning of the report:

If no research with a Highly Pathogenic Agent or Select Agent has been performed or is planned to be performed under this grant.

If your IBC or equivalent body or official has determined, for example, by conducting a risk assessment, that the work being planned or performed under this grant may be conducted at a biocontainment safety level that is lower than BSL3.

If the work involves Select Agents and/or Highly Pathogenic Agents, also address the following points:

Any changes in the use of the Agent(s) or Toxin(s) including its restricted experiments that have resulted in a change in the required biocontainment level, and any resultant change in location, if applicable, as determined by your IBC or equivalent body or official.

If work with a new or additional Agent(s)/Toxin(s) is proposed in the upcoming project period, provide:

- A list of the new and/or additional Agent(s) that will be studied;
- A description of the work that will be done with the Agent(s), and whether or not the work is a restricted experiment;
- The title and location for each biocontainment resource/facility, including the name of the organization that operates the facility, and the biocontainment level at which the work will be conducted, with documentation of approval by your IBC or equivalent body or official. It is important to note if the work is being done in a new location.

STAFF CONTACTS

The Grants Management Specialist is responsible for the negotiation, award and administration of this project and for interpretation of Grants Administration policies and provisions. The Program Official is responsible for the scientific, programmatic and technical aspects of this project. These individuals work together in overall project administration. Prior approval requests (signed by an Authorized Organizational Representative) should be submitted in writing to the Grants Management Specialist. Requests may be made via e-mail.

Grants Management Specialist: Tseday G Girma
Email: (b) (6) **Phone**: (b) (6) **Fax**: 301-493-0597

Program Official: Erik J. Stemmy
Email: (b) (6) **Phone**: (b) (6)

SPREADSHEET SUMMARY
GRANT NUMBER: 2R01AI110964-06 REVISED

INSTITUTION: ECOHEALTH ALLIANCE, INC.

Budget	Year 6	Year 7	Year 8	Year 9	Year 10
Salaries and Wages	$170,123	$170,123	$170,123	$170,123	$170,123
Fringe Benefits	$53,590	$53,590	$53,590	$53,590	$53,590
Personnel Costs (Subtotal)	$223,713	$223,713	$223,713	$223,713	$223,713
Consultant Services	$49,750	$49,750	$49,750	$49,750	$49,750
Materials & Supplies	$20,850	$14,850	$14,850	$14,850	$14,850
Travel	$15,027	$15,027	$15,027	$15,027	$15,027
Subawards/Consortium/Contractual Costs	$229,651	$229,651	$229,651	$229,651	$229,651
Publication Costs		$6,000	$6,000	$6,000	$6,000
TOTAL FEDERAL DC	$538,991	$538,991	$538,991	$538,991	$538,991
TOTAL FEDERAL F&A	$122,989	$98,989	$98,989	$98,989	$98,989
TOTAL COST	$661,980	$637,980	$637,980	$637,980	$637,980

Facilities and Administrative Costs	Year 6	Year 7	Year 8	Year 9	Year 10
F&A Cost Rate 1	32%	32%	32%	32%	32%
F&A Cost Base 1	$384,340	$309,340	$309,340	$309,340	$309,340
F&A Costs 1	$122,989	$98,989	$98,989	$98,989	$98,989

Notice of Award

RESEARCH **Issue Date:** 05/27/2014

Department of Health and Human Services
National Institutes of Health
NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Grant Number: 1R01AI110964-01
FAIN: R01AI110964

Principal Investigator(s):
PETER DASZAK, PHD

Project Title: Understanding the Risk of Bat Coronavirus Emergence

Aleksei
President
460 West 34th Street
17th Floor
New York, NY 100012317

Award e-mailed to: (b) (6)

Budget Period: 06/01/2014 – 05/31/2015
Project Period: 06/01/2014 – 05/31/2019

Dear Business Official:

The National Institutes of Health hereby awards a grant in the amount of $666,442 (see "Award Calculation" in Section I and "Terms and Conditions" in Section III) to ECOHEALTH ALLIANCE, INC. in support of the above referenced project. This award is pursuant to the authority of 42 USC 241 42 CFR 52 and is subject to the requirements of this statute and regulation and of other referenced, incorporated or attached terms and conditions.

Acceptance of this award including the "Terms and Conditions" is acknowledged by the grantee when funds are drawn down or otherwise obtained from the grant payment system.

Each publication, press release, or other document about research supported by an NIH award must include an acknowledgment of NIH award support and a disclaimer such as "Research reported in this publication was supported by the National Institute Of Allergy And Infectious Diseases of the National Institutes of Health under Award Number R01AI110964. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health." Prior to issuing a press release concerning the outcome of this research, please notify the NIH awarding IC in advance to allow for coordination.

Award recipients must promote objectivity in research by establishing standards that provide a reasonable expectation that the design, conduct and reporting of research funded under NIH awards will be free from bias resulting from an Investigator's Financial Conflict of Interest (FCOI), in accordance with the 2011 revised regulation at 42 CFR Part 50 Subpart F. The Institution shall submit all FCOI reports to the NIH through the eRA Commons FCOI Module. The regulation does not apply to Phase I Small Business Innovative Research (SBIR) and Small Business Technology Transfer (STTR) awards. Consult the NIH website http://grants.nih.gov/grants/policy/coi/ for a link to the regulation and additional important information.

If you have any questions about this award, please contact the individual(s) referenced in Section IV.

Sincerely yours,

Laura A. Pone
Grants Management Officer
NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Additional information follows

SECTION I – AWARD DATA – 1R01AI110964-01

Award Calculation (U.S. Dollars)

Salaries and Wages	$167,708
Fringe Benefits	$54,168
Supplies	$21,400
Travel Costs	$35,918
Other Costs	$10,000
Consortium/Contractual Cost	$227,663
Federal Direct Costs	$516,857
Federal F&A Costs	$149,585
Approved Budget	$666,442
Federal Share	$666,442
TOTAL FEDERAL AWARD AMOUNT	$666,442
AMOUNT OF THIS ACTION (FEDERAL SHARE)	$666,442

SUMMARY TOTALS FOR ALL YEARS		
YR	**THIS AWARD**	**CUMULATIVE TOTALS**
1	$666,442	$666,442
2	$630,445	$630,445
3	$611,090	$611,090
4	$597,112	$597,112
5	$581,646	$581,646

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

Fiscal Information:

CFDA Number:	93.855
EIN:	1311726494A1
Document Number:	RAI110964A
PMS Account Type:	P (Subaccount)
Fiscal Year:	2014

IC	CAN	2014	2015	2016	2017	2018
AI	8472350	$666,442	$630,445	$611,090	$597,112	$581,646

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

NIH Administrative Data:
PCC: M51C / **OC**: 414A / **Released**: (b) (6) 05/20/2014
Award Processed: 05/08/2014 01:52:21 PM

SECTION II – PAYMENT/HOTLINE INFORMATION – 1R01AI110964-01

For payment and HHS Office of Inspector General Hotline information, see the NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm

SECTION III – TERMS AND CONDITIONS – 1R01AI110964-01

This award is based on the application submitted to, and as approved by, NIH on the above-titled project and is subject to the terms and conditions incorporated either directly or by reference in the following:

a. The grant program legislation and program regulation cited in this Notice of Award.

b. Conditions on activities and expenditure of funds in other statutory requirements, such as those included in appropriations acts.
c. 45 CFR Part 74 or 45 CFR Part 92 as applicable.
d. The NIH Grants Policy Statement, including addenda in effect as of the beginning date of the budget period.
e. This award notice, INCLUDING THE TERMS AND CONDITIONS CITED BELOW.

(See NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm for certain references cited above.)

An unobligated balance may be carried over into the next budget period without Grants Management Officer prior approval.

This grant is subject to Streamlined Noncompeting Award Procedures (SNAP).

This award is subject to the requirements of 2 CFR Part 25 for institutions to receive a Dun & Bradstreet Universal Numbering System (DUNS) number and maintain an active registration in the Central Contractor Registration. Should a consortium/subaward be issued under this award, a DUNS requirement must be included. See http://grants.nih.gov/grants/policy/awardconditions.htm for the full NIH award term implementing this requirement and other additional information.

This award has been assigned the Federal Award Identification Number (FAIN) R01AI110964. Recipients must document the assigned FAIN on each consortium/subaward issued under this award.

Based on the project period start date of this project, this award is likely subject to the Transparency Act subaward and executive compensation reporting requirement of 2 CFR Part 170. There are conditions that may exclude this award; see http://grants.nih.gov/grants/policy/awardconditions.htm for additional award applicability information.

In accordance with P.L. 110-161, compliance with the NIH Public Access Policy is now mandatory. For more information, see NOT-OD-08-033 and the Public Access website: http://publicaccess.nih.gov/.

Treatment of Program Income:
Additional Costs

SECTION IV – AI Special Terms and Conditions – 1R01AI110964-01

THIS AWARD CONTAINS GRANT SPECIFIC RESTRICTIONS. THESE RESTRICTIONS MAY ONLY BE LIFTED BY A REVISED NOTICE OF AWARD.

RESTRICTION: This award is issued with the knowledge that subjects may be involved within the period of support, but definite plans were not set forth in the application as per 45 CFR 46.118. No human subjects may be involved in any project supported by this award until all requirements for Human Subjects research as identified in the PHS398/SF424 Instructions have been provided to and approved by NIH.

RESTRICTION: The present award is being made without a currently valid certification of IRB approval for this project with the following restriction: Only activities that are clearly severable and independent from activities that involve human subjects may be conducted pending the NIAID's acceptance of the certification of IRB review and approval.

No funds may be drawn down from the payment system and no obligations may be made against Federal funds for any research involving human subjects prior to the NIAID's notification to the grantee that the identified issues have been resolved and this restriction removed.

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This award includes funds for subcontract/consortium activity with Wuhan Institute of Virology, CHINA and is budgeted as follows:

	-Yr 1	-Yr 2	-Yr 3	-Yr 4	-Yr 5
Total Direct Costs	$123,699	$128,718	$147,335	$147,335	$147,335
F&A Costs @ 8%(MTDC)	$9,896	$10,297	$11,787	$11,787	$11,787
TOTAL COSTS	$133,595	$139,015	$159,122	$159,122	$159,122

Consortiums are to be established and administered as described in the NIH Grants Policy Statement. This written agreement with the consortium must address the negotiated arrangements for meeting the scientific, administrative, financial, and reporting requirements for this grant.
~~~~~~~~~
This award includes funds for subcontract/consortium activity with East China Normal University, CHINA and is budgeted as follows:

	-Yr 1	-Yr 2	-Yr 3	-Yr 4	-Yr 5
Total Direct Costs	$87,100	$67,300	$50,108	$39,167	$14,850
F&A Costs @ 8%(MTDC)	$6,968	$5,384	$4,009	$3,133	$2,404
TOTAL COSTS	$94,068	$72,684	$54,117	$42,300	$32,454

Consortiums are to be established and administered as described in the NIH Grants Policy Statement. This written agreement with the consortium must address the negotiated arrangements for meeting the scientific, administrative, financial, and reporting requirements for this grant.
~~~~~~~~~
Select Agents:
Awardee of a project that at any time involves a restricted experiment with a select agent, is responsible for notifying and receiving prior approval from the NIAID. Please be advised that changes in the use of a Select Agent will be considered a change in scope and require NIH awarding office prior approval. The approval is necessary for new select agent experiments as well as changes in on-going experiments that would require change in the biosafety plan and/or biosafety containment level. An approval to conduct a restricted experiment granted to an individual cannot be assumed an approval to other individuals who conduct the same restricted experiment as defined in the Select Agents Regulation 42 CFR Part 73, Section 13.b (http://www.selectagents.gov/Regulations.html).

Highly Pathogenic Agent:
NIAID defines a Highly Pathogenic Agent as an infectious Agent or Toxin that may warrant a biocontainment safety level of BSL3 or higher according to the current edition of the CDC/NIH Biosafety in Microbiological and Biomedical Laboratories (BMBL) (http://www.cdc.gov/OD/ohs/biosfty/bmbl5/bmbl5toc.htm). Research funded under this grant must adhere to the BMBL, including using the BMBL-recommended biocontainment level at a minimum. If your Institutional Biosafety Committee (or equivalent body) or designated institutional biosafety official recommend a higher biocontainment level, the highest recommended containment level must be used.
When submitting future Progress Reports indicate at the beginning of the report:

If no research with a Highly Pathogenic Agent or Select Agent has been performed or is planned to be performed under this grant.

If your IBC or equivalent body or official has determined, for example, by conducting a risk assessment, that the work being planned or performed under this grant may be conducted at a biocontainment safety level that is lower than BSL3.

If the work involves Select Agents and/or Highly Pathogenic Agents, also address the following points:

Any changes in the use of the Agent(s) or Toxin(s) including its restricted experiments that have resulted in a change in the required biocontainment level, and any resultant change in location, if applicable, as determined by your IBC or equivalent body or official.
~~~~~~~~~

If work with a new or additional Agent(s)/Toxin(s) is proposed in the upcoming project period, provide:

o A list of the new and/or additional Agent(s) that will be studied;
o A description of the work that will be done with the Agent(s), and whether or not the work is a restricted experiment;
o The title and location for each biocontainment resource/facility, including the name of the organization that operates the facility, and the biocontainment level at which the work will be conducted, with documentation of approval by your IBC or equivalent body or official. It is important to note if the work is being done in a new location.

STAFF CONTACTS

The Grants Management Specialist is responsible for the negotiation, award and administration of this project and for interpretation of Grants Administration policies and provisions. The Program Official is responsible for the scientific, programmatic and technical aspects of this project. These individuals work together in overall project administration. Prior approval requests (signed by an Authorized Organizational Representative) should be submitted in writing to the Grants Management Specialist. Requests may be made via e-mail.

Grants Management Specialist: Laura A. Pone
Email: (b) (6) **Phone**: (b) (6) **Fax**: 301-493-0597

Program Official: Erik J. Stemmy
Email: (b) (6) **Phone**: (b) (6)

SPREADSHEET SUMMARY
GRANT NUMBER: 1R01AI110964-01

INSTITUTION: ECOHEALTH ALLIANCE, INC.

Budget	Year 1	Year 2	Year 3	Year 4	Year 5
Salaries and Wages	$167,708	$167,708	$167,708	$167,708	$167,708
Fringe Benefits	$54,168	$54,168	$54,168	$54,168	$54,168
Supplies	$21,400	$19,250	$7,250	$7,000	$3,500
Travel Costs	$35,918	$35,918	$35,918	$35,918	$35,918
Other Costs	$10,000	$13,550	$11,050	$9,800	$9,400
Consortium/Contractual Cost	$227,663	$211,699	$213,239	$201,422	$191,576
TOTAL FEDERAL DC	$516,857	$502,293	$489,333	$476,016	$462,270
TOTAL FEDERAL F&A	$149,585	$128,152	$121,757	$121,096	$119,376
TOTAL COST	$666,442	$630,445	$611,090	$597,112	$581,646

Facilities and Administrative Costs	Year 1	Year 2	Year 3	Year 4	Year 5
F&A Cost Rate 1	44.1%	44.1%	44.1%	44.1%	44.1%
F&A Cost Base 1	$339,194	$290,594	$276,094	$274,594	$270,694
F&A Costs 1	$149,585	$128,152	$121,757	$121,096	$119,376

(b) (5)

[redacted]

(b) (5)

From: Tabak, Lawrence (NIH/OD) [E]
To: Lauer, Michael (NIH/OD) [E]
Subject: Re: Draft response for review -- FW: Request for information: Senate Qs - Wuhan Institute of Virology
Date: Wednesday, April 15, 2020 7:24:37 AM

So we don't technically fund them directly, the grantee in NY does?

From: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Date: Wednesday, April 15, 2020 at 7:23 AM
To: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Cc: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Subject: Re: Draft response for review -- FW: Request for information: Senate Qs - Wuhan Institute of Virology

Hi Larry – on the Type 1 total is 749,976. On the Type 2, looks like the total is 76,301 (so far). Thus total is 749,976+76,301=826,277.

It's a subcontract going through New York.

Mike

From: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Date: Wednesday, April 15, 2020 at 7:12 AM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Subject: Re: Draft response for review -- FW: Request for information: Senate Qs - Wuhan Institute of Virology

Mike – sorry – what is the total amount Wuhan has received since 2014?

Does the money go to NY and they send to Wuhan or do we send to Wuhan directly.

Thanks
Larry

From: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Date: Wednesday, April 15, 2020 at 7:11 AM
To: "Tabak, Lawrence (NIH/OD) [E]" (b) (6), "Erbelding, Emily (NIH/NIAID) [E]" (b) (6)
Cc: "Marston, Hilary (NIH/NIAID) [E]" (b) (6), "Lauer, Michael (NIH/OD) [E]" (b) (6)
Subject: Re: Draft response for review -- FW: Request for information: Senate Qs - Wuhan Institute of Virology

Thanks – just sent you budget details.

Mike

From: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Date: Tuesday, April 14, 2020 at 10:12 PM
To: "Erbelding, Emily (NIH/NIAID) [E]" (b) (6)
Cc: "Marston, Hilary (NIH/NIAID) [E]" (b) (6), "Lauer, Michael (NIH/OD) [E]" (b) (6)
Subject: Re: Draft response for review -- FW: Request for information: Senate Qs - Wuhan Institute of Virology

Thanks Emily.
Looping in Mike Lauer,
Larry

From: "Erbelding, Emily (NIH/NIAID) [E]" (b) (6)
Date: Tuesday, April 14, 2020 at 10:11 PM
To: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Cc: "Marston, Hilary (NIH/NIAID) [E]" (b) (6)
Subject: Fwd: Draft response for review -- FW: Request for information: Senate Qs - Wuhan Institute of Virology

I am forwarding draft response below to inquiry from Rubio et al earlier.

PI is Peter Dazsak, Eco Health alliance in NYC. Wuhan subcontract is approximately 74k per year. I will try to find more accurate subcontract numbers.

Sent from my iPad

Begin forwarded message:

> **From:** "Abbey, Lillian (NIH/NIAID) [E]" (b) (6)
> **Date:** April 14, 2020 at 4:24:34 PM EDT
> **To:** "Cassetti, Cristina (NIH/NIAID) [E]" (b) (6), "Erbelding, Emily (NIH/NIAID) [E]" (b) (6)
> **Cc:** "Ford, Andrew (NIH/NIAID) [E]" (b) (6), "Bateman, Karen (NIH/NIAID) [E]" (b) (6), "Werner, Alyssa (NIH/NIAID) [E]" (b) (6), "Mulach, Barbara (NIH/NIAID) [E]" (b) (6)
> **Subject: Draft response for review -- FW: Request for information: Senate Qs - Wuhan Institute of Virology**
>
> Dear Cristina and Emily,
> Incorporated below in red font is a draft response Andrew developed based on his discussion with Erik. (b) (5) Also, Andrew provided the attached publication from mid-March, noting that we may want to share it with the OD.
>
> DRAFT RESPONSE:

Project Number:	2R01AI110964-06	**Contact PI / Project Leader:**	DASZAK, PETER
Title:	UNDERSTANDING THE RISK OF BAT CORONAVIRUS EMERGENCE	**Awardee Organization:**	ECOHEALTH ALLIANCE, INC.

https://projectreporter.nih.gov/project_info_description.cfm?aid=9819304&icde=49588715&ddparam=&ddvalue=&ddsub=&cr=1&csb=default&cs=ASC&pball=

1. What are the goals of the main grant:

(b) (5)

2. What are the specific activities supported by the sub to the Wuhan lab and the total costs associated with these activities. Please verify if the creation of recombinant bat in Wuhan is included in their research activities.

(b) (5)

Total award information is available in Reporter at link above but budget information about subcontracts is not publicly available as these awards are administered by the grantee institution.

From: Crawford, Chase (NIH/NIAID) [E] <(b) (6)
Sent: Monday, April 13, 2020 5:41 PM
To: NIAID BUGS (b) (6)
Cc: Auchincloss, Hugh (NIH/NIAID) [E] (b) (6); Harper, Jill (NIH/NIAID) [E] (b) (6); NIAID OCGR Leg (b) (6)
Subject: Request for information: Senate Qs - Wuhan Institute of Virology

Hi BUGS,

Staff to Senator Marco Rubio (R-FL) has forwarded an email to Building 1 from the White Coat Waste Project (see bottom of email chain). The forwarded message links to recent

articles in The Daily Mail and the Washington Examiner on NIH support for previous coronavirus studies involving the Wuhan Institute of Virology. Building 1 has asked if NIAID has any information related to this research that we can share with staff to Senators Rubio and Mike Braun (R-IN).

To help us better understand this congressional request, is there any background information that you can provide on the activities discussed in the articles referenced below?

Thanks,
Chase
(b) (6)

From: LaMontagne, Karen (NIH/OD) [E] (b) (6)
Sent: Monday, April 13, 2020 4:23 PM
To: NIAID OCGR Leg <NIAIDOCGRLeg@mail.nih.gov>
Subject: Senate Qs - Wuhan Institute of Virology

Hi, NIAID,

Separately, we have heard from the offices of Senators Rubio and Braun about these linked articles:

White Coat Waste
Daily Mail
Washington Examiner

Both offices have asked if there's any information we can share with them related to this matter. Thanks in advance for anything you can provide.

Karen

From: Michelle Mitchell (b) (6)>
Date: Monday, April 13, 2020 at 3:42 PM
To: Karen LaMontagne (b) (6)
Subject: Sen. Rubio question - NIH funding Wuhan virus lab

Hey Karen,

Sen. Rubio's staff, Ansley Rhyne, forwarded the email below that she received regarding NIH funding for the Wuhan Institute of Virology. Her boss, along with Rep. Gaetz are working on a letter to ensure no taxpayer dollars are sent to that Institute.

Ansley requested our input. Would you ask NIAID for any information on this issue that we could be shared with Ansley?

Thank you.

MM

From: Justin Goodman <justin@whitecoatwaste.org>
Sent: Monday, April 13, 2020 2:36 PM
To:
Subject: Laura- NIH funding Wuhan virus lab

I hope you had a nice weekend and are staying safe and healthy. I wanted to make sure you saw that our taxpayer watchdog group just exposed that **the National Institutes of Health (NIH) has been sending tax dollars to the controversial Wuhan Institute of Virology for years, including for dangerous lab experiments on coronavirus-infected bats captured from caves.** The Daily Mail, Washington Examiner, Drudge and others ran stories about the troubling find over the weekend.

We're working with Rep. Matt Gaetz (R-FL) and others on a sign-on letter about this and would love to work with you and Senator Rubio as well to ensure no more tax dollars are shipped to the Wuhan Institute of Virology.

I'd be happy to send over more info if you're interested and answer any questions you may have.

Thanks for looking,

Justin

Justin Goodman, M.A.
Vice President, Advocacy and Public Policy
White Coat Waste Project

Taxpayers shouldn't be forced to pay $20 billion+
*for **wasteful** government animal experiments.*

PO Box 26029
Washington, DC 20001
Phone: 860.882.2492
Donate | Blog | Web | Twitter | Facebook

From: Lauer, Michael (NIH/OD) [E]
To: Black, Jodi (NIH/OD) [E]
Subject: Re: Direct Reply w/ OD Clearance - Wuhan Institute of Virology (WF390335)
Date: Thursday, April 30, 2020 8:34:42 AM
Attachments: image001.png

Thanks Jodi!

Mike

From: "Black, Jodi (NIH/OD) [E]" (b) (6)
Date: Thursday, April 30, 2020 at 8:32 AM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Subject: Re: Direct Reply w/ OD Clearance - Wuhan Institute of Virology (WF390335)

Hi Mike, I'm checking with OPERA for options.

Best,
Jodi

Jodi B. Black, PhD, MMSc
Deputy Director
Office of Extramural Research, NIH

From: Mike Lauer (b) (6)
Date: Thursday, April 30, 2020 at 7:15 AM
To: "Pearson, Katrina (NIH/OD) [E]" (b) (6), "Haugen, Brian (NIH/OD) [E]" (b) (6), Jodi OER (b) (6)
Cc: "Brining, Sheryl (NIH/OD) [E]" (b) (6), OER Executive Secretariat (b) (6), liza bundesen (b) (6), "Schwetz, Tara (NIH/OD) [E]" (b) (6), Mike Lauer (b) (6)
Subject: Re: Direct Reply w/ OD Clearance - Wuhan Institute of Virology (WF390335)

Many thanks Katrina for checking and confirming the results.

Hi Aesha – I'll continue to work on this.

Best, Mike

From: "Pearson, Katrina (NIH/OD) [E]" (b) (6)
Date: Wednesday, April 29, 2020 at 11:41 PM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6), "Haugen, Brian (NIH/OD) [E]" (b) (6), "Black, Jodi (NIH/OD) [E]" (b) (6)

Cc: "Brining, Sheryl (NIH/OD) [E]" (b) (6), OER Executive Secretariat (b) (6), "Bundesen, Liza (NIH/OD) [E]" (b) (6), "Schwetz, Tara (NIH/OD) [E]" (b) (6)
Subject: RE: Direct Reply w/ OD Clearance - Wuhan Institute of Virology (WF390335)

Hi Mike,

(b) (5)

See breakdown below and FACTS snapshots attached.

(b) (5)

Katrina

Katrina Pearson
Office: (b) (6) /Mobile: (b) (6)
Website: http://report.nih.gov

From: Lauer, Michael (NIH/OD) [E] (b) (6)
Sent: Wednesday, April 29, 2020 8:22 PM
To: Pearson, Katrina (NIH/OD) [E] (b) (6); Haugen, Brian (NIH/OD) [E] (b) (6); Black, Jodi (NIH/OD) [E] (b) (6)
Cc: Lauer, Michael (NIH/OD) [E] (b) (6); Brining, Sheryl (NIH/OD) [E] (b) (6); OER Executive Secretariat (b) (6); Bundesen, Liza (NIH/OD) [E] (b) (6); Schwetz, Tara (NIH/OD) [E]

[redacted]
Subject: FW: Direct Reply w/ OD Clearance - Wuhan Institute of Virology (WF390335)

Hi Katrina and Brian

Please see the letter from Senator McSally and Congressman Gaetz. [redacted]

Hi Jodi – [redacted]

Many thanks!

Mike

From: OER Executive Secretariat [redacted]
Date: Wednesday, April 29, 2020 at 10:21 AM
To: "Lauer, Michael (NIH/OD) [E]" [redacted], "Black, Jodi (NIH/OD) [E]" [redacted]
Cc: "Bundesen, Liza (NIH/OD) [E]" [redacted], "Kosub, David (NIH/OD) [E]" [redacted], "Joshi, Pritty (NIH/OD) [E]" [redacted], "Showe, Melanie (NIH/OD) [E]" [redacted]
Subject: Direct Reply w/ OD Clearance - Wuhan Institute of Virology (WF390335)

Hi Mike and Jodi –
Please see the attached letter from Members of Congress who write with concerns about NIH's past and current relationship with China's bio-agent laboratory Wuhan Institute of Virology (WIV) and to ensure no additional tax dollars are directed to this institution. OER has been asked to draft a direct reply for OD Clearance. Would you mind forwarding me a draft response for OD clearance. Please let me know if you have any questions or if you feel this should be assigned to another SME for drafting.

Thanks,

Best Regards,
Aesha Brandy, MBA*
Program Analyst
NIH Office of Extramural Research
Immediate Office of the Director

Building 1, Room 150
Bethesda, MD 20814
[redacted]
[redacted]
**Contractor*

Page appears blank in original copy

From: Lauer, Michael (NIH/OD) [E]
To: Wojtowicz, Emma (NIH/OD) [E]; Kosub, David (NIH/OD) [E]; OER Press Group
Cc: Myles, Renate (NIH/OD) [E]; Fine, Amanda (NIH/OD) [E]
Subject: Re: Media Inquiry from PolitiFact
Date: Wednesday, February 3, 2021 11:03:05 PM

No worries, Emma, thanks so much!

Mike

From: "Wojtowicz, Emma (NIH/OD) [E]" (b) (6)
Date: Wednesday, February 3, 2021 at 11:02 PM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6), "Kosub, David (NIH/OD) [E]" (b) (6), OER Press Group (b) (6)
Cc: "Myles, Renate (NIH/OD) [E]" (b) (6), "Fine, Amanda (NIH/OD) [E]" (b) (6)
Subject: Re: Media Inquiry from PolitiFact

That is my fault. Thank you!

From: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Date: Wednesday, February 3, 2021 at 10:30:04 PM
To: "Wojtowicz, Emma (NIH/OD) [E]" (b) (6), "Kosub, David (NIH/OD) [E]" (b) (6), "OER Press Group" (b) (6)
Cc: "Myles, Renate (NIH/OD) [E]" (b) (6), "Fine, Amanda (NIH/OD) [E]" (b) (6), "Lauer, Michael (NIH/OD) [E]" (b) (6)
Subject: Re: Media Inquiry from PolitiFact

Hi Emma – sorry, see attached. My apologies, I'm a bit confused by the different email trails.

Mike

From: "Wojtowicz, Emma (NIH/OD) [E]" (b) (6)
Date: Wednesday, February 3, 2021 at 6:45 PM
To: "Kosub, David (NIH/OD) [E]" (b) (6), OER Press Group (b) (6), "Lauer, Michael (NIH/OD) [E]" (b) (6)
Cc: "Myles, Renate (NIH/OD) [E]" (b) (6), "Fine, Amanda (NIH/OD) [E]" (b) (6)
Subject: RE: Media Inquiry from PolitiFact

+Mike, thanks for your review on the other EcoHealth inquiry.

Sorry to keep nudging, (b) (5). Do you think you will be able to get back to us

tonight with the language we asked for?

Thank you!
Emma

From: Kosub, David (NIH/OD) [E] (b) (6)
Sent: Wednesday, February 3, 2021 2:45 PM
To: Wojtowicz, Emma (NIH/OD) [E] (b) (6); OER Press Group (b) (6)
Cc: Myles, Renate (NIH/OD) [E] (b) (6); Fine, Amanda (NIH/OD) [E] (b) (6)
Subject: RE: Media Inquiry from PolitiFact

Hi yes, working on it. sorry for radio silence.
D

From: Wojtowicz, Emma (NIH/OD) [E] (b) (6)
Sent: Wednesday, February 3, 2021 2:40 PM
To: OER Press Group (b) (6)
Cc: Myles, Renate (NIH/OD) [E] (b) (6); Fine, Amanda (NIH/OD) [E] (b) (6)
Subject: RE: Media Inquiry from PolitiFact

Hi All-

Sorry to ping you, but I wanted to make sure that you saw my email below and will get back to us soon with language. We also are waiting to hear back on the other EcoHealth inquiry that we sent to Mike this morning, please see attached.

Thank you-
Emma

From: Wojtowicz, Emma (NIH/OD) [E]
Sent: Wednesday, February 3, 2021 12:44 PM
To: OER Press Group (b) (6)
Cc: Myles, Renate (NIH/OD) [E] (b) (6); Fine, Amanda (NIH/OD) [E] (b) (6)
Subject: FW: Media Inquiry from PolitiFact

Hello OER-

As you are aware, we have been receiving many inquiries about EcoHealth as a result of Fox segment reporting that the original grant supported gain-of-function research. Please see the inquiry below

from PolitiFact asking for clarification on the relationship between the grants. Can you please help us and provide language explaining how the original grant was for 5 years and renewed in 2019 and what that means. Once we have this language we will go back to Fox as well.

Thank you in advance for your help-
Emma

From: Noah Kim (b) (6)
Sent: Wednesday, February 3, 2021 11:46 AM
To: Wojtowicz, Emma (NIH/OD) [E] (b) (6)
Cc: Myles, Renate (NIH/OD) [E] (b) (6); Fine, Amanda (NIH/OD) [E] (b) (6)
Subject: Re: Media Inquiry from PolitiFact

Hi Emma,

Thanks a lot for this, I really appreciate it. Would you mind explaining the difference between grants 1R01AI110964-01 and 2R01AI110964-06? My guess is that grant 1R01AI110964-01 is a sub-award of the larger grant 2R01AI110964-06, but it would be good to get some clarification.

For context, the Fox segment we're looking into addresses a similar statement that the NIH sent them. The Fox commentator claims that the NIH addressed his questions about project 2R01AI110964-06 even though he had asked about project 1R01AI110964-01. He then goes onto claim that project 1R01AI110964-01 included gain-of-function research at the Wuhan Institute, but not 2R01AI110964-06. The relevant clip starts around 10:22 in this video.

In order to debunk this, I'm hoping to address the specific allegations made by the commentator, and it would be very helpful to get some clarification.

Best,
Noah

On Wed, Feb 3, 2021 at 11:00 AM Wojtowicz, Emma (NIH/OD) [E] (b) (6) wrote:

> Hi Noah-
>
> Thanks for checking with us. Attributable to NIH generally:
>
> EcoHealth Alliance Inc. is the grantee organization, which made sub-awards to Wuhan Institute of Virology (Wuhan), East China Normal University (Shanghai), the Institute of Pathogen Biology (Beijing), and Duke-NUS Medical School (Singapore). Publicly available information about the grant to EcoHealth Alliance Inc. is available on NIH RePORTER at this link. For Information about the

distribution to sub-awardees please visit USASpending.gov and switch from “Prime Awards” to “Sub-Awards” in the upper right corner.

To clarify, the research supported under the grant to EcoHealth Alliance Inc. characterized the function of newly discovered bat spike proteins and naturally occurring pathogens and did not involve the enhancement of the pathogenicity or transmissibility of the viruses studied. Therefore, after review NIAID determined the awards were not subject to either the Gain-of-Function Research Funding Pause or its successor, the DHHS Framework for Guiding Funding Decisions about Proposed Research Involving Enhanced Potential Pandemic Pathogens.

For additional background, here is the Director’s statement about NIH lifting the pause on gain-of-function research: https://www.nih.gov/about-nih/who-we-are/nih-director/statements/nih-lifts-funding-pause-gain-function-research.

The Office of the Director of National Intelligence issued a statement on their investigation into the origins of the outbreak. Any questions related to the origins of the outbreak should be directed to ODNI.

Thank you-
Emma

Emma Wojtowicz
Public Affairs Specialist
National Institutes of Health
Tel: (b) (6)
Email: (b) (6)
Web: http://www.nih.gov

NIH . . . Turning Discovery Into Health

From: Noah Kim (b) (6)
Sent: Wednesday, February 3, 2021 10:11 AM
To: Wojtowicz, Emma (NIH/OD) [E] (b) (6)
Subject: Media Inquiry from PolitiFact

Hi Emma,

My name is Noah Kim, and I'm a reporter with PolitiFact.

We're trying to debunk a viral claim that's circulating social media about Dr. Fauci. It's a variation on other conspiracy theories that have cropped up over the source of this pandemic.

The thrust of the claim is that Dr. Fauci advocated for gain-of-function research in 2011. This

appears to be true. However, the claim goes further than that, saying that "Fauci's National Institute of Allergy and Infectious Diseases" funded gain-of-function research at the Wuhan Institute of Virology, and that it is a "near certainty" that Sars-Cov-2 was lab-made.

I was wondering if you'd mind sending me a statement/any materials pushing back on these claims.

I'd be especially curious to know if there's any truth to the fact that the NIH funded the Wuhan Institute of Virology. (This wouldn't establish the veracity of the conspiracy theory, but it would allow me to share with our readers how this conspiracy theory may have originated from a germ of truth.) I'd also be curious to know the scientific basis behind why we know it is extremely unlikely that Sars-Cov-2 was manufactured or engineered at the Wuhan Institute.

Thanks a lot for your time and help,
Noah

From:	Wojtowicz, Emma (NIH/OD) [E]
To:	Lauer, Michael (NIH/OD) [E]; Rabin, Elise (NIH/OD) [E]; Kosub, David (NIH/OD) [E]; Bulls, Michelle G. (NIH/OD) [E]
Cc:	OER Press Group; Ta, Kristin (NIH/OD) [E]; Myles, Renate (NIH/OD) [E]; Fine, Amanda (NIH/OD) [E]
Subject:	RE: Media Response Review: Politifact - Difference in EcoHealth Alliance Grants
Date:	Thursday, February 4, 2021 12:22:01 PM

Thanks, Mike!

From: Lauer, Michael (NIH/OD) [E] (b) (6)
Sent: Thursday, February 4, 2021 12:21 PM
To: Wojtowicz, Emma (NIH/OD) [E] (b) (6); Rabin, Elise (NIH/OD) [E] (b) (6); Kosub, David (NIH/OD) [E] (b) (6); Bulls, Michelle G. (NIH/OD) [E] (b) (6)
Cc: OER Press Group (b) (6); Ta, Kristin (NIH/OD) [E] (b) (6); Myles, Renate (NIH/OD) [E] (b) (6); Fine, Amanda (NIH/OD) [E] (b) (6); Lauer, Michael (NIH/OD) [E] (b) (6)
Subject: Re: Media Response Review: Politifact - Difference in EcoHealth Alliance Grants

Thanks Emma – I think this looks fine.

Mike

From: "Wojtowicz, Emma (NIH/OD) [E]" (b) (6)
Date: Thursday, February 4, 2021 at 11:42 AM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6), "Rabin, Elise (NIH/OD) [E]" (b) (6), "Kosub, David (NIH/OD) [E]" (b) (6), "Bulls, Michelle G. (NIH/OD) [E]" (b) (6)
Cc: OER Press Group (b) (6), "Ta, Kristin (NIH/OD) [E]" (b) (6), "Myles, Renate (NIH/OD) [E]" (b) (6), "Fine, Amanda (NIH/OD) [E]" (b) (6)
Subject: RE: Media Response Review: Politifact - Difference in EcoHealth Alliance Grants

Hi Mike and Elise-

Thanks for the grant language. (b) (5) Please review the response below and let us know if we captured every accurately and if you have any edits/concerns.

Thank you-
Emma

Would you mind explaining the difference between grants 1R01AI110964-01 and 2R01AI110964-06?

From: Lauer, Michael (NIH/OD) [E] (b) (6)
Sent: Wednesday, February 3, 2021 10:29 PM
To: Rabin, Elise (NIH/OD) [E] (b) (6); Kosub, David (NIH/OD) [E] (b) (6); Bulls, Michelle G. (NIH/OD) [E] (b) (6); Wojtowicz, Emma (NIH/OD) [E] (b) (6)
Cc: OER Press Group (b) (6); Ta, Kristin (NIH/OD) [E] (b) (6); Lauer, Michael (NIH/OD) [E] (b) (6)
Subject: Re: Media Response Review: Politifact - Difference in EcoHealth Alliance Grants

Thanks Elise – looks fine. I'm looping in Emma. Sorry if I'm confused by different email trails.

Mike

From: "Rabin, Elise (NIH/OD) [E]" (b) (6)
Date: Wednesday, February 3, 2021 at 6:58 PM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6), "Kosub, David (NIH/OD) [E]" (b) (6), "Bulls, Michelle G. (NIH/OD) [E]" (b) (6)
Cc: OER Press Group (b) (6), "Ta, Kristin (NIH/OD) [E]" (b) (6)

Subject: RE: Media Response Review: Politifact - Difference in EcoHealth Alliance Grants

Hi Mike –

(b) (5)

Thoughts – recognizing that Emma is waiting?

- Elise

From: Lauer, Michael (NIH/OD) [E] (b) (6)
Sent: Wednesday, February 3, 2021 5:40 PM
To: Kosub, David (NIH/OD) [E] (b) (6); Bulls, Michelle G. (NIH/OD) [E] (b) (6)
Cc: OER Press Group (b) (6); Ta, Kristin (NIH/OD) [E] (b) (6); Lauer, Michael (NIH/OD) [E] (b) (6)
Subject: Re: Media Response Review: Politifact - Difference in EcoHealth Alliance Grants

Many thanks – could you send me the proposed response? I'm having trouble figuring it out.

Mike

From: "Kosub, David (NIH/OD) [E]" (b) (6)
Date: Wednesday, February 3, 2021 at 5:10 PM
To: "Bulls, Michelle G. (NIH/OD) [E]" (b) (6), "Lauer, Michael (NIH/OD) [E]" (b) (6)
Cc: OER Press Group (b) (6), "Ta, Kristin (NIH/OD) [E]" (b) (6)
Subject: RE: Media Response Review: Politifact - Difference in EcoHealth Alliance Grants

Thanks Michelle.
Mike, appreciate any additional thoughts you may have on Michelle's revised response. OCPL is hoping for a response on this and the other request Emma made earlier (which I can re-forward to you).

Thanks
David

From: Bulls, Michelle G. (NIH/OD) [E] (b) (6)
Sent: Wednesday, February 3, 2021 4:50 PM
To: Kosub, David (NIH/OD) [E] (b) (6); Lauer, Michael (NIH/OD) [E] (b) (6)
Cc: OER Press Group (b) (6); Ta, Kristin (NIH/OD) [E] (b) (6); Bulls, Michelle G. (NIH/OD) [E] (b) (6)
Subject: RE: Media Response Review: Politifact - Difference in EcoHealth Alliance Grants

Hi David,
Just seeing this, (b) (5). See below for possible revisions.

From: Kosub, David (NIH/OD) [E] (b) (6)
Sent: Wednesday, February 3, 2021 2:32 PM
To: Lauer, Michael (NIH/OD) [E] (b) (6); Bulls, Michelle G. (NIH/OD) [E] (b) (6)
Cc: OER Press Group (b) (6); Ta, Kristin (NIH/OD) [E] (b) (6)
Subject: Media Response Review: Politifact - Difference in EcoHealth Alliance Grants

Good day Mike and OPERA,

A reporter with Politifact would like NIH to explain the difference between 1R01AI110964-01 and 2R01AI110964-06 awarded to EcoHealth Alliance. Though we can help the reporter decipher the relationship between the grants as requested by OCPL (i.e. difference between -01 original award and -06 renewal), (b) (5) This question stems from a Fox segment reporting that the original grant supported gain-of-function research. Appreciate your thoughts.

Proposed Response for the first part of the question:

(b) (5)

From: Wojtowicz, Emma (NIH/OD) [E] (b) (6)
Sent: Wednesday, February 3, 2021 12:44 PM
To: OER Press Group (b) (6)
Cc: Myles, Renate (NIH/OD) [E] (b) (6); Fine, Amanda (NIH/OD) [E] (b) (6)
Subject: FW: Media Inquiry from PolitiFact

Hello OER-

As you are aware, we have been receiving many inquiries about EcoHealth as a result of Fox segment reporting that the original grant supported gain-of-function research. Please see the inquiry below from PolitiFact asking for clarification on the relationship between the grants. Can you please help us and provide language explaining how the original grant was for 5 years and renewed in 2019 and what that means. Once we have this language we will go back to Fox as well.

Thank you in advance for your help-
Emma

From: Noah Kim (b) (6)
Sent: Wednesday, February 3, 2021 11:46 AM
To: Wojtowicz, Emma (NIH/OD) [E] (b) (6)
Cc: Myles, Renate (NIH/OD) [E] (b) (6); Fine, Amanda (NIH/OD) [E] (b) (6)
Subject: Re: Media Inquiry from PolitiFact

Hi Emma,

Thanks a lot for this, I really appreciate it. Would you mind explaining the difference between grants 1R01AI110964-01 and 2R01AI110964-06? My guess is that grant 1R01AI110964-01 is a sub-award of the larger grant 2R01AI110964-06, but it would be good to get some clarification.

For context, the Fox segment we're looking into addresses a similar statement that the NIH sent them. The Fox commentator claims that the NIH addressed his questions about project 2R01AI110964-06 even though he had asked about project 1R01AI110964-01. He then goes onto claim that project 1R01AI110964-01 included gain-of-function research at the Wuhan Institute, but not 2R01AI110964-06. The relevant clip starts around 10:22 in this video.

In order to debunk this, I'm hoping to address the specific allegations made by the commentator, and it would be very helpful to get some clarification.

Best,
Noah

On Wed, Feb 3, 2021 at 11:00 AM Wojtowicz, Emma (NIH/OD) [E] [redacted] (b) (6) wrote:

> Hi Noah-
>
> Thanks for checking with us. Attributable to NIH generally:
>
> EcoHealth Alliance Inc. is the grantee organization, which made sub-awards to Wuhan Institute of Virology (Wuhan), East China Normal University (Shanghai), the Institute of Pathogen Biology (Beijing), and Duke-NUS Medical School (Singapore). Publicly available information about the grant to EcoHealth Alliance Inc. is available on NIH RePORTER at this link. For Information about the distribution to sub-awardees please visit USASpending.gov and switch from "Prime Awards" to "Sub-Awards" in the upper right corner.
>
> To clarify, the research supported under the grant to EcoHealth Alliance Inc. characterized the function of newly discovered bat spike proteins and naturally occurring pathogens and did not involve the enhancement of the pathogenicity or transmissibility of the viruses studied. Therefore, after review NIAID determined the awards were not subject to either the Gain-of-Function Research Funding Pause or its successor, the DHHS Framework for Guiding Funding Decisions about Proposed Research Involving Enhanced Potential Pandemic Pathogens.
>
> For additional background, here is the Director's statement about NIH lifting the pause on gain-of-function research: https://www.nih.gov/about-nih/who-we-are/nih-director/statements/nih-lifts-funding-pause-gain-function-research.
>
> The Office of the Director of National Intelligence issued a statement on their investigation into the origins of the outbreak. Any questions related to the origins of the outbreak should be directed to ODNI.
>
> Thank you-
> Emma
>
> Emma Wojtowicz
> Public Affairs Specialist
> National Institutes of Health
> Tel: [redacted] (b) (6)
> Email: [redacted] (b) (6)
> Web: http://www.nih.gov
>
> NIH . . . Turning Discovery Into Health

From: Noah Kim (b) (6)
Sent: Wednesday, February 3, 2021 10:11 AM
To: Wojtowicz, Emma (NIH/OD) [E] (b) (6)
Subject: Media Inquiry from PolitiFact

Hi Emma,

My name is Noah Kim, and I'm a reporter with PolitiFact.

We're trying to debunk a viral claim that's circulating social media about Dr. Fauci. It's a variation on other conspiracy theories that have cropped up over the source of this pandemic.

The thrust of the claim is that Dr. Fauci advocated for gain-of-function research in 2011. This appears to be true. However, the claim goes further than that, saying that "Fauci's National Institute of Allergy and Infectious Diseases" funded gain-of-function research at the Wuhan Institute of Virology, and that it is a "near certainty" that Sars-Cov-2 was lab-made.

I was wondering if you'd mind sending me a statement/any materials pushing back on these claims.

I'd be especially curious to know if there's any truth to the fact that the NIH funded the Wuhan Institute of Virology. (This wouldn't establish the veracity of the conspiracy theory, but it would allow me to share with our readers how this conspiracy theory may have originated from a germ of truth.) I'd also be curious to know the scientific basis behind why we know it is extremely unlikely that Sars-Cov-2 was manufactured or engineered at the Wuhan Institute.

Thanks a lot for your time and help,
Noah

From: Lauer, Michael (NIH/OD) [E]
To: Kosub, David (NIH/OD) [E]; Black, Jodi (NIH/OD) [E]
Cc: OER Press Group; Lauer, Michael (NIH/OD) [E]
Subject: Re: OER PRESS/NEED YOUR HELP: Media inquiries on EcoHealth Alliance
Date: Wednesday, April 29, 2020 2:43:49 PM
Attachments: SR_29Apr2020_020207_56918587[1].csv
Screen Shot 2020-04-29 at 2.40.00 PM.png

Hi David – our WG meeting is on break. (b) (5) Attached are the tables from RePORTER and from QVR – (b) (5)

Many thanks, Mike

From: "Kosub, David (NIH/OD) [E]" (b) (6)
Date: Wednesday, April 29, 2020 at 2:31 PM
To: "Black, Jodi (NIH/OD) [E]" (b) (6), "Lauer, Michael (NIH/OD) [E]" (b) (6)
Cc: OER Press Group (b) (6)
Subject: FW: OER PRESS/NEED YOUR HELP: Media inquiries on EcoHealth Alliance

Hi Jodi,
Would you be able to clear the revised statement from OCPL below in Mike's absence? They requested a response and are getting inundated with requests on this
THanks
David

From: Lauer, Michael (NIH/OD) [E] (b) (6)
Sent: Wednesday, April 29, 2020 2:04 PM
To: Fine, Amanda (NIH/OD) [E] (b) (6)
Cc: Myles, Renate (NIH/OD) [E] (b) (6); Wojtowicz, Emma (NIH/OD) [E] (b) (6); Black, Jodi (NIH/OD) [E] (b) (6); OER Press Group (b) (6); Lauer, Michael (NIH/OD) [E] (b) (6)
Subject: Re: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance

Hi Amanda – Sorry, I'm tied up this afternoon – here's the table of the history of the grant.

Thanks, Mike

> **From:** "Fine, Amanda (NIH/OD) [E]" (b) (6)
> **Date:** Wednesday, April 29, 2020 at 1:48 PM
> **To:** "Lauer, Michael (NIH/OD) [E]" (b) (6)
> **Cc:** "Myles, Renate (NIH/OD) [E]" (b) (6), "Wojtowicz, Emma (NIH/OD) [E]" (b) (6), "Black, Jodi (NIH/OD) [E]" (b) (6), OER Press Group (b) (6)
> **Subject:** RE: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance
>
> Just to update you we've received a few more inquiries on this. Hoping to get back to them as soon as possible. We know you're swamped but when you have a moment let us know if we are able to share the below response.
>
> Thanks!
> Amanda

From: Fine, Amanda (NIH/OD) [E]
Sent: Wednesday, April 29, 2020 12:38 PM
To: Lauer, Michael (NIH/OD) [E] (b) (6)
Cc: Myles, Renate (NIH/OD) [E] (b) (6); Wojtowicz, Emma (NIH/OD) [E] (b) (6); Black, Jodi (NIH/OD) [E] (b) (6); OER Press Group (b) (6)
Subject: FW: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance

Hi Mike-

Sorry for the delay, (b) (5)

(b) (5)

Thanks,
Amanda

From: Lauer, Michael (NIH/OD) [E] (b) (6)
Sent: Tuesday, April 28, 2020 7:09 PM
To: Fine, Amanda (NIH/OD) [E] (b) (6)
Cc: Myles, Renate (NIH/OD) [E] (b) (6); Wojtowicz, Emma (NIH/OD) [E] (b) (6); Black, Jodi (NIH/OD) [E] (b) (6); OER Press Group (b) (6); Lauer, Michael (NIH/OD) [E] (b) (6)
Subject: Re: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance

Hi Amanda

(b) (5)

(b) (5)

Many thanks, Mike

From: "Fine, Amanda (NIH/OD) [E]" (b) (6)
Date: Tuesday, April 28, 2020 at 5:54 PM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Cc: "Myles, Renate (NIH/OD) [E]" (b) (6), "Wojtowicz, Emma (NIH/OD) [E]" (b) (6), "Black, Jodi (NIH/OD) [E]" (b) (6), OER Press Group (b) (6)
Subject: RE: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance

Hi Mike-

As you are probably can guess we're getting a lot of media inquiries on this topic. There have been several articles that cite the April 19 letter from you to EcoHealth Alliance. Since this letter is now somewhat public, the first paragraph has definitely been quoted in several places, (b) (5)

(b) (5)

.
Thanks for your guidance,
Amanda

From: Lauer, Michael (NIH/OD) [E] (b) (6)
Sent: Tuesday, April 28, 2020 1:39 PM
To: Fine, Amanda (NIH/OD) [E] (b) (6); Myles, Renate (NIH/OD) [E] (b) (6); Black, Jodi (NIH/OD) [E] (b) (6); Showe, Melanie (NIH/OD) [E] (b) (6)
Cc: Wojtowicz, Emma (NIH/OD) [E] (b) (6); OER Press Group (b) (6); Lauer, Michael (NIH/OD) [E] (b) (6)
Subject: Re: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance

Hi Amanda – (b) (5)

(b) (5)

Many thanks, Mike

From: "Fine, Amanda (NIH/OD) [E]" (b) (6)
Date: Tuesday, April 28, 2020 at 12:40 PM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6), "Myles, Renate (NIH/OD) [E]" (b) (6), "Black, Jodi (NIH/OD) [E]" (b) (6), "Showe, Melanie (NIH/OD) [E]" (b) (6)
Cc: "Wojtowicz, Emma (NIH/OD) [E]" (b) (6), OER Press Group (b) (6)
Subject: RE: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance

Hi Mike-

Thanks, regarding the highlighted below, (b) (5)

Amanda

From: Lauer, Michael (NIH/OD) [E] (b) (6)
Sent: Tuesday, April 28, 2020 12:12 PM
To: Fine, Amanda (NIH/OD) [E] (b) (6); Myles, Renate (NIH/OD) [E] (b) (6); Black, Jodi (NIH/OD) [E] (b) (6); Showe, Melanie (NIH/OD) [E] (b) (6)
Cc: Wojtowicz, Emma (NIH/OD) [E] (b) (6); OER Press Group (b) (6); Lauer, Michael (NIH/OD) [E] (b) (6)
Subject: Re: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance

Hi Amanda – (b) (5)

Thanks, Mike

From: "Fine, Amanda (NIH/OD) [E]" (b) (6)
Date: Tuesday, April 28, 2020 at 12:05 PM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6), "Myles, Renate (NIH/OD) [E]" (b) (6), "Black, Jodi (NIH/OD) [E]" (b) (6), "Showe, Melanie (NIH/OD) [E]" (b) (6)
Cc: "Wojtowicz, Emma (NIH/OD) [E]" (b) (6), OER Press Group (b) (6)
Subject: RE: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance

Hi Mike-

Science magazine asked for the “law or regulation” that gives NIH authority to stop funding a grant midstream in the absence of fraud or other findings of misconduct?

Based on what we discussed yesterday, how do you recommend we respond? (b) (5)

Thanks!

Amanda

From: Lauer, Michael (NIH/OD) [E] (b) (6)
Sent: Monday, April 27, 2020 7:21 PM
To: Myles, Renate (NIH/OD) [E] (b) (6); Fine, Amanda (NIH/OD) [E] (b) (6); Black, Jodi (NIH/OD) [E] (b) (6); Showe, Melanie (NIH/OD) [E] (b) (6)
Cc: Wojtowicz, Emma (NIH/OD) [E] (b) (6); OER Press Group (b) (6); Lauer, Michael (NIH/OD) [E] (b) (6)
Subject: Re: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance

Hi Renate – (b) (5)

Best, Mike

From: "Myles, Renate (NIH/OD) [E]" (b) (6)
Date: Monday, April 27, 2020 at 7:20 PM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6), "Fine, Amanda (NIH/OD) [E]" (b) (6), "Black, Jodi (NIH/OD) [E]" (b) (6), "Showe, Melanie (NIH/OD) [E]" (b) (6)
Cc: "Wojtowicz, Emma (NIH/OD) [E]" (b) (6), OER Press Group (b) (6)
Subject: RE: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance

Hi Mike:

(b) (5)

Thanks,
Renate

From: Lauer, Michael (NIH/OD) [E] (b) (6)
Sent: Monday, April 27, 2020 7:14 PM
To: Fine, Amanda (NIH/OD) [E] (b) (6); Black, Jodi (NIH/OD) [E] (b) (6); Showe, Melanie (NIH/OD) [E] (b) (6)
Cc: Myles, Renate (NIH/OD) [E] (b) (6); Wojtowicz, Emma (NIH/OD) [E] (b) (6); OER Press Group (b) (6); Lauer, Michael (NIH/OD) [E] (b) (6)
Subject: Re: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance

Hi Amanda

Here's a revised paragraph (b) (5)

Thanks, Mike

(b) (5)

(b) (5)

From: "Fine, Amanda (NIH/OD) [E]" (b) (6)
Date: Monday, April 27, 2020 at 6:22 PM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6), "Black, Jodi (NIH/OD) [E]" (b) (6), "Showe, Melanie (NIH/OD) [E]" (b) (6)
Cc: "Myles, Renate (NIH/OD) [E]" (b) (6), "Wojtowicz, Emma (NIH/OD) [E]" (b) (6), OER Press Group (b) (6)
Subject: RE: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance

Hi Mike-

Thanks for sharing the report. (b) (5)

Thanks in advance for your guidance,
Amanda

(b) (5)

From: Lauer, Michael (NIH/OD) [E] (b) (6)
Sent: Monday, April 27, 2020 5:45 PM
To: Fine, Amanda (NIH/OD) [E] (b) (6); Black, Jodi (NIH/OD) [E] (b) (6); Showe, Melanie (NIH/OD) [E] (b) (6)
Cc: Myles, Renate (NIH/OD) [E] (b) (6); Wojtowicz, Emma (NIH/OD) [E]

(b) (6); OER Press Group (b) (6); Lauer, Michael (NIH/OD) [E] (b) (6)
Subject: Re: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance

Hi Amanda – (b) (5) But I'm not seeing this in any public venue.

Best, Mike

From: "Fine, Amanda (NIH/OD) [E]" (b) (6)
Date: Monday, April 27, 2020 at 4:27 PM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6), "Black, Jodi (NIH/OD) [E]" (b) (6), "Showe, Melanie (NIH/OD) [E]" (b) (6)
Cc: "Myles, Renate (NIH/OD) [E]" (b) (6), "Wojtowicz, Emma (NIH/OD) [E]" (b) (6), OER Press Group (b) (6)
Subject: RE: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance

Thanks Mike-and is that response public?

From: Lauer, Michael (NIH/OD) [E] (b) (6)
Sent: Monday, April 27, 2020 4:17 PM
To: Fine, Amanda (NIH/OD) [E] (b) (6); Black, Jodi (NIH/OD) [E] (b) (6); Showe, Melanie (NIH/OD) [E] (b) (6)
Cc: Myles, Renate (NIH/OD) [E] (b) (6); Wojtowicz, Emma (NIH/OD) [E] (b) (6); OER Press Group (b) (6); Lauer, Michael (NIH/OD) [E] (b) (6)
Subject: Re: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance

Hi Amanda – (b) (5)

Best, Mike

From: "Fine, Amanda (NIH/OD) [E]" (b) (6)
Date: Monday, April 27, 2020 at 3:40 PM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6), "Black, Jodi (NIH/OD) [E]" (b) (6), "Showe, Melanie (NIH/OD) [E]" (b) (6)
Cc: "Myles, Renate (NIH/OD) [E]" (b) (6), "Wojtowicz, Emma (NIH/OD) [E]" (b) (6), OER Press Group (b) (6)
Subject: RE: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance

Hi Mike-

Thanks so much again for your input. One question we're not sure how to answer, (b) (5) Do you have guidance on how to respond to that question?

Thanks!
Amanda

From: Lauer, Michael (NIH/OD) [E] (b) (6)
Sent: Monday, April 27, 2020 2:39 PM

To: Fine, Amanda (NIH/OD) [E] (b) (6); Black, Jodi (NIH/OD) [E] (b) (6); Showe, Melanie (NIH/OD) [E] (b) (6); Lauer, Michael (NIH/OD) [E] (b) (6)
Cc: Myles, Renate (NIH/OD) [E] (b) (6); Wojtowicz, Emma (NIH/OD) [E] (b) (6); OER Press Group (b) (6)
Subject: Re: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance

Please send me an invite with your conference line, thanks

From: "Fine, Amanda (NIH/OD) [E]" (b) (6)
Date: Monday, April 27, 2020 at 2:32 PM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6), "Black, Jodi (NIH/OD) [E]" (b) (6), "Showe, Melanie (NIH/OD) [E]" (b) (6)
Cc: "Myles, Renate (NIH/OD) [E]" (b) (6), "Wojtowicz, Emma (NIH/OD) [E]" (b) (6), OER Press Group (b) (6)
Subject: RE: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance

Either work. What number should we call or do you want to use the OCPL conference line?

From: Lauer, Michael (NIH/OD) [E] (b) (6)
Sent: Monday, April 27, 2020 2:29 PM
To: Fine, Amanda (NIH/OD) [E] (b) (6); Black, Jodi (NIH/OD) [E] (b) (6); Showe, Melanie (NIH/OD) [E] (b) (6)
Cc: Myles, Renate (NIH/OD) [E] (b) (6); Wojtowicz, Emma (NIH/OD) [E] (b) (6); OER Press Group (b) (6); Lauer, Michael (NIH/OD) [E] (b) (6)
Subject: Re: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance

Probably best for us to talk – I'm "free" from 3:05 to 3:25 if that works.

Thanks, Mike

From: "Fine, Amanda (NIH/OD) [E]" (b) (6)
Date: Monday, April 27, 2020 at 2:21 PM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6), "Black, Jodi (NIH/OD) [E]" (b) (6)
Cc: "Myles, Renate (NIH/OD) [E]" (b) (6), "Wojtowicz, Emma (NIH/OD) [E]" (b) (6), OER Press Group (b) (6)
Subject: FOR INPUT AND GUIDANCE: Media inquiries on EcoHealth Alliance

Hi Mike and Jodi-

NIAID has been receiving inquiries about the EcoHealth Alliance grant. In addition to the 2 listed below in Jen's email they received a similar one from Newsweek. We want to answer these questions. Would you provide guidance on how best to answer them? Thanks and hope you're both staying well.

Newsweek:

From: Fred Guterl <f.guterl@newsweek.com>

Hi, we're running a story tomorrow morning at 10 am that mentions Dr. Fauci and we'd like to ask for a comment.

The story is about the possibility that SARS-Cov-2 is a product of gain of function research at the Wuhan Institute of Virology. The story mentions Dr. Fauci as an early proponent of the work of Ron Fouchier et al. ten years ago, quotes from his Washington Post article of 2011 on the importance of the research as a way of preparing for a pandemic. We trace the lifting of the moratorium and subsequent accusations that the NIH was acting to too little transparency in approving projects.

Sorry to spring this on you on Sunday night. Many thanks in advance.

Best,
Fred

From: Routh, Jennifer (NIH/NIAID) [E] (b) (6)
Sent: Monday, April 27, 2020 1:38 PM
To: Myles, Renate (NIH/OD) [E] (b) (6); Fine, Amanda (NIH/OD) [E] (b) (6)
Cc: Billet, Courtney (NIH/NIAID) [E] (b) (6); Stover, Kathy (NIH/NIAID) [E] (b) (6); Haskins, Melinda (NIH/NIAID) [E] (b) (6)
Subject: EcoHealth Alliance grant / Wuhan lab
Importance: High

Hi Renate –

NIAID received media inquiries last week from Snopes and Politifact related to the NIAID grant to EcoHealth Alliance (see below). Kathy and I just had a conversation with NIAID grants management and learned that OER communicated with this grantee on Friday and we believe media inquiries on this topic would be best handled by OER now. Happy to discuss more via phone. We are holding on any responses to media on this topic right now.

INQUIRY FROM SNOPES

QUESTION:
This is Dan Evon from the fact-checking website Snopes. We've been receiving questions about a recent article published in the Daily Mail that claims the Obama administration provided a $3.7 million grant to the Wuhan Institute of Virology, and I was hoping to get some more information from you.

The Daily Mail appears to be referring to NIAID award R01AI110964. That award went to the EcoHealth Alliance in New York and subsequently funded a research paper from the Wuhan Institute.

Has NIH issued any direct grants to the Wuhan Institute of Virology? The NIH RePORT tool shows funding to Wuhan University in 2019 and 2018, but not (unless I missed something) from previous years.

Did NIH provide a $3.7 million grant to the Wuhan Institute of Virology between 2008 and 2016? Can you tell me more about the grants awarded to Wuhan University in 2018 and 2019?

Any information you can provide would be greatly appreciated.

INQUIRY FROM POLITIFACT

QUESTION:
We're fielding a claim that NIH gave a $3.7 million grant to a virology lab in Wuhan in 2015. Can you share any relevant grant or contract activity around that time and place?

NIAID PROVIDED THIS RESPONSE (general cleared language):
(b) (5)

REPORTER FOLLOWED UP WITH THESE QUESTIONS:
Focusing on the money, does this Spending.gov summary (Grant tab; see Wuhan University) tell me how much the Wuhan lab in question got from the overall $3.7 million? (b) (5) Also, is the project done, and has any money due to Wuhan been withdrawn/put on hold, etc? Lastly, if you want to make sure I see the scientific articles specific to the Wuhan research, please feel free to highlight them. I will go through the results list, but it's always better if you make sure I don't miss one.

(b) (5)

Jennifer Routh [E]
News and Science Writing Branch
Office of Communications and Government Relations
National Institute of Allergy and Infectious Diseases (NIAID)
NIH/HHS
31 Center Drive Room 7A17C
Bethesda, MD 20892
Direct: (b) (6)
(b) (6)

Search Criteria:

Search in: Projects AdminIC: All; Principal Investigator / Project Leader: Daszak; Project Number (split): 110964; Fiscal Year: All Fiscal Years

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NIH Spending Categorization	Project Terms	Project Title	Public Health Relevance	Administering IC	Application ID	Award Notice Date	FOA	Project Number	Type	Activity	IC	Serial Number	Support Year	Suffix	Program Official Information	Project Start Date	Project End Date	Study Section
No NIH Category available.	Acute;Acute Diarrhea;Address;Amino Acid Sequence;Animals;base;Behavior;Behavioral;Biological;biosecurity;Cells;China;Chiroptera;Clinic;Clinic Visits;Clinical;Communities;community clinic;Coronavirus;Coronavirus Infections;Coupled;Data;Data Analyses;Development;Disease Outbreaks;epidemiologic data;Epithelial Cells;experimental study;exposed human population;exposure route;Exposure to;Family suidae;follow-up;food security;Future;genetic element;Genome;Geographic Distribution;Geography;global health;Habitats;Health;high risk;high risk population;Human;human population study;humanized mouse;In Vitro;in vivo;Individual;Infection;Influenza;Investigation;laboratory experiment;Lead;Maps;Middle East Respiratory Syndrome Coronavirus;Modeling;Molecular;Monoclonal Antibodies;mouse model;Nature;novel;pandemic disease;Paper;Patients;Phylogenetic Analysis;Phylogeny;Prevalence;prevent; Principal	Understanding the Risk of Bat Coronavirus Emergence	Program Director/Principal Investigator: Daszak; PeterRenewal: Understanding the Risk of Bat Coronavirus EmergenceProject NarrativeMost emerging human viruses come from wildlife; and these represent a significant threat topublic health and biosecurity in the US and globally; as was demonstrated by the SARScoronavirus pandemic of 2002-03. This project seeks to understand what factors allowcoronaviruses; including close relatives to SARS; to evolve and jump into the human populationby studying viral diversity in their animal reservoirs (bats); surveying people that live in high-riskcommunities in China for evidence of	NIAID	9819304	24-Jul-19	PA-18-484	2R01AI110964-06	2	R01	AI	110964	6	STEMMY, ERIK J	1-Jun-14	24-Apr-20	Clinical Research and Field Studies of Infectious Diseases Study Section (CRFS)
Clinical Research;Emerging Infectious Diseases;Genetics;Infectious Diseases;Rare Diseases	Acute;Animals;Asia;Binding;Binding Sites;Biological Assay;biosecurity;Blood specimen;Cell Culture Techniques;Cell Line;Cells;Chimeric Proteins;China;Chiroptera;Clinical;Coronavirus;coronavirus receptor;Data;Dipeptidyl-Peptidase IV;Disease;Ecosystem;Epidemic;Evolution;experimental study;Exposure to;field study;Frequencies;Future;Genbank;Gene Proteins;Genes;Genetic;Genetic Recombination;Genetic Variation;Genomics;Geography;global health;high risk;Human;human population study;humanized mouse;improved;In Vitro;in vivo;Infection;interest;Interview;Investigation;Laboratory Study;Mammals;mathematical model;Mathematics;Middle East;Middle East Respiratory Syndrome Coronavirus;Modeling;Molecular;mutant;Nature;novel;Occupational Exposure;pandemic disease;Pattern;Phylogenetic Analysis;Phylogeny;predictive modeling;Primates;Process;Property;Public Health;public health relevance;receptor;receptor	Understanding the Risk of Bat Coronavirus Emergence	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).	NIAID	9491676	18-Jun-18	PA-11-260	5R01AI110964-05	5	R01	AI	110964	5	STEMMY, ERIK J	1-Jun-14	31-May-19	Clinical Research and Field Studies of Infectious Diseases Study Section (CRFS)

	A Cell;Animals;Asia;Binding;Binding Sites;Biological Assay;biosecurity;Blood specimen;Cell Culture Techniques;Cell Line;Cells;Chimeric Proteins;China;Chiroptera;Clinical;Coronaviridae;Coronavirus;coronavirus receptor;Data;Dipeptidyl-Peptidase IV;Disease;Ecosystem;Epidemic;Evolution;experimental study;Exposure to;field study;Frequencies;Future;Genbank;Gene Proteins;Genes;Genetic;Genetic Recombination;Genetic Variation;Genomics;Geography;global health;high risk;Human;human population study;humanized mouse;improved;In Vitro;in vivo;Infection;interest;Interview;Investigation;Laboratory Study;Mammals;mathematical model;Mathematics;Middle East;Middle East Respiratory Syndrome Coronavirus;Modeling;Molecular;mutant;Nature;novel;Occupational Exposure;pandemic disease;Pattern;Phylogenetic Analysis;Phylogeny;predictive modeling;Primates;Process;Property;Public Health;public health relevance receptor;receptor	Understanding the Risk of Bat Coronavirus Emergence	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).	NIAID	9320765	26-May-17	PA-11-260	5R01AI110964-04	5	R01	AI	110964	4	STEMMY, ERIK J	1-Jun-14	31-May-19	Clinical Research and Field Studies of Infectious Diseases Study Section (CRFS)
Clinical Research;Emerging Infectious Diseases;Genetics;Infectious Diseases																
	A Cell;Animals;Asia;Binding;Binding Sites;Biological Assay;biosecurity;Blood specimen;Cell Culture Techniques;Cell Line;Cells;Chimeric Proteins;China;Chiroptera;Clinical;Coronavirus;coronavirus receptor;Data;Dipeptidyl-Peptidase IV;Disease;Ecosystem;Epidemic;Evolution;Exposure to;field study;Frequencies;Future;Genbank;Genes;Genetic;Genetic Recombination;Genetic Variation;Genomics;global health;Health;high risk;Human;human population study;humanized mouse;improved;In Vitro;in vitro Assay;in vivo;Infection;interest;Interview;Investigation;Laboratory Study;Life;Mammals;Marketing;mathematical model;Middle East;Middle East Respiratory Syndrome Coronavirus;Modeling;Molecular;mutant;Nature;novel;Occupational Exposure;pandemic disease;Pattern;Phylogenetic Analysis;Phylogeny;predictive modeling;Primates;Process;Property;Public Health;receptor;receptor	Understanding the Risk of Bat Coronavirus Emergence	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).	NIAID	9086286	22-Jul-16	PA-11-260	5R01AI110964-03	5	R01	AI	110964	3	STEMMY, ERIK J	1-Jun-14	31-May-19	Clinical Research and Field Studies of Infectious Diseases Study Section (CRFS)
Biotechnology;Clinical Research;Emerging Infectious Diseases;Genetics;Infectious Diseases																

	A Cell;Animals;Asia;Binding;Binding Sites;Biological Assay;biosecurity;Blood specimen;Cell Culture Techniques;Cell Line;Cells;Chimeric Proteins;China;Chiroptera;Clinical;Coronavirus;coronavirus receptor;Data;Dipeptidyl-Peptidase IV;Disease;Ecosystem;Epidemic;Evolution;Exposure to;field study;Frequencies;Future;Genbank;Genes;Genetic;Genetic Recombination;Genetic Variation;Genomics;global health;high risk;Human;human population study;Human Virus;improved;In Vitro;in vitro Assay;in vivo;Infection;interest;Interview;Investigation;Laboratory Study;Life;Mammals;Marketing;mathematical model;Middle East;Middle East Respiratory Syndrome Coronavirus;Modeling;Molecular;Mus;mutant;Nature;novel;Occupational Exposure;pandemic disease;Pattern;Phylogenetic Analysis;Phylogeny;predictive modeling;Primates;Process;Property;Public Health;public health relevance receptor;receptor	Understanding the Risk of Bat Coronavirus Emergence	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).	NIAID	8853810	10-Jun-15	PA-11-260	5R01AI110964-02	5	R01	AI	110964	2	STEMMY, ERIK J	1-Jun-14	31-May-19	Biotechnology;Clinical Research;Emerging Infectious Diseases;Genetics;Infectious Diseases	Clinical Research and Field Studies of Infectious Diseases Study Section (CRFS)
	A Cell;Animals;Asia;Binding;Binding Sites;Biological Assay;biosecurity;Blood specimen;Cell Culture Techniques;Cell Line;Cells;Chimeric Proteins;China;Chiroptera;Clinical;Coronavirus;coronavirus receptor;Data;Dipeptidyl-Peptidase IV;Disease;Ecosystem;Epidemic;Evolution;Exposure to;field study;Frequencies;Future;Genbank;Genes;Genetic;Genetic Recombination;Genetic Variation;Genomics;global health;high risk;Human;human population study;Human Virus;improved;In Vitro;in vitro Assay;in vivo;Infection;interest;Interview;Investigation;Laboratory Study;Life;Mammals;Marketing;mathematical model;Middle East;Modeling;Molecular;Mus;mutant;Nature;novel;Occupational Exposure;pandemic disease;Pattern;Phylogenetic Analysis;Phylogeny;positional cloning;predictive modeling;Primates;Process;Property;Public Health;public health relevance;receptor;receptor	Understanding the Risk of Bat Coronavirus Emergence	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).	NIAID	8674931	27-May-14	PA-11-260	1R01AI110964-01	1	R01	AI	110964	1	STEMMY, ERIK J	1-Jun-14	31-May-19	Biotechnology;Emerging Infectious Diseases;Genetics;Infectious Diseases	Clinical Research and Field Studies of Infectious Diseases Study Section (CRFS)

Subproject Number	Contact PI Person ID	Contact PI / Project Leader	Other PI or Project Leader(s)	Congressional District	Department	DUNS Number	FIPS	Latitude	Longitude	Organization ID (IPF)	Organization Name	Organization City	Organization State	Organization Type	Organization Zip	Organization Country	ARRA Indicator	Budget Start Date	Budget End Date	CFDA Code	Funding Mechanism
	6575431	DASZAK, PETER	Not Applicable	10	Unavailable	77090066	US	40.75413	-73.99829	4415701	ECOHEALTH ALLIANCE, INC.	NEW YORK	NY	Other Domestic Non-Profits	10001-2320	UNITED STATES		24-Jul-19	24-Apr-20	855	Research Projects
	6575431	DASZAK, PETER	Not Applicable	10	Unavailable	77090066	US	40.75413	-73.99829	4415701	ECOHEALTH ALLIANCE, INC.	NEW YORK	NY	Other Domestic Non-Profits	10001-2320	UNITED STATES		1-Jun-18	31-May-19	855	Research Projects

6575431	DASZAK, PETER	Not Applicable	10	Unavailable	77090066	US	40.75413	-73.99829	4415701	ECOHEALTH ALLIANCE, INC.	NEW YORK	NY	Other Domestic Non-Profits	10001-2320	UNITED STATES	1-Jun-17	31-May-18	855	Research Projects

6575431	DASZAK, PETER	Not Applicable	10	Unavailable	77090066	US	40.75413	-73.99829	4415701	ECOHEALTH ALLIANCE, INC.	NEW YORK	NY	Other Domestic Non-Profits	10001-2320	UNITED STATES	1-Jun-16	31-May-17	855	Research Projects

6575431	DASZAK, PETER	Not Applicable	10	Unavailable	77090066	US	40.75413	-73.99829	4415701	ECOHEALTH ALLIANCE, INC.	NEW YORK	NY	Other Domestic Non-Profits	10001-2320	UNITED STATES	1-Jun-15	31-May-16	855	Research Projects

6575431	DASZAK, PETER	Not Applicable	10	Unavailable	77090066	US	40.75413	-73.99829	4415701	ECOHEALTH ALLIANCE, INC.	NEW YORK	NY	Other Domestic Non-Profits	10001-2320	UNITED STATES	1-Jun-14	31-May-15	855	Research Projects

FY	Funding IC	FY Direct Costs	FY Indirect Costs	FY Total Cost by IC	FY Total Cost (Sub Projects)
2019	NIAID	262862	29299	292161	
2018	NIAID	462270	119376	581646	

2017	NIAID	476016	121096	597112
2016	NIAID	489333	121757	611090

2015 NIAID 502293 128152 630445

2014 NIAID 516857 149585 666442

	* T Act IC Project RFA Appl Id	FY Council	Links	PI Name	Status Grp (Status Cd) %tile / Score	Study Sec Admin PCC NI / ESI	Project Title Org Name (State)	Awd TC Awd DC Bud Start
1	2 R01 AI110964-06 PA-18-484 9819304	2019 2019-05	Snap Abs SS NoA Acctg Hist **eIMG** Docs GF PUB Like Who	DASZAK, PETER	(b) (5)		Understanding the Risk of Bat Coronavirus Emergence ECOHEALTH ALLIANCE, INC. (NY)	$292,161 $262,862 2019/07/24
2	5 R01 AI110964-05 PA-11-260 9491676	2018 -	Snap Abs NoA Acctg Hist **eIMG** Docs GF PUB Like Who	DASZAK, PETER			Understanding the Risk of Bat Coronavirus Emergence ECOHEALTH ALLIANCE, INC. (NY)	$581,646 $462,270 2018/06/01
3	5 R01 AI110964-04 PA-11-260 9320765	2017 -	Snap Abs NoA Acctg Hist **eIMG** Docs GF PUB Like Who	DASZAK, PETER			Understanding the Risk of Bat Coronavirus Emergence ECOHEALTH ALLIANCE, INC. (NY)	$597,112 $476,016 2017/06/01
4	5 R01 AI110964-03 PA-11-260 9086286	2016 -	Snap Abs NoA Acctg Hist **eIMG** Docs GF PUB Like Who	DASZAK, PETER			Understanding the Risk of Bat Coronavirus Emergence ECOHEALTH ALLIANCE, INC. (NY)	$611,090 $489,333 2016/06/01
5	5 R01 AI110964-02 PA-11-260 8853810	2015 -	Snap Abs NoA Acctg Hist **eIMG** Docs GF PUB Like Who	DASZAK, PETER			Understanding the Risk of Bat Coronavirus Emergence ECOHEALTH ALLIANCE, INC. (NY)	$630,445 $502,293 2015/06/01
6	1 R01 AI110964-01 PA-11-260 8674931	2014 2014-01	Snap Abs SS NoA Acctg Hist **eIMG** Docs GF PUB Like Who	DASZAK, PETER			Understanding the Risk of Bat Coronavirus Emergence ECOHEALTH ALLIANCE, INC. (NY)	$666,442 $516,857 2014/06/01

From: Lauer, Michael (NIH/OD) [E]
To: Black, Jodi (NIH/OD) [E]
Subject: Re: request for a call...
Date: Thursday, April 16, 2020 8:13:28 AM

Got voice mail – I'm at (b) (6)

From: "Black, Jodi (NIH/OD) [E]" (b) (6)
Date: Thursday, April 16, 2020 at 8:07 AM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Subject: Re: request for a call...

Ok. Should I call you? Or you could call me (b) (6)

Best,
Jodi

Jodi B. Black, PhD, MMSc
Deputy Director
Office of Extramural Research, NIH

From: Mike Lauer (b) (6)
Date: Thursday, April 16, 2020 at 7:57 AM
To: Jodi OER (b) (6)
Cc: Mike Lauer (b) (6)
Subject: FW: request for a call...

Good morning Jodi – we discussed this grant at 0730 meeting. (b) (5)

Happy to talk.

Thanks, Mike

From: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Date: Wednesday, April 15, 2020 at 5:14 PM
To: "Black, Jodi (NIH/OD) [E]" (b) (6), "Bulls, Michelle G. (NIH/OD) [E]" (b) (6)
Cc: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Subject: Re: request for a call...

FYI – some email exchanges from earlier today.

Thanks, Mike

From: "Black, Jodi (NIH/OD) [E]" (b) (6)
Date: Wednesday, April 15, 2020 at 4:07 PM
To: "Bulls, Michelle G. (NIH/OD) [E]" (b) (6)
Cc: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Subject: Re: request for a call...

Ok thanks for working on this with Emily.

Best,
Jodi

Jodi B. Black, PhD, MMSc
Deputy Director
Office of Extramural Research, NIH

From: Michelle Bulls (b) (6)
Date: Wednesday, April 15, 2020 at 3:49 PM
To: Jodi OER (b) (6)
Cc: Mike Lauer (b) (6), Michelle Bulls (b) (6)
Subject: FW: request for a call...

FYI. Urgent.

(b) (5)

(b) (5)

Waiting to hear back from Emily and will set up time to talk to Jodi tomorrow.

Thanks,
Michelle

From: Linde, Emily (NIH/NIAID) [E] (b) (6)
Sent: Wednesday, April 15, 2020 12:03 PM
To: Bulls, Michelle G. (NIH/OD) [E] (b) (6); Ta, Kristin (NIH/OD) [E] (b) (6); Tarwater, Robert (NIH/OD) [E] (b) (6); Dean, Diane

(NIH/OD) [E] (b) (6)

Subject: request for a call...

Hello,

(b) (5)

Can we have a call to discuss (b) (5)

Many thanks,

Emily

Emily Linde

Director, Grants Management Program
NIAID, NIH, DHHS
Telephone Number: (b) (6)
Email Address: (b) (6)

From: Bulls, Michelle G. (NIH/OD) [E]
To: Black, Jodi (NIH/OD) [E]
Cc: Lauer, Michael (NIH/OD) [E]
Subject: RE: request for a call...
Date: Thursday, April 16, 2020 9:04:33 AM

Ok (b) (5)

From: Black, Jodi (NIH/OD) [E] (b) (6)
Sent: Thursday, April 16, 2020 8:44 AM
To: Bulls, Michelle G. (NIH/OD) [E] (b) (6)
Cc: Lauer, Michael (NIH/OD) [E] (b) (6)
Subject: Re: request for a call...

Hi Michelle, (b) (5)

Best,
Jodi

Jodi B. Black, PhD, MMSc
Deputy Director
Office of Extramural Research, NIH

From: Michelle Bulls (b) (6)
Date: Thursday, April 16, 2020 at 8:37 AM
To: Jodi OER (b) (6)
Cc: Mike Lauer (b) (6)
Subject: RE: request for a call...

Happy to help.

From: Black, Jodi (NIH/OD) [E] (b) (6)
Sent: Wednesday, April 15, 2020 4:07 PM
To: Bulls, Michelle G. (NIH/OD) [E] (b) (6)
Cc: Lauer, Michael (NIH/OD) [E] (b) (6)
Subject: Re: request for a call...

Ok thanks for working on this with Emily.

Best,
Jodi

Jodi B. Black, PhD, MMSc

Deputy Director
Office of Extramural Research, NIH

From: Michelle Bulls (b) (6)
Date: Wednesday, April 15, 2020 at 3:49 PM
To: Jodi OER (b) (6)
Cc: Mike Lauer (b) (6), Michelle Bulls (b) (6)
Subject: FW: request for a call...

FYI. Urgent.

(b) (5)

(b) (5)

Waiting to hear back from Emily and will set up time to talk to Jodi tomorrow.

Thanks,
Michelle

From: Linde, Emily (NIH/NIAID) [E] (b) (6)
Sent: Wednesday, April 15, 2020 12:03 PM
To: Bulls, Michelle G. (NIH/OD) [E] (b) (6); Ta, Kristin (NIH/OD) [E] (b) (6); Tarwater, Robert (NIH/OD) [E] (b) (6); Dean, Diane (NIH/OD) [E] (b) (6)
Subject: request for a call...

Hello,

(b) (5)

Can we have a call to (b) (5)

Many thanks,

Emily

Emily Linde

Director, Grants Management Program
NIAID, NIH, DHHS
Telephone Number: (b) (6)
Email Address: (b) (6)

From: Black, Jodi (NIH/OD) [E]
To: Lauer, Michael (NIH/OD) [E]
Subject: Re: URGENT
Date: Monday, April 20, 2020 12:14:55 PM
Attachments: Urgent request re Wuhan lab research .msg
NoA R01AI110964-01[4][1].pdf
Screen Shot 2020-04-20 at 11.09.54 AM[2][3].png
NoA R01AI110964-06[8][2].pdf

HI, I just spoke to Matthew and let him know the eRA was open for soft launch and explained the issues. Emily was probably waiting for the "system to come back up".

He is on it

Best,
Jodi

Jodi B. Black, PhD, MMSc
Deputy Director
Office of Extramural Research, NIH

From: Mike Lauer (b) (6)
Date: Monday, April 20, 2020 at 11:53 AM
To: Jodi OER (b) (6)
Subject: FW: URGENT

Hi Jodi – do you have a few minutes now for a quick phone call?

From: "Black, Jodi (NIH/OD) [E]" (b) (6)
Date: Monday, April 20, 2020 at 11:38 AM
To: "Tabak, Lawrence (NIH/OD) [E]" (b) (6), "Lauer, Michael (NIH/OD) [E]" (b) (6)
Subject: Re: URGENT

(b) (5) .. I'm asking NIAID for the information.

Best,
Jodi

Jodi B. Black, PhD, MMSc
Deputy Director
Office of Extramural Research, NIH

From: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Date: Monday, April 20, 2020 at 11:11 AM
To: Mike Lauer (b) (6)
Cc: Jodi OER (b) (6)
Subject: URGENT

Screen shot from world reporter – (b) (5)

Call with Secretary at 11;45

From: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Date: Monday, April 20, 2020 at 10:50 AM
To: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Cc: "Lauer, Michael (NIH/OD) [E]" (b) (6), "Black, Jodi (NIH/OD) [E]" (b) (6)
Subject: Urgent request re Wuhan lab research

Hi Larry

Other sites in China – see 4th attachment.

(b) (5)

Thanks, Mike

From: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Date: Wednesday, April 15, 2020 at 7:03 AM
To: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Cc: "Schwetz, Tara (NIH/OD) [E]" (b) (6), "Wolinetz, Carrie (NIH/OD) [E]" (b) (6), "Lauer, Michael (NIH/OD) [E]" (b) (6)
Subject: Re: Wuhan lab research

Good morning – see Section IV of the NoAs:

- Type 1: Wuhan gets 134K to 159K per year.
- Type 2: Wuhan gets $76,301.

Thanks, Mike

From: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Date: Tuesday, April 14, 2020 at 10:05 PM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Cc: "Schwetz, Tara (NIH/OD) [E]" (b) (6), "Wolinetz, Carrie (NIH/OD) [E]" (b) (6)
Subject: Re: Wuhan lab research

https://projectreporter.nih.gov/project_info_description.cfm?aid=9819304&icde=49593891&ddparam=&ddvalue=&ddsub=&cr=1&csb=default&cs=ASC&pball=

can we get subproject info – costs to Wuhan?

From: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Date: Tuesday, April 14, 2020 at 10:00 PM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Cc: "Schwetz, Tara (NIH/OD) [E]" (b) (6), "Wolinetz, Carrie (NIH/OD) [E]" (b) (6)
Subject: Re: Wuhan lab research

Is this what they are referring to: https://worldreport.nih.gov/app/#!/

From: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Date: Tuesday, April 14, 2020 at 9:50 PM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Cc: "Schwetz, Tara (NIH/OD) [E]" (b) (6), "Wolinetz, Carrie (NIH/OD) [E]" (b) (6)
Subject: FW: Wuhan lab research

Can I get this information asap please?

From: "Pence, Laura (HHS/ASL)" (b) (6)
Date: Tuesday, April 14, 2020 at 9:47 PM
To: "Tabak, Lawrence (NIH/OD) [E]" (b) (6), "Wolinetz, Carrie (NIH/OD) [E]" (b) (6), "Schwetz, Tara (NIH/OD) [E]" (b) (6)
Subject: Wuhan lab research

Hi! Can we get info on this ASAP? Need for the morning. Sorry for the fire drill.

Begin forwarded message:

From: "Arbes, Sarah (HHS/ASL)" (b) (6)
Date: April 14, 2020 at 9:30:23 PM EDT
To: "Hallett, Adrienne (NIH/OD) [E]" (b) (6), "Pence, Laura (HHS/ASL)" (b) (6)
Cc: "Morse, Sara (HHS/ASL)" (b) (6)
Subject: For AMA in the morning

Adrienne and Laura –

Can you please help me run ground truth to this article?: https://www.soundhealthandlastingwealth.com/health-news/u-s-government-gave-3-7million-grant-to-wuhan-lab-that-experimented-on-coronavirus-source-bats/

Congressman Gaetz is publicly criticizing HHS/NIH for funding the Wuhan laboratory's bat research. Here's this quote from another article: "I'm disgusted to learn that for years the US government has been funding dangerous and cruel animal experiments at the Wuhan Institute, which may have contributed to the global spread of coronavirus, and research at other labs in China that have virtually no oversight from US authorities."

- How long have we been giving research dollars to this lab?
- How much have we given?
- For what purpose?
- If asked to defend our research dollars going to this lab for this purpose, what do you recommend we say?
- Anything else we should know?

Thanks much!
Sarah

From: Lauer, Michael (NIH/OD) [E]
To: Tabak, Lawrence (NIH/OD) [E]
Cc: Lauer, Michael (NIH/OD) [E]; Black, Jodi (NIH/OD) [E]
Subject: Urgent request re Wuhan lab research
Date: Monday, April 20, 2020 10:50:01 AM
Attachments: FACTS Snapshot for 2-R01-AI110964-06 DASZAK, PETER QVR.pdf
NoA R01AI110964-06.pdf
NoA R01AI110964-01.pdf
Screen Shot 2020-04-20 at 10.43.02 AM.png
Screen Shot 2020-04-20 at 10.45.14 AM.png
Importance: High

(b) (5)

(b) (5)

RESEARCH
Department of Health and Human Services
National Institutes of Health

Federal Award Date: 08/05/2019

NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Grant Number: 2R01AI110964-06 REVISED
FAIN: R01AI110964

Principal Investigator(s):
PETER DASZAK, PHD

Project Title: Understanding the Risk of Bat Coronavirus Emergence

Dr. Daszak, Peter
PD/PI
460 West 34th Street
Suite 1701
New York, NY 100012320

Award e-mailed to: (b) (6)

Period Of Performance:
Budget Period: 07/24/2019 – 06/30/2020
Project Period: 06/01/2014 – 06/30/2024

Dear Business Official:

The National Institutes of Health hereby revises this award to reflect a decrease in the amount of $71,770 (see "Award Calculation" in Section I and "Terms and Conditions" in Section III) to ECOHEALTH ALLIANCE, INC. in support of the above referenced project. This award is pursuant to the authority of 42 USC 241 42 CFR 52 and is subject to the requirements of this statute and regulation and of other referenced, incorporated or attached terms and conditions.

Acceptance of this award including the "Terms and Conditions" is acknowledged by the grantee when funds are drawn down or otherwise obtained from the grant payment system.

Each publication, press release, or other document about research supported by an NIH award must include an acknowledgment of NIH award support and a disclaimer such as "Research reported in this publication was supported by the National Institute Of Allergy And Infectious Diseases of the National Institutes of Health under Award Number R01AI110964. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health." Prior to issuing a press release concerning the outcome of this research, please notify the NIH awarding IC in advance to allow for coordination.

Award recipients must promote objectivity in research by establishing standards that provide a reasonable expectation that the design, conduct and reporting of research funded under NIH awards will be free from bias resulting from an Investigator's Financial Conflict of Interest (FCOI), in accordance with the 2011 revised regulation at 42 CFR Part 50 Subpart F. The Institution shall submit all FCOI reports to the NIH through the eRA Commons FCOI Module. The regulation does not apply to Phase I Small Business Innovative Research (SBIR) and Small Business Technology Transfer (STTR) awards. Consult the NIH website http://grants.nih.gov/grants/policy/coi/ for a link to the regulation and additional important information.

If you have any questions about this award, please contact the individual(s) referenced in Section IV.

Sincerely yours,

Tseday G Girma
Grants Management Officer
NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Additional information follows

SECTION I – AWARD DATA – 2R01AI110964-06 REVISED

Award Calculation (U.S. Dollars)

Salaries and Wages	$170,123
Fringe Benefits	$53,590
Personnel Costs (Subtotal)	$223,713
Consultant Services	$49,750
Materials & Supplies	$20,850
Travel	$15,027
Subawards/Consortium/Contractual Costs	$229,651
Federal Direct Costs	$538,991
Federal F&A Costs	$122,989
Approved Budget	$661,980
Total Amount of Federal Funds Obligated (Federal Share)	$661,980
TOTAL FEDERAL AWARD AMOUNT	$661,980
AMOUNT OF THIS ACTION (FEDERAL SHARE)	($-71,770)

SUMMARY TOTALS FOR ALL YEARS		
YR	**THIS AWARD**	**CUMULATIVE TOTALS**
6	$661,980	$661,980
7	$637,980	$637,980
8	$637,980	$637,980
9	$637,980	$637,980
10	$637,980	$637,980

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

Fiscal Information:

CFDA Name:	Allergy and Infectious Diseases Research
CFDA Number:	93.855
EIN:	1311726494A1
Document Number:	RAI110964B
PMS Account Type:	P (Subaccount)
Fiscal Year:	2019

IC	CAN	2019	2020	2021	2022	2023
AI	8472364	$661,980	$637,980	$637,980	$637,980	$637,980

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

NIH Administrative Data:
PCC: M51C B / **OC**: 414B / **Released**: (b) (6) 08/02/2019
Award Processed: 08/05/2019 12:01:51 AM

SECTION II – PAYMENT/HOTLINE INFORMATION – 2R01AI110964-06 REVISED

For payment and HHS Office of Inspector General Hotline information, see the NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm

SECTION III – TERMS AND CONDITIONS – 2R01AI110964-06 REVISED

This award is based on the application submitted to, and as approved by, NIH on the above-titled project and is subject to the terms and conditions incorporated either directly or by reference in the following:

a. The grant program legislation and program regulation cited in this Notice of Award.
b. Conditions on activities and expenditure of funds in other statutory requirements, such as those included in appropriations acts.

c. 45 CFR Part 75.
d. National Policy Requirements and all other requirements described in the NIH Grants Policy Statement, including addenda in effect as of the beginning date of the budget period.
e. Federal Award Performance Goals: As required by the periodic report in the RPPR or in the final progress report when applicable.
f. This award notice, INCLUDING THE TERMS AND CONDITIONS CITED BELOW.

(See NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm for certain references cited above.)

Research and Development (R&D): All awards issued by the National Institutes of Health (NIH) meet the definition of "Research and Development" at 45 CFR Part§ 75.2**.** As such, auditees should identify NIH awards as part of the R&D cluster on the Schedule of Expenditures of Federal Awards (SEFA). The auditor should test NIH awards for compliance as instructed in Part V, Clusters of Programs. NIH recognizes that some awards may have another classification for purposes of indirect costs. The auditor is not required to report the disconnect (i.e., the award is classified as R&D for Federal Audit Requirement purposes but non-research for indirect cost rate purposes), unless the auditee is charging indirect costs at a rate other than the rate(s) specified in the award document(s).

An unobligated balance may be carried over into the next budget period without Grants Management Officer prior approval.

This grant is subject to Streamlined Noncompeting Award Procedures (SNAP).

This award is subject to the requirements of 2 CFR Part 25 for institutions to receive a Dun & Bradstreet Universal Numbering System (DUNS) number and maintain an active registration in the System for Award Management (SAM). Should a consortium/subaward be issued under this award, a DUNS requirement must be included. See http://grants.nih.gov/grants/policy/awardconditions.htm for the full NIH award term implementing this requirement and other additional information.

This award has been assigned the Federal Award Identification Number (FAIN) R01AI110964. Recipients must document the assigned FAIN on each consortium/subaward issued under this award.

Based on the project period start date of this project, this award is likely subject to the Transparency Act subaward and executive compensation reporting requirement of 2 CFR Part 170. There are conditions that may exclude this award; see http://grants.nih.gov/grants/policy/awardconditions.htm for additional award applicability information.

In accordance with P.L. 110-161, compliance with the NIH Public Access Policy is now mandatory. For more information, see NOT-OD-08-033 and the Public Access website: http://publicaccess.nih.gov/.

In accordance with the regulatory requirements provided at 45 CFR 75.113 and Appendix XII to 45 CFR Part 75, recipients that have currently active Federal grants, cooperative agreements, and procurement contracts with cumulative total value greater than $10,000,000 must report and maintain information in the System for Award Management (SAM) about civil, criminal, and administrative proceedings in connection with the award or performance of a Federal award that reached final disposition within the most recent five-year period. The recipient must also make semiannual disclosures regarding such proceedings. Proceedings information will be made publicly available in the designated integrity and performance system (currently the Federal Awardee Performance and Integrity Information System (FAPIIS)). Full reporting requirements and procedures are found in Appendix XII to 45 CFR Part 75. This term does not apply to NIH fellowships.

Treatment of Program Income:
Additional Costs

SECTION IV – AI Special Terms and Conditions – 2R01AI110964-06 REVISED

Clinical Trial Indicator: No
This award does not support any NIH-defined Clinical Trials. See the NIH Grants Policy Statement Section 1.2 for NIH definition of Clinical Trial.

REVISED AWARD: This award is revised to adjust the budget in accordance with the letter from Aleksei Chmura/ECOHealth Alliance.

Supersedes previous Notice of Award dated **07/24/2019**.

****
This Notice of Award (NoA) includes funds for activity with **The University of North Carolina at Chapel Hill** in the amount of **$77,750** (**$50,000** direct costs + **$27,750**F&A costs).

This Notice of Award (NoA) includes funds for activity with **Wuhan Institute of Virology** in the amount of **$76,301** (**$70,649** direct costs + **$5,652** F&A costs).

This Notice of Award (NoA) includes funds for activity with **Institute of Pathogen Biology** in the amount of **$75,600** (**$70,000** direct costs + **$5,600** F&A costs).

****
The Research Performance Progress Report (RPPR), Section G.9 (Foreign component), includes reporting requirements for all research performed outside of the United States. Research conducted at the following site(s) must be reported in your RPPR:

Wuhan Institute of Virology, CHINA

Institute of Pathogen Biology, CHINA

East China Normal University, CHINA

Duke-NUS Medical School, SINGAPORE

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This award reflects current Federal policies regarding Facilities & Administrative (F&A) Costs for foreign grantees including foreign sub-awardees, and domestic awards with foreign sub-awardees. Please see: Chapter 16 Grants to Foreign Organizations, International Organizations, and Domestic Grants with Foreign Components, Section 16.6 “Allowable and Unallowable Cost” of the NIH Grants Policy.

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This award may include collaborations with and/or between foreign organizations. Please be advised that short term travel visa expenses are an allowable expense on this grant, if justified as critical and necessary for the conduct of the project.

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The budget period anniversary start date for future year(s) will be **July** 1.

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Dissemination of study data will be in accord with the Recipient’s accepted genomic data sharing plan as stated in the page(s) **203** of the application. Failure to adhere to the sharing plan as mutually agreed upon by the Recipient and the NIAID may result in Enforcement Actions as described in the NIH Grants Policy Statement.

****
This award is subject to the Clinical Terms of Award referenced in the NIH Guide for Grants and Contracts, July 8, 2002, NOT AI-02-032. These terms and conditions are hereby incorporated by

reference, and can be accessed via the following World Wide Web address: https://www.niaid.nih.gov/grants-contracts/niaid-clinical-terms-award All submissions required by the NIAID Clinical Terms of Award must be forwarded electronically or by mail to the responsible NIAID Program Official identified on this Notice of Award.

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Awardees who conduct research involving Select Agents (see 42 CFR 73 for the Select Agent list; and 7 CFR 331 and 9 CFR 121 for the relevant animal and plant pathogens at http://www.selectagents.gov/Regulations.html) must complete registration with CDC (or APHIS, depending on the agent) before using NIH funds. No funds can be used for research involving Select Agents if the final registration certificate is denied.

Prior to conducting a restricted experiment with a Select Agent or Toxin, awardees must notify the NIAID and must request and receive approval from CDC or APHIS.

****

Select Agents:
Awardee of a project that at any time involves a restricted experiment with a select agent, is responsible for notifying and receiving prior approval from the NIAID. Please be advised that changes in the use of a Select Agent will be considered a change in scope and require NIH awarding office prior approval. The approval is necessary for new select agent experiments as well as changes in on-going experiments that would require change in the biosafety plan and/or biosafety containment level. An approval to conduct a restricted experiment granted to an individual cannot be assumed an approval to other individuals who conduct the same restricted experiment as defined in the Select Agents Regulation 42 CFR Part 73, Section 13.b (http://www.selectagents.gov/Regulations.html).

Highly Pathogenic Agent:
NIAID defines a Highly Pathogenic Agent as an infectious Agent or Toxin that may warrant a biocontainment safety level of BSL3 or higher according to the current edition of the CDC/NIH Biosafety in Microbiological and Biomedical Laboratories (BMBL) (http://www.cdc.gov/OD/ohs/biosfty/bmbl5/bmbl5toc.htm). Research funded under this grant must adhere to the BMBL, including using the BMBL-recommended biocontainment level at a minimum. If your Institutional Biosafety Committee (or equivalent body) or designated institutional biosafety official recommend a higher biocontainment level, the highest recommended containment level must be used.
When submitting future Progress Reports indicate at the beginning of the report:

If no research with a Highly Pathogenic Agent or Select Agent has been performed or is planned to be performed under this grant.

If your IBC or equivalent body or official has determined, for example, by conducting a risk assessment, that the work being planned or performed under this grant may be conducted at a biocontainment safety level that is lower than BSL3.

If the work involves Select Agents and/or Highly Pathogenic Agents, also address the following points:

Any changes in the use of the Agent(s) or Toxin(s) including its restricted experiments that have resulted in a change in the required biocontainment level, and any resultant change in location, if applicable, as determined by your IBC or equivalent body or official.

If work with a new or additional Agent(s)/Toxin(s) is proposed in the upcoming project period, provide:

- A list of the new and/or additional Agent(s) that will be studied;
- A description of the work that will be done with the Agent(s), and whether or not the work is a restricted experiment;
- The title and location for each biocontainment resource/facility, including the name of the organization that operates the facility, and the biocontainment level at which the work will be conducted, with documentation of approval by your IBC or equivalent body or official. It is important to note if the work is being done in a new location.

STAFF CONTACTS

The Grants Management Specialist is responsible for the negotiation, award and administration of this project and for interpretation of Grants Administration policies and provisions. The Program Official is responsible for the scientific, programmatic and technical aspects of this project. These individuals work together in overall project administration. Prior approval requests (signed by an Authorized Organizational Representative) should be submitted in writing to the Grants Management Specialist. Requests may be made via e-mail.

Grants Management Specialist: Tseday G Girma
Email: (b) (6) **Phone**: (b) (6) **Fax**: 301-493-0597

Program Official: Erik J. Stemmy
Email: (b) (6) **Phone**: (b) (6)

SPREADSHEET SUMMARY
GRANT NUMBER: 2R01AI110964-06 REVISED

INSTITUTION: ECOHEALTH ALLIANCE, INC.

Budget	Year 6	Year 7	Year 8	Year 9	Year 10
Salaries and Wages	$170,123	$170,123	$170,123	$170,123	$170,123
Fringe Benefits	$53,590	$53,590	$53,590	$53,590	$53,590
Personnel Costs (Subtotal)	$223,713	$223,713	$223,713	$223,713	$223,713
Consultant Services	$49,750	$49,750	$49,750	$49,750	$49,750
Materials & Supplies	$20,850	$14,850	$14,850	$14,850	$14,850
Travel	$15,027	$15,027	$15,027	$15,027	$15,027
Subawards/Consortium/Contractual Costs	$229,651	$229,651	$229,651	$229,651	$229,651
Publication Costs		$6,000	$6,000	$6,000	$6,000
TOTAL FEDERAL DC	$538,991	$538,991	$538,991	$538,991	$538,991
TOTAL FEDERAL F&A	$122,989	$98,989	$98,989	$98,989	$98,989
TOTAL COST	$661,980	$637,980	$637,980	$637,980	$637,980

Facilities and Administrative Costs	Year 6	Year 7	Year 8	Year 9	Year 10
F&A Cost Rate 1	32%	32%	32%	32%	32%
F&A Cost Base 1	$384,340	$309,340	$309,340	$309,340	$309,340
F&A Costs 1	$122,989	$98,989	$98,989	$98,989	$98,989

Notice of Award

RESEARCH **Issue Date:** 05/27/2014

Department of Health and Human Services
National Institutes of Health
NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Grant Number: 1R01AI110964-01
FAIN: R01AI110964

Principal Investigator(s):
PETER DASZAK, PHD

Project Title: Understanding the Risk of Bat Coronavirus Emergence

Aleksei
President
460 West 34th Street
17th Floor
New York, NY 100012317

Award e-mailed to: (b) (6)

Budget Period: 06/01/2014 – 05/31/2015
Project Period: 06/01/2014 – 05/31/2019

Dear Business Official:

The National Institutes of Health hereby awards a grant in the amount of $666,442 (see "Award Calculation" in Section I and "Terms and Conditions" in Section III) to ECOHEALTH ALLIANCE, INC. in support of the above referenced project. This award is pursuant to the authority of 42 USC 241 42 CFR 52 and is subject to the requirements of this statute and regulation and of other referenced, incorporated or attached terms and conditions.

Acceptance of this award including the "Terms and Conditions" is acknowledged by the grantee when funds are drawn down or otherwise obtained from the grant payment system.

Each publication, press release, or other document about research supported by an NIH award must include an acknowledgment of NIH award support and a disclaimer such as "Research reported in this publication was supported by the National Institute Of Allergy And Infectious Diseases of the National Institutes of Health under Award Number R01AI110964. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health." Prior to issuing a press release concerning the outcome of this research, please notify the NIH awarding IC in advance to allow for coordination.

Award recipients must promote objectivity in research by establishing standards that provide a reasonable expectation that the design, conduct and reporting of research funded under NIH awards will be free from bias resulting from an Investigator's Financial Conflict of Interest (FCOI), in accordance with the 2011 revised regulation at 42 CFR Part 50 Subpart F. The Institution shall submit all FCOI reports to the NIH through the eRA Commons FCOI Module. The regulation does not apply to Phase I Small Business Innovative Research (SBIR) and Small Business Technology Transfer (STTR) awards. Consult the NIH website http://grants.nih.gov/grants/policy/coi/ for a link to the regulation and additional important information.

If you have any questions about this award, please contact the individual(s) referenced in Section IV.

Sincerely yours,

Laura A. Pone
Grants Management Officer
NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Additional information follows

SECTION I – AWARD DATA – 1R01AI110964-01

Award Calculation (U.S. Dollars)

Salaries and Wages	$167,708
Fringe Benefits	$54,168
Supplies	$21,400
Travel Costs	$35,918
Other Costs	$10,000
Consortium/Contractual Cost	$227,663
Federal Direct Costs	$516,857
Federal F&A Costs	$149,585
Approved Budget	$666,442
Federal Share	$666,442
TOTAL FEDERAL AWARD AMOUNT	$666,442
AMOUNT OF THIS ACTION (FEDERAL SHARE)	$666,442

SUMMARY TOTALS FOR ALL YEARS		
YR	**THIS AWARD**	**CUMULATIVE TOTALS**
1	$666,442	$666,442
2	$630,445	$630,445
3	$611,090	$611,090
4	$597,112	$597,112
5	$581,646	$581,646

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

Fiscal Information:

CFDA Number:	93.855
EIN:	1311726494A1
Document Number:	RAI110964A
PMS Account Type:	P (Subaccount)
Fiscal Year:	2014

IC	CAN	2014	2015	2016	2017	2018
AI	8472350	$666,442	$630,445	$611,090	$597,112	$581,646

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

NIH Administrative Data:
PCC: M51C / **OC**: 414A / **Released**: (b) (6) 05/20/2014
Award Processed: 05/08/2014 01:52:21 PM

SECTION II – PAYMENT/HOTLINE INFORMATION – 1R01AI110964-01

For payment and HHS Office of Inspector General Hotline information, see the NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm

SECTION III – TERMS AND CONDITIONS – 1R01AI110964-01

This award is based on the application submitted to, and as approved by, NIH on the above-titled project and is subject to the terms and conditions incorporated either directly or by reference in the following:

a. The grant program legislation and program regulation cited in this Notice of Award.

b. Conditions on activities and expenditure of funds in other statutory requirements, such as those included in appropriations acts.
c. 45 CFR Part 74 or 45 CFR Part 92 as applicable.
d. The NIH Grants Policy Statement, including addenda in effect as of the beginning date of the budget period.
e. This award notice, INCLUDING THE TERMS AND CONDITIONS CITED BELOW.

(See NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm for certain references cited above.)

An unobligated balance may be carried over into the next budget period without Grants Management Officer prior approval.

This grant is subject to Streamlined Noncompeting Award Procedures (SNAP).

This award is subject to the requirements of 2 CFR Part 25 for institutions to receive a Dun & Bradstreet Universal Numbering System (DUNS) number and maintain an active registration in the Central Contractor Registration. Should a consortium/subaward be issued under this award, a DUNS requirement must be included. See http://grants.nih.gov/grants/policy/awardconditions.htm for the full NIH award term implementing this requirement and other additional information.

This award has been assigned the Federal Award Identification Number (FAIN) R01AI110964. Recipients must document the assigned FAIN on each consortium/subaward issued under this award.

Based on the project period start date of this project, this award is likely subject to the Transparency Act subaward and executive compensation reporting requirement of 2 CFR Part 170. There are conditions that may exclude this award; see http://grants.nih.gov/grants/policy/awardconditions.htm for additional award applicability information.

In accordance with P.L. 110-161, compliance with the NIH Public Access Policy is now mandatory. For more information, see NOT-OD-08-033 and the Public Access website: http://publicaccess.nih.gov/.

Treatment of Program Income:
Additional Costs

SECTION IV – AI Special Terms and Conditions – 1R01AI110964-01

THIS AWARD CONTAINS GRANT SPECIFIC RESTRICTIONS. THESE RESTRICTIONS MAY ONLY BE LIFTED BY A REVISED NOTICE OF AWARD.

RESTRICTION: This award is issued with the knowledge that subjects may be involved within the period of support, but definite plans were not set forth in the application as per 45 CFR 46.118. No human subjects may be involved in any project supported by this award until all requirements for Human Subjects research as identified in the PHS398/SF424 Instructions have been provided to and approved by NIH.

RESTRICTION: The present award is being made without a currently valid certification of IRB approval for this project with the following restriction: Only activities that are clearly severable and independent from activities that involve human subjects may be conducted pending the NIAID's acceptance of the certification of IRB review and approval.

No funds may be drawn down from the payment system and no obligations may be made against Federal funds for any research involving human subjects prior to the NIAID's notification to the grantee that the identified issues have been resolved and this restriction removed.

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This award includes funds for subcontract/consortium activity with Wuhan Institute of Virology, CHINA and is budgeted as follows:

	-Yr 1	-Yr 2	-Yr 3	-Yr 4	-Yr 5
Total Direct Costs	$123,699	$128,718	$147,335	$147,335	$147,335
F&A Costs @ 8%(MTDC)	$9,896	$10,297	$11,787	$11,787	$11,787
TOTAL COSTS	$133,595	$139,015	$159,122	$159,122	$159,122

Consortiums are to be established and administered as described in the NIH Grants Policy Statement. This written agreement with the consortium must address the negotiated arrangements for meeting the scientific, administrative, financial, and reporting requirements for this grant.
~~~~~~~~~
This award includes funds for subcontract/consortium activity with East China Normal University, CHINA and is budgeted as follows:

	-Yr 1	-Yr 2	-Yr 3	-Yr 4	-Yr 5
Total Direct Costs	$87,100	$67,300	$50,108	$39,167	$14,850
F&A Costs @ 8%(MTDC)	$6,968	$5,384	$4,009	$3,133	$2,404
TOTAL COSTS	$94,068	$72,684	$54,117	$42,300	$32,454

Consortiums are to be established and administered as described in the NIH Grants Policy Statement. This written agreement with the consortium must address the negotiated arrangements for meeting the scientific, administrative, financial, and reporting requirements for this grant.
~~~~~~~~~
Select Agents:
Awardee of a project that at any time involves a restricted experiment with a select agent, is responsible for notifying and receiving prior approval from the NIAID. Please be advised that changes in the use of a Select Agent will be considered a change in scope and require NIH awarding office prior approval. The approval is necessary for new select agent experiments as well as changes in on-going experiments that would require change in the biosafety plan and/or biosafety containment level. An approval to conduct a restricted experiment granted to an individual cannot be assumed an approval to other individuals who conduct the same restricted experiment as defined in the Select Agents Regulation 42 CFR Part 73, Section 13.b (http://www.selectagents.gov/Regulations.html).

Highly Pathogenic Agent:
NIAID defines a Highly Pathogenic Agent as an infectious Agent or Toxin that may warrant a biocontainment safety level of BSL3 or higher according to the current edition of the CDC/NIH Biosafety in Microbiological and Biomedical Laboratories (BMBL) (http://www.cdc.gov/OD/ohs/biosfty/bmbl5/bmbl5toc.htm). Research funded under this grant must adhere to the BMBL, including using the BMBL-recommended biocontainment level at a minimum. If your Institutional Biosafety Committee (or equivalent body) or designated institutional biosafety official recommend a higher biocontainment level, the highest recommended containment level must be used.
When submitting future Progress Reports indicate at the beginning of the report:

If no research with a Highly Pathogenic Agent or Select Agent has been performed or is planned to be performed under this grant.

If your IBC or equivalent body or official has determined, for example, by conducting a risk assessment, that the work being planned or performed under this grant may be conducted at a biocontainment safety level that is lower than BSL3.

If the work involves Select Agents and/or Highly Pathogenic Agents, also address the following points:

Any changes in the use of the Agent(s) or Toxin(s) including its restricted experiments that have resulted in a change in the required biocontainment level, and any resultant change in location, if applicable, as determined by your IBC or equivalent body or official.
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If work with a new or additional Agent(s)/Toxin(s) is proposed in the upcoming project period, provide:

o A list of the new and/or additional Agent(s) that will be studied;
o A description of the work that will be done with the Agent(s), and whether or not the work is a restricted experiment;
o The title and location for each biocontainment resource/facility, including the name of the organization that operates the facility, and the biocontainment level at which the work will be conducted, with documentation of approval by your IBC or equivalent body or official. It is important to note if the work is being done in a new location.

STAFF CONTACTS

The Grants Management Specialist is responsible for the negotiation, award and administration of this project and for interpretation of Grants Administration policies and provisions. The Program Official is responsible for the scientific, programmatic and technical aspects of this project. These individuals work together in overall project administration. Prior approval requests (signed by an Authorized Organizational Representative) should be submitted in writing to the Grants Management Specialist. Requests may be made via e-mail.

Grants Management Specialist: Laura A. Pone
Email: (b) (6) **Phone**: (b) (6) **Fax**: 301-493-0597

Program Official: Erik J. Stemmy
Email: (b) (6) **Phone**: (b) (6)

SPREADSHEET SUMMARY
GRANT NUMBER: 1R01AI110964-01

INSTITUTION: ECOHEALTH ALLIANCE, INC.

Budget	Year 1	Year 2	Year 3	Year 4	Year 5
Salaries and Wages	$167,708	$167,708	$167,708	$167,708	$167,708
Fringe Benefits	$54,168	$54,168	$54,168	$54,168	$54,168
Supplies	$21,400	$19,250	$7,250	$7,000	$3,500
Travel Costs	$35,918	$35,918	$35,918	$35,918	$35,918
Other Costs	$10,000	$13,550	$11,050	$9,800	$9,400
Consortium/Contractual Cost	$227,663	$211,699	$213,239	$201,422	$191,576
TOTAL FEDERAL DC	$516,857	$502,293	$489,333	$476,016	$462,270
TOTAL FEDERAL F&A	$149,585	$128,152	$121,757	$121,096	$119,376
TOTAL COST	$666,442	$630,445	$611,090	$597,112	$581,646

Facilities and Administrative Costs	Year 1	Year 2	Year 3	Year 4	Year 5
F&A Cost Rate 1	44.1%	44.1%	44.1%	44.1%	44.1%
F&A Cost Base 1	$339,194	$290,594	$276,094	$274,594	$270,694
F&A Costs 1	$149,585	$128,152	$121,757	$121,096	$119,376

Collaborator/Site (Site ID: 262256)	Site Flags	Budget Period	Budget Amt	Verified By	Verified Date
ZHU, GUANGJIAN EAST CHINA NORMAL UNIVERSITY School of Life Science, B327 Science building, 3663 Zhongshan Beilu Shanghai 200062	Animals: Y FWA: Humans: N				

Collaborator/Site (Site ID: 262253)	Site Flags	Budget Period	Budget Amt	Verified By	Verified Date
GUO, LI INSTITUTE OF PATHOGEN BIOLOGY Dong Dan San Tiao, No. 9 Dongcheng District Beijing 100730	Animals: N FWA: Y Humans: Y				

Collaborator/Site (Site ID: 262252)	Site Flags	Budget Period	Budget Amt	Verified By	Verified Date
REN, LILI INSTITUTE OF PATHOGEN BIOLOGY Dong Dan San Tiao, No. 9 Dongcheng District Beijing 100730	Animals: N FWA: Y Humans: Y				

~~~~~~~~~

This award includes funds for subcontract/consortium activity with East China Normal University, CHINA and is budgeted as follows:

	-Yr 1	-Yr 2	-Yr 3	-Yr 4	-Yr 5
Total Direct Costs	$87,100	$67,300	$50,108	$39,167	$14,850
F&A Costs @ 8%(MTDC)	$6,968	$5,384	$4,009	$3,133	$2,404
TOTAL COSTS	$94,068	$72,684	$54,117	$42,300	$32,454
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Notice of Award

RESEARCH **Issue Date:** 05/27/2014

Department of Health and Human Services
National Institutes of Health
NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Grant Number: 1R01AI110964-01
FAIN: R01AI110964

Principal Investigator(s):
PETER DASZAK, PHD

Project Title: Understanding the Risk of Bat Coronavirus Emergence

Aleksei
President
460 West 34th Street
17th Floor
New York, NY 100012317

Award e-mailed to: (b) (6)

Budget Period: 06/01/2014 – 05/31/2015
Project Period: 06/01/2014 – 05/31/2019

Dear Business Official:

The National Institutes of Health hereby awards a grant in the amount of $666,442 (see "Award Calculation" in Section I and "Terms and Conditions" in Section III) to ECOHEALTH ALLIANCE, INC. in support of the above referenced project. This award is pursuant to the authority of 42 USC 241 42 CFR 52 and is subject to the requirements of this statute and regulation and of other referenced, incorporated or attached terms and conditions.

Acceptance of this award including the "Terms and Conditions" is acknowledged by the grantee when funds are drawn down or otherwise obtained from the grant payment system.

Each publication, press release, or other document about research supported by an NIH award must include an acknowledgment of NIH award support and a disclaimer such as "Research reported in this publication was supported by the National Institute Of Allergy And Infectious Diseases of the National Institutes of Health under Award Number R01AI110964. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health." Prior to issuing a press release concerning the outcome of this research, please notify the NIH awarding IC in advance to allow for coordination.

Award recipients must promote objectivity in research by establishing standards that provide a reasonable expectation that the design, conduct and reporting of research funded under NIH awards will be free from bias resulting from an Investigator's Financial Conflict of Interest (FCOI), in accordance with the 2011 revised regulation at 42 CFR Part 50 Subpart F. The Institution shall submit all FCOI reports to the NIH through the eRA Commons FCOI Module. The regulation does not apply to Phase I Small Business Innovative Research (SBIR) and Small Business Technology Transfer (STTR) awards. Consult the NIH website http://grants.nih.gov/grants/policy/coi/ for a link to the regulation and additional important information.

If you have any questions about this award, please contact the individual(s) referenced in Section IV.

Sincerely yours,

Laura A. Pone
Grants Management Officer
NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Additional information follows

SECTION I – AWARD DATA – 1R01AI110964-01

Award Calculation (U.S. Dollars)

Salaries and Wages	$167,708
Fringe Benefits	$54,168
Supplies	$21,400
Travel Costs	$35,918
Other Costs	$10,000
Consortium/Contractual Cost	$227,663
Federal Direct Costs	$516,857
Federal F&A Costs	$149,585
Approved Budget	$666,442
Federal Share	$666,442
TOTAL FEDERAL AWARD AMOUNT	$666,442
AMOUNT OF THIS ACTION (FEDERAL SHARE)	$666,442

SUMMARY TOTALS FOR ALL YEARS		
YR	**THIS AWARD**	**CUMULATIVE TOTALS**
1	$666,442	$666,442
2	$630,445	$630,445
3	$611,090	$611,090
4	$597,112	$597,112
5	$581,646	$581,646

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

Fiscal Information:

CFDA Number:	93.855
EIN:	1311726494A1
Document Number:	RAI110964A
PMS Account Type:	P (Subaccount)
Fiscal Year:	2014

IC	CAN	2014	2015	2016	2017	2018
AI	8472350	$666,442	$630,445	$611,090	$597,112	$581,646

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

NIH Administrative Data:
PCC: M51C / **OC**: 414A / **Released**: (b) (6) 05/20/2014
Award Processed: 05/08/2014 01:52:21 PM

SECTION II – PAYMENT/HOTLINE INFORMATION – 1R01AI110964-01

For payment and HHS Office of Inspector General Hotline information, see the NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm

SECTION III – TERMS AND CONDITIONS – 1R01AI110964-01

This award is based on the application submitted to, and as approved by, NIH on the above-titled project and is subject to the terms and conditions incorporated either directly or by reference in the following:

a. The grant program legislation and program regulation cited in this Notice of Award.

b. Conditions on activities and expenditure of funds in other statutory requirements, such as those included in appropriations acts.
c. 45 CFR Part 74 or 45 CFR Part 92 as applicable.
d. The NIH Grants Policy Statement, including addenda in effect as of the beginning date of the budget period.
e. This award notice, INCLUDING THE TERMS AND CONDITIONS CITED BELOW.

(See NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm for certain references cited above.)

An unobligated balance may be carried over into the next budget period without Grants Management Officer prior approval.

This grant is subject to Streamlined Noncompeting Award Procedures (SNAP).

This award is subject to the requirements of 2 CFR Part 25 for institutions to receive a Dun & Bradstreet Universal Numbering System (DUNS) number and maintain an active registration in the Central Contractor Registration. Should a consortium/subaward be issued under this award, a DUNS requirement must be included. See http://grants.nih.gov/grants/policy/awardconditions.htm for the full NIH award term implementing this requirement and other additional information.

This award has been assigned the Federal Award Identification Number (FAIN) R01AI110964. Recipients must document the assigned FAIN on each consortium/subaward issued under this award.

Based on the project period start date of this project, this award is likely subject to the Transparency Act subaward and executive compensation reporting requirement of 2 CFR Part 170. There are conditions that may exclude this award; see http://grants.nih.gov/grants/policy/awardconditions.htm for additional award applicability information.

In accordance with P.L. 110-161, compliance with the NIH Public Access Policy is now mandatory. For more information, see NOT-OD-08-033 and the Public Access website: http://publicaccess.nih.gov/.

Treatment of Program Income:
Additional Costs

SECTION IV – AI Special Terms and Conditions – 1R01AI110964-01

THIS AWARD CONTAINS GRANT SPECIFIC RESTRICTIONS. THESE RESTRICTIONS MAY ONLY BE LIFTED BY A REVISED NOTICE OF AWARD.

RESTRICTION: This award is issued with the knowledge that subjects may be involved within the period of support, but definite plans were not set forth in the application as per 45 CFR 46.118. No human subjects may be involved in any project supported by this award until all requirements for Human Subjects research as identified in the PHS398/SF424 Instructions have been provided to and approved by NIH.

RESTRICTION: The present award is being made without a currently valid certification of IRB approval for this project with the following restriction: Only activities that are clearly severable and independent from activities that involve human subjects may be conducted pending the NIAID's acceptance of the certification of IRB review and approval.

No funds may be drawn down from the payment system and no obligations may be made against Federal funds for any research involving human subjects prior to the NIAID's notification to the grantee that the identified issues have been resolved and this restriction removed.

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This award includes funds for subcontract/consortium activity with Wuhan Institute of Virology, CHINA and is budgeted as follows:

	-Yr 1	-Yr 2	-Yr 3	-Yr 4	-Yr 5
Total Direct Costs	$123,699	$128,718	$147,335	$147,335	$147,335
F&A Costs @ 8%(MTDC)	$9,896	$10,297	$11,787	$11,787	$11,787
TOTAL COSTS	$133,595	$139,015	$159,122	$159,122	$159,122

Consortiums are to be established and administered as described in the NIH Grants Policy Statement. This written agreement with the consortium must address the negotiated arrangements for meeting the scientific, administrative, financial, and reporting requirements for this grant.
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This award includes funds for subcontract/consortium activity with East China Normal University, CHINA and is budgeted as follows:

	-Yr 1	-Yr 2	-Yr 3	-Yr 4	-Yr 5
Total Direct Costs	$87,100	$67,300	$50,108	$39,167	$14,850
F&A Costs @ 8%(MTDC)	$6,968	$5,384	$4,009	$3,133	$2,404
TOTAL COSTS	$94,068	$72,684	$54,117	$42,300	$32,454

Consortiums are to be established and administered as described in the NIH Grants Policy Statement. This written agreement with the consortium must address the negotiated arrangements for meeting the scientific, administrative, financial, and reporting requirements for this grant.
~~~~~~~~~
Select Agents:
Awardee of a project that at any time involves a restricted experiment with a select agent, is responsible for notifying and receiving prior approval from the NIAID. Please be advised that changes in the use of a Select Agent will be considered a change in scope and require NIH awarding office prior approval. The approval is necessary for new select agent experiments as well as changes in on-going experiments that would require change in the biosafety plan and/or biosafety containment level. An approval to conduct a restricted experiment granted to an individual cannot be assumed an approval to other individuals who conduct the same restricted experiment as defined in the Select Agents Regulation 42 CFR Part 73, Section 13.b (http://www.selectagents.gov/Regulations.html).

Highly Pathogenic Agent:
NIAID defines a Highly Pathogenic Agent as an infectious Agent or Toxin that may warrant a biocontainment safety level of BSL3 or higher according to the current edition of the CDC/NIH Biosafety in Microbiological and Biomedical Laboratories (BMBL) (http://www.cdc.gov/OD/ohs/biosfty/bmbl5/bmbl5toc.htm). Research funded under this grant must adhere to the BMBL, including using the BMBL-recommended biocontainment level at a minimum. If your Institutional Biosafety Committee (or equivalent body) or designated institutional biosafety official recommend a higher biocontainment level, the highest recommended containment level must be used.
When submitting future Progress Reports indicate at the beginning of the report:

If no research with a Highly Pathogenic Agent or Select Agent has been performed or is planned to be performed under this grant.

If your IBC or equivalent body or official has determined, for example, by conducting a risk assessment, that the work being planned or performed under this grant may be conducted at a biocontainment safety level that is lower than BSL3.

If the work involves Select Agents and/or Highly Pathogenic Agents, also address the following points:

Any changes in the use of the Agent(s) or Toxin(s) including its restricted experiments that have resulted in a change in the required biocontainment level, and any resultant change in location, if applicable, as determined by your IBC or equivalent body or official.
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If work with a new or additional Agent(s)/Toxin(s) is proposed in the upcoming project period, provide:

o A list of the new and/or additional Agent(s) that will be studied;
o A description of the work that will be done with the Agent(s), and whether or not the work is a restricted experiment;
o The title and location for each biocontainment resource/facility, including the name of the organization that operates the facility, and the biocontainment level at which the work will be conducted, with documentation of approval by your IBC or equivalent body or official. It is important to note if the work is being done in a new location.

STAFF CONTACTS

The Grants Management Specialist is responsible for the negotiation, award and administration of this project and for interpretation of Grants Administration policies and provisions. The Program Official is responsible for the scientific, programmatic and technical aspects of this project. These individuals work together in overall project administration. Prior approval requests (signed by an Authorized Organizational Representative) should be submitted in writing to the Grants Management Specialist. Requests may be made via e-mail.

Grants Management Specialist: Laura A. Pone
Email: (b) (6) **Phone**: (b) (6) **Fax**: 301-493-0597

Program Official: Erik J. Stemmy
Email: (b) (6) **Phone**: (b) (6)

SPREADSHEET SUMMARY
GRANT NUMBER: 1R01AI110964-01

INSTITUTION: ECOHEALTH ALLIANCE, INC.

Budget	Year 1	Year 2	Year 3	Year 4	Year 5
Salaries and Wages	$167,708	$167,708	$167,708	$167,708	$167,708
Fringe Benefits	$54,168	$54,168	$54,168	$54,168	$54,168
Supplies	$21,400	$19,250	$7,250	$7,000	$3,500
Travel Costs	$35,918	$35,918	$35,918	$35,918	$35,918
Other Costs	$10,000	$13,550	$11,050	$9,800	$9,400
Consortium/Contractual Cost	$227,663	$211,699	$213,239	$201,422	$191,576
TOTAL FEDERAL DC	$516,857	$502,293	$489,333	$476,016	$462,270
TOTAL FEDERAL F&A	$149,585	$128,152	$121,757	$121,096	$119,376
TOTAL COST	$666,442	$630,445	$611,090	$597,112	$581,646

Facilities and Administrative Costs	Year 1	Year 2	Year 3	Year 4	Year 5
F&A Cost Rate 1	44.1%	44.1%	44.1%	44.1%	44.1%
F&A Cost Base 1	$339,194	$290,594	$276,094	$274,594	$270,694
F&A Costs 1	$149,585	$128,152	$121,757	$121,096	$119,376

NIH	GUANGDONG ENTOMOLOGICAL INSTITUTE	Understanding the Risk of Bat Coronavirus Emergence	ZHU, GUANJIN	CHINA	GUANGZHOU
NIH	CENTER FOR DISEASE CONTROL AND PREVENTION OF GUANGDONG	Understanding the Risk of Bat Coronavirus Emergence	KE, CHANGWEN	CHINA	Guangzhou
NIH	YUNNAN INSTITUTE OF ENDEMIC DISEASES CONTROL AND PREVENTION	Understanding the Risk of Bat Coronavirus Emergence	ZHANG, YUN-ZHI	CHINA	Dali
NIH	WUHAN INSTITUTE OF VIROLOGY, CHINESE ACADEMY OF SCIENCES	Understanding the Risk of Bat Coronavirus Emergence	SHI, ZHENGLI	CHINA	WUHAN
NIH	SCHOOL OF PUBLIC HEALTH, WUHAN UNIVERSITY	Understanding the Risk of Bat Coronavirus Emergence	LI, SHIYUE	CHINA	Wuhan

RESEARCH
Department of Health and Human Services
National Institutes of Health

Federal Award Date: 08/05/2019

NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Grant Number: 2R01AI110964-06 REVISED
FAIN: R01AI110964

Principal Investigator(s):
PETER DASZAK, PHD

Project Title: Understanding the Risk of Bat Coronavirus Emergence

Dr. Daszak, Peter
PD/PI
460 West 34th Street
Suite 1701
New York, NY 100012320

Award e-mailed to: (b) (6)

Period Of Performance:
Budget Period: 07/24/2019 – 06/30/2020
Project Period: 06/01/2014 – 06/30/2024

Dear Business Official:

The National Institutes of Health hereby revises this award to reflect a decrease in the amount of $71,770 (see "Award Calculation" in Section I and "Terms and Conditions" in Section III) to ECOHEALTH ALLIANCE, INC. in support of the above referenced project. This award is pursuant to the authority of 42 USC 241 42 CFR 52 and is subject to the requirements of this statute and regulation and of other referenced, incorporated or attached terms and conditions.

Acceptance of this award including the "Terms and Conditions" is acknowledged by the grantee when funds are drawn down or otherwise obtained from the grant payment system.

Each publication, press release, or other document about research supported by an NIH award must include an acknowledgment of NIH award support and a disclaimer such as "Research reported in this publication was supported by the National Institute Of Allergy And Infectious Diseases of the National Institutes of Health under Award Number R01AI110964. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health." Prior to issuing a press release concerning the outcome of this research, please notify the NIH awarding IC in advance to allow for coordination.

Award recipients must promote objectivity in research by establishing standards that provide a reasonable expectation that the design, conduct and reporting of research funded under NIH awards will be free from bias resulting from an Investigator's Financial Conflict of Interest (FCOI), in accordance with the 2011 revised regulation at 42 CFR Part 50 Subpart F. The Institution shall submit all FCOI reports to the NIH through the eRA Commons FCOI Module. The regulation does not apply to Phase I Small Business Innovative Research (SBIR) and Small Business Technology Transfer (STTR) awards. Consult the NIH website http://grants.nih.gov/grants/policy/coi/ for a link to the regulation and additional important information.

If you have any questions about this award, please contact the individual(s) referenced in Section IV.

Sincerely yours,

Tseday G Girma
Grants Management Officer
NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES

Additional information follows

SECTION I – AWARD DATA – 2R01AI110964-06 REVISED

Award Calculation (U.S. Dollars)

Salaries and Wages	$170,123
Fringe Benefits	$53,590
Personnel Costs (Subtotal)	$223,713
Consultant Services	$49,750
Materials & Supplies	$20,850
Travel	$15,027
Subawards/Consortium/Contractual Costs	$229,651
Federal Direct Costs	$538,991
Federal F&A Costs	$122,989
Approved Budget	$661,980
Total Amount of Federal Funds Obligated (Federal Share)	$661,980
TOTAL FEDERAL AWARD AMOUNT	$661,980
AMOUNT OF THIS ACTION (FEDERAL SHARE)	($-71,770)

SUMMARY TOTALS FOR ALL YEARS		
YR	**THIS AWARD**	**CUMULATIVE TOTALS**
6	$661,980	$661,980
7	$637,980	$637,980
8	$637,980	$637,980
9	$637,980	$637,980
10	$637,980	$637,980

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

Fiscal Information:

CFDA Name:	Allergy and Infectious Diseases Research
CFDA Number:	93.855
EIN:	1311726494A1
Document Number:	RAI110964B
PMS Account Type:	P (Subaccount)
Fiscal Year:	2019

IC	CAN	2019	2020	2021	2022	2023
AI	8472364	$661,980	$637,980	$637,980	$637,980	$637,980

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

NIH Administrative Data:
PCC: M51C B / **OC**: 414B / **Released**: (b) (6) 08/02/2019
Award Processed: 08/05/2019 12:01:51 AM

SECTION II – PAYMENT/HOTLINE INFORMATION – 2R01AI110964-06 REVISED

For payment and HHS Office of Inspector General Hotline information, see the NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm

SECTION III – TERMS AND CONDITIONS – 2R01AI110964-06 REVISED

This award is based on the application submitted to, and as approved by, NIH on the above-titled project and is subject to the terms and conditions incorporated either directly or by reference in the following:

a. The grant program legislation and program regulation cited in this Notice of Award.
b. Conditions on activities and expenditure of funds in other statutory requirements, such as those included in appropriations acts.

c. 45 CFR Part 75.
d. National Policy Requirements and all other requirements described in the NIH Grants Policy Statement, including addenda in effect as of the beginning date of the budget period.
e. Federal Award Performance Goals: As required by the periodic report in the RPPR or in the final progress report when applicable.
f. This award notice, INCLUDING THE TERMS AND CONDITIONS CITED BELOW.

(See NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm for certain references cited above.)

Research and Development (R&D): All awards issued by the National Institutes of Health (NIH) meet the definition of "Research and Development" at 45 CFR Part§ 75.2**.** As such, auditees should identify NIH awards as part of the R&D cluster on the Schedule of Expenditures of Federal Awards (SEFA). The auditor should test NIH awards for compliance as instructed in Part V, Clusters of Programs. NIH recognizes that some awards may have another classification for purposes of indirect costs. The auditor is not required to report the disconnect (i.e., the award is classified as R&D for Federal Audit Requirement purposes but non-research for indirect cost rate purposes), unless the auditee is charging indirect costs at a rate other than the rate(s) specified in the award document(s).

An unobligated balance may be carried over into the next budget period without Grants Management Officer prior approval.

This grant is subject to Streamlined Noncompeting Award Procedures (SNAP).

This award is subject to the requirements of 2 CFR Part 25 for institutions to receive a Dun & Bradstreet Universal Numbering System (DUNS) number and maintain an active registration in the System for Award Management (SAM). Should a consortium/subaward be issued under this award, a DUNS requirement must be included. See http://grants.nih.gov/grants/policy/awardconditions.htm for the full NIH award term implementing this requirement and other additional information.

This award has been assigned the Federal Award Identification Number (FAIN) R01AI110964. Recipients must document the assigned FAIN on each consortium/subaward issued under this award.

Based on the project period start date of this project, this award is likely subject to the Transparency Act subaward and executive compensation reporting requirement of 2 CFR Part 170. There are conditions that may exclude this award; see http://grants.nih.gov/grants/policy/awardconditions.htm for additional award applicability information.

In accordance with P.L. 110-161, compliance with the NIH Public Access Policy is now mandatory. For more information, see NOT-OD-08-033 and the Public Access website: http://publicaccess.nih.gov/.

In accordance with the regulatory requirements provided at 45 CFR 75.113 and Appendix XII to 45 CFR Part 75, recipients that have currently active Federal grants, cooperative agreements, and procurement contracts with cumulative total value greater than $10,000,000 must report and maintain information in the System for Award Management (SAM) about civil, criminal, and administrative proceedings in connection with the award or performance of a Federal award that reached final disposition within the most recent five-year period. The recipient must also make semiannual disclosures regarding such proceedings. Proceedings information will be made publicly available in the designated integrity and performance system (currently the Federal Awardee Performance and Integrity Information System (FAPIIS)). Full reporting requirements and procedures are found in Appendix XII to 45 CFR Part 75. This term does not apply to NIH fellowships.

Treatment of Program Income:
Additional Costs

SECTION IV – AI Special Terms and Conditions – 2R01AI110964-06 REVISED

Clinical Trial Indicator: No
This award does not support any NIH-defined Clinical Trials. See the NIH Grants Policy Statement Section 1.2 for NIH definition of Clinical Trial.

REVISED AWARD: This award is revised to adjust the budget in accordance with the letter from Aleksei Chmura/ECOHealth Alliance.

Supersedes previous Notice of Award dated **07/24/2019**.

****
This Notice of Award (NoA) includes funds for activity with **The University of North Carolina at Chapel Hill** in the amount of **$77,750** (**$50,000** direct costs + **$27,750**F&A costs).

This Notice of Award (NoA) includes funds for activity with **Wuhan Institute of Virology** in the amount of **$76,301** (**$70,649** direct costs + **$5,652** F&A costs).

This Notice of Award (NoA) includes funds for activity with **Institute of Pathogen Biology** in the amount of **$75,600** (**$70,000** direct costs + **$5,600** F&A costs).

****
The Research Performance Progress Report (RPPR), Section G.9 (Foreign component), includes reporting requirements for all research performed outside of the United States. Research conducted at the following site(s) must be reported in your RPPR:

Wuhan Institute of Virology, CHINA

Institute of Pathogen Biology, CHINA

East China Normal University, CHINA

Duke-NUS Medical School, SINGAPORE

****
This award reflects current Federal policies regarding Facilities & Administrative (F&A) Costs for foreign grantees including foreign sub-awardees, and domestic awards with foreign sub-awardees. Please see: Chapter 16 Grants to Foreign Organizations, International Organizations, and Domestic Grants with Foreign Components, Section 16.6 “Allowable and Unallowable Cost” of the NIH Grants Policy.

****
This award may include collaborations with and/or between foreign organizations. Please be advised that short term travel visa expenses are an allowable expense on this grant, if justified as critical and necessary for the conduct of the project.

****
The budget period anniversary start date for future year(s) will be **July** 1.

****
Dissemination of study data will be in accord with the Recipient’s accepted genomic data sharing plan as stated in the page(s) **203** of the application. Failure to adhere to the sharing plan as mutually agreed upon by the Recipient and the NIAID may result in Enforcement Actions as described in the NIH Grants Policy Statement.

****
This award is subject to the Clinical Terms of Award referenced in the NIH Guide for Grants and Contracts, July 8, 2002, NOT AI-02-032. These terms and conditions are hereby incorporated by

reference, and can be accessed via the following World Wide Web address: https://www.niaid.nih.gov/grants-contracts/niaid-clinical-terms-award All submissions required by the NIAID Clinical Terms of Award must be forwarded electronically or by mail to the responsible NIAID Program Official identified on this Notice of Award.

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Awardees who conduct research involving Select Agents (see 42 CFR 73 for the Select Agent list; and 7 CFR 331 and 9 CFR 121 for the relevant animal and plant pathogens at http://www.selectagents.gov/Regulations.html) must complete registration with CDC (or APHIS, depending on the agent) before using NIH funds. No funds can be used for research involving Select Agents if the final registration certificate is denied.

Prior to conducting a restricted experiment with a Select Agent or Toxin, awardees must notify the NIAID and must request and receive approval from CDC or APHIS.

****

Select Agents:
Awardee of a project that at any time involves a restricted experiment with a select agent, is responsible for notifying and receiving prior approval from the NIAID. Please be advised that changes in the use of a Select Agent will be considered a change in scope and require NIH awarding office prior approval. The approval is necessary for new select agent experiments as well as changes in on-going experiments that would require change in the biosafety plan and/or biosafety containment level. An approval to conduct a restricted experiment granted to an individual cannot be assumed an approval to other individuals who conduct the same restricted experiment as defined in the Select Agents Regulation 42 CFR Part 73, Section 13.b (http://www.selectagents.gov/Regulations.html).

Highly Pathogenic Agent:
NIAID defines a Highly Pathogenic Agent as an infectious Agent or Toxin that may warrant a biocontainment safety level of BSL3 or higher according to the current edition of the CDC/NIH Biosafety in Microbiological and Biomedical Laboratories (BMBL) (http://www.cdc.gov/OD/ohs/biosfty/bmbl5/bmbl5toc.htm). Research funded under this grant must adhere to the BMBL, including using the BMBL-recommended biocontainment level at a minimum. If your Institutional Biosafety Committee (or equivalent body) or designated institutional biosafety official recommend a higher biocontainment level, the highest recommended containment level must be used.
When submitting future Progress Reports indicate at the beginning of the report:

If no research with a Highly Pathogenic Agent or Select Agent has been performed or is planned to be performed under this grant.

If your IBC or equivalent body or official has determined, for example, by conducting a risk assessment, that the work being planned or performed under this grant may be conducted at a biocontainment safety level that is lower than BSL3.

If the work involves Select Agents and/or Highly Pathogenic Agents, also address the following points:

Any changes in the use of the Agent(s) or Toxin(s) including its restricted experiments that have resulted in a change in the required biocontainment level, and any resultant change in location, if applicable, as determined by your IBC or equivalent body or official.

If work with a new or additional Agent(s)/Toxin(s) is proposed in the upcoming project period, provide:

- A list of the new and/or additional Agent(s) that will be studied;
- A description of the work that will be done with the Agent(s), and whether or not the work is a restricted experiment;
- The title and location for each biocontainment resource/facility, including the name of the organization that operates the facility, and the biocontainment level at which the work will be conducted, with documentation of approval by your IBC or equivalent body or official. It is important to note if the work is being done in a new location.

STAFF CONTACTS

The Grants Management Specialist is responsible for the negotiation, award and administration of this project and for interpretation of Grants Administration policies and provisions. The Program Official is responsible for the scientific, programmatic and technical aspects of this project. These individuals work together in overall project administration. Prior approval requests (signed by an Authorized Organizational Representative) should be submitted in writing to the Grants Management Specialist. Requests may be made via e-mail.

Grants Management Specialist: Tseday G Girma
Email: (b) (6) **Phone**: (b) (6) **Fax**: 301-493-0597

Program Official: Erik J. Stemmy
Email: (b) (6) **Phone**: (b) (6)

SPREADSHEET SUMMARY
GRANT NUMBER: 2R01AI110964-06 REVISED

INSTITUTION: ECOHEALTH ALLIANCE, INC.

Budget	Year 6	Year 7	Year 8	Year 9	Year 10
Salaries and Wages	$170,123	$170,123	$170,123	$170,123	$170,123
Fringe Benefits	$53,590	$53,590	$53,590	$53,590	$53,590
Personnel Costs (Subtotal)	$223,713	$223,713	$223,713	$223,713	$223,713
Consultant Services	$49,750	$49,750	$49,750	$49,750	$49,750
Materials & Supplies	$20,850	$14,850	$14,850	$14,850	$14,850
Travel	$15,027	$15,027	$15,027	$15,027	$15,027
Subawards/Consortium/Contractual Costs	$229,651	$229,651	$229,651	$229,651	$229,651
Publication Costs		$6,000	$6,000	$6,000	$6,000
TOTAL FEDERAL DC	$538,991	$538,991	$538,991	$538,991	$538,991
TOTAL FEDERAL F&A	$122,989	$98,989	$98,989	$98,989	$98,989
TOTAL COST	$661,980	$637,980	$637,980	$637,980	$637,980

Facilities and Administrative Costs	Year 6	Year 7	Year 8	Year 9	Year 10
F&A Cost Rate 1	32%	32%	32%	32%	32%
F&A Cost Base 1	$384,340	$309,340	$309,340	$309,340	$309,340
F&A Costs 1	$122,989	$98,989	$98,989	$98,989	$98,989

From: Lauer, Michael (NIH/OD) [E]
To: Jorgenson, Lyric (NIH/OD) [E]
Cc: Lauer, Michael (NIH/OD) [E]
Subject: USE THIS ONE. Re: For our 5 PM today. See page 11
Date: Tuesday, May 11, 2021 5:52:43 PM
Attachments: PLOS WIV 2017 Daszak ppat.1006698[1].pdf

Hi Lyric – I highlighted what I think is the relevant text. Page 11.

Thanks, Mike

From: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Date: Tuesday, May 11, 2021 at 10:25 AM
To: "Jorgenson, Lyric (NIH/OD) [E]" (b) (6)
Cc: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Subject: For our 5 PM today

Hi Lyric – could we talk about this paper?

Many thanks, Mike

PLOS | PATHOGENS

RESEARCH ARTICLE

Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus

Ben Hu[1☯], Lei-Ping Zeng[1☯], Xing-Lou Yang[1☯], Xing-Yi Ge[1], Wei Zhang[1], Bei Li[1], Jia-Zheng Xie[1], Xu-Rui Shen[1], Yun-Zhi Zhang[2,3], Ning Wang[1], Dong-Sheng Luo[1], Xiao-Shuang Zheng[1], Mei-Niang Wang[1], Peter Daszak[4], Lin-Fa Wang[5], Jie Cui[1]*, Zheng-Li Shi[1]*

1 CAS Key Laboratory of Special Pathogens and Biosafety, Center for Emerging Infectious Diseases of Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China, **2** Yunnan Institute of Endemic Diseases Control and Prevention, Dali, China, **3** Dali University, Dali, China, **4** EcoHealth Alliance, New York, New York, United States of America, **5** Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore

☯ These authors contributed equally to this work.
* jiecui@wh.iov.cn (JC); zlshi@wh.iov.cn (Z-LS)

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Data Availability Statement: All relevant data are within the paper and its Supporting Information files. The complete genome sequences of the 11 bat SARS-related coronaviruses newly identified in this study have been deposited in the GenBank database and assigned accession numbers KY417142 to KY417152, respectively.

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Abstract

A large number of SARS-related coronaviruses (SARSr-CoV) have been detected in horseshoe bats since 2005 in different areas of China. However, these bat SARSr-CoVs show sequence differences from SARS coronavirus (SARS-CoV) in different genes (S, ORF8, ORF3, *etc*) and are considered unlikely to represent the direct progenitor of SARS-CoV. Herein, we report the findings of our 5-year surveillance of SARSr-CoVs in a cave inhabited by multiple species of horseshoe bats in Yunnan Province, China. The full-length genomes of 11 newly discovered SARSr-CoV strains, together with our previous findings, reveals that the SARSr-CoVs circulating in this single location are highly diverse in the S gene, ORF3 and ORF8. Importantly, strains with high genetic similarity to SARS-CoV in the hypervariable N-terminal domain (NTD) and receptor-binding domain (RBD) of the S1 gene, the ORF3 and ORF8 region, respectively, were all discovered in this cave. In addition, we report the first discovery of bat SARSr-CoVs highly similar to human SARS-CoV in ORF3b and in the split ORF8a and 8b. Moreover, SARSr-CoV strains from this cave were more closely related to SARS-CoV in the non-structural protein genes ORF1a and 1b compared with those detected elsewhere. Recombination analysis shows evidence of frequent recombination events within the S gene and around the ORF8 between these SARSr-CoVs. We hypothesize that the direct progenitor of SARS-CoV may have originated after sequential recombination events between the precursors of these SARSr-CoVs. Cell entry studies demonstrated that three newly identified SARSr-CoVs with different S protein sequences are all able to use human ACE2 as the receptor, further exhibiting the close relationship between strains in this cave and SARS-CoV. This work provides new insights into the origin and evolution of SARS-CoV and highlights the necessity of preparedness for future emergence of SARS-like diseases.

Scientific and technological basis special project (2013FY113500) to YZZ and ZLS from the Ministry of Science and Technology of China, the Strategic Priority Research Program of the Chinese Academy of Sciences (XDPB0301) to ZLS, the National Institutes of Health (NIAID R01AI110964), the USAID Emerging Pandemic Threats (EPT) PREDICT program to PD and ZLS, CAS Pioneer Hundred Talents Program to JC, NRF-CRP grant (NRF-CRP10-2012-05) to LFW and WIV "One-Three-Five" Strategic Program (WIV-135-TP1) to JC and ZLS. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing interests: The authors have declared that no competing interests exist.

Author summary

Increasing evidence has been gathered to support the bat origin of SARS coronavirus (SARS-CoV) in the past decade. However, none of the currently known bat SARSr-CoVs is thought to be the direct ancestor of SARS-CoV. Herein, we report the identification of a diverse group of bat SARSr-CoVs in a single cave in Yunnan, China. Importantly, all of the building blocks of SARS-CoV genome, including the highly variable S gene, ORF8 and ORF3, could be found in the genomes of different SARSr-CoV strains from this single location. Based on the analysis of full-length genome sequences of the newly identified bat SARSr-CoVs, we speculate that the direct ancestor of SARS-CoV may have arisen from sequential recombination events between the precursors of these bat SARSr-CoVs prior to spillover to an intermediate host. In addition, we found bat SARSr-CoV strains with different S proteins that can all use the receptor of SARS-CoV in humans (ACE2) for cell entry, suggesting diverse SARSr-CoVs capable of direct transmission to humans are circulating in bats in this cave. Our current study therefore offers a clearer picture on the evolutionary origin of SARS-CoV and highlights the risk of future emergence of SARS-like diseases.

Introduction

Severe Acute Respiratory Syndrome (SARS) is a severe emerging viral disease with high fatality characterized by fever, headache and severe respiratory symptoms including cough, dyspnea and pneumonia [1]. Due to its high transmissibility among humans, after its first emergence in southern China in late 2002, it rapidly led to a global pandemic in 2003 and was marked as one of the most significant public health threats in the 21st century [2,3]. The causative agent, SARS coronavirus (SARS-CoV), has been previously assigned to group 2b CoV and is now a member of the lineage B of genus *Betacoronavirus* in the family *Coronaviridae* [4]. It shares similar genome organization with other coronaviruses, but exhibits a unique genomic structure which includes a number of specific accessory genes, including ORF3a, 3b, ORF6, ORF7a, 7b, ORF8a, 8b and 9b [5,6].

Masked palm civets (*Paguma larvata*) were initially hypothesized to be the animal origin of SARS-CoV [7,8]. However, since a large number of genetically diverse SARS-related coronaviruses (SARSr-CoV) have been detected in multiple species of horseshoe bats (genus *Rhinolophus*) from different areas of China and Europe in the aftermath of SARS, it is prevailingly considered that SARS-CoV originated in horseshoe bats with civets acting as the intermediate amplifying and transmitting host [9–16]. Recently we have reported four novel SARSr-CoVs from Chinese horseshoe bats that shared much higher genomic sequence similarity to the epidemic strains, particularly in their S gene, of which two strains (termed WIV1 and WIV16) have been successfully cultured *in vitro* [17,18]. These newly identified SARSr-CoVs have been demonstrated to use the same cellular receptor (angiotensin converting enzyme-2 [ACE-2]) as SARS-CoV does and replicate efficiently in primary human airway cells [17–19].

Despite the cumulative evidence for the emergence of SARS-CoV from bats, all bat SARSr-CoVs described so far are clearly distinct from SARS-CoV in the S gene and/or one or more accessory genes such as ORF3 and ORF8, suggesting they are likely not the direct ancestor of SARS-CoV. Thus a critical gap remains in our understanding of how and where SARS-CoV originated from bat reservoirs. Previously, we reported a number of bat SARSr-CoVs with diverse S protein sequences from a single cave in Yunnan Province, including the four strains

mentioned above most closely related to SARS-CoV [17,18]. Here we report the latest results of our 5-year longitudinal surveillance of bat SARSr-CoVs in this single location and systematic evolutionary analysis using full-length genome sequences of 15 SARSr-CoV strains (11 novel ones and 4 from previous studies). Efficiency of human ACE2 usage and the functions of accessory genes ORF8 and 8a were also evaluated for some of the newly identified strains.

Results

Continued circulation of diverse SARSr-CoVs in bats from a single location

We have carried out a five-year longitudinal surveillance (April 2011 to October 2015) on SARSr-CoVs in bats from a single habitat in proximity to Kunming city, Yunnan province, China, which was mainly inhabited by horseshoe bats. A total of 602 alimentary specimens (anal swabs or feces) were collected and tested for the presence of CoVs by a Pan-CoV RT-PCR targeting the 440-nt RdRp fragment that is conserved among all known α- and β-CoVs [20]. In total, 84 samples tested positive for CoVs. Sequencing of the PCR amplicons revealed the presence of SARSr-CoVs in the majority (64/84) of the CoV-positive samples (Table 1). Host species identification by amplification of either *Cytb* or *ND1* gene suggested that most (57/64) of the SARSr-CoV positive samples were from *Rhinolophus sinicus*, while the remaining 7 samples were from *Rhinolophus ferrumequinum*, *Rhinolophus affinis* and from *Aselliscus stoliczkanus* which belongs to the family *Hipposideridae*.

Based on the preliminary analysis of the partial RdRp sequences, all of the 64 bat SARSr-CoV sequences showed high similarity among themselves and with other reported bat SARSr-CoVs and SARS-CoVs from humans and civets. To understand the genetic diversity of these bat SARSr-CoVs, the most variable region of the SARSr-CoV S gene, corresponding to the receptor-binding domain (RBD) of SARS-CoV, were amplified and sequenced. Due to low viral load in some samples, RBD sequences were successfully amplified only from 49 samples. These RBD sequences displayed high genetic diversity and could be divided into two large clades, both of which included multiple genotypes. Clade 1 strains shared an identical size and higher amino acid (aa) sequence identity with SARS-CoV RBD, while clade 2 had a shorter size than SARS-CoV S due to two deletions (5 and 12–13 aa, respectively) (S1 Fig). Co-infections by two strains of different clades were detected in two samples, Rs3262 and Rs4087 (S1 Fig).

Table 1. Summary of SARSr-CoV detection in bats from a single habitat in Kunming, Yunnan.

Sampling time	Sample type	Sample Numbers			SARSr-CoV + bat species (No.)
		Total	CoV +	SARSr-CoV +	
April, 2011	anal swab	14	1	1	*R. sinicus* (1)
October, 2011	anal swab	8	3	3	*R. sinicus* (3)
May, 2012	anal swab & feces	54	9	4	*R. sinicus* (4)
September, 2012	feces	39	20	19	*R. sinicus* (16)
					R. ferrumequinum (3)
April, 2013	feces	52	21	16	*R. sinicus* (16)
July, 2013	anal swab & feces	115	9	8	*R. sinicus* (8)
May, 2014	feces	131	8	4	*A. stoliczkamus* (3)
					R. affinis (1)
October, 2014	anal swab	19	4	4	*R. sinicus* (4)
May, 2015	feces	145	3	0	
October, 2015	anal swab	25	6	5	*R. sinicus* (5)
Total		***602***	***84***	***64***	***R (61) A (3)***

https://doi.org/10.1371/journal.ppat.1006698.t001

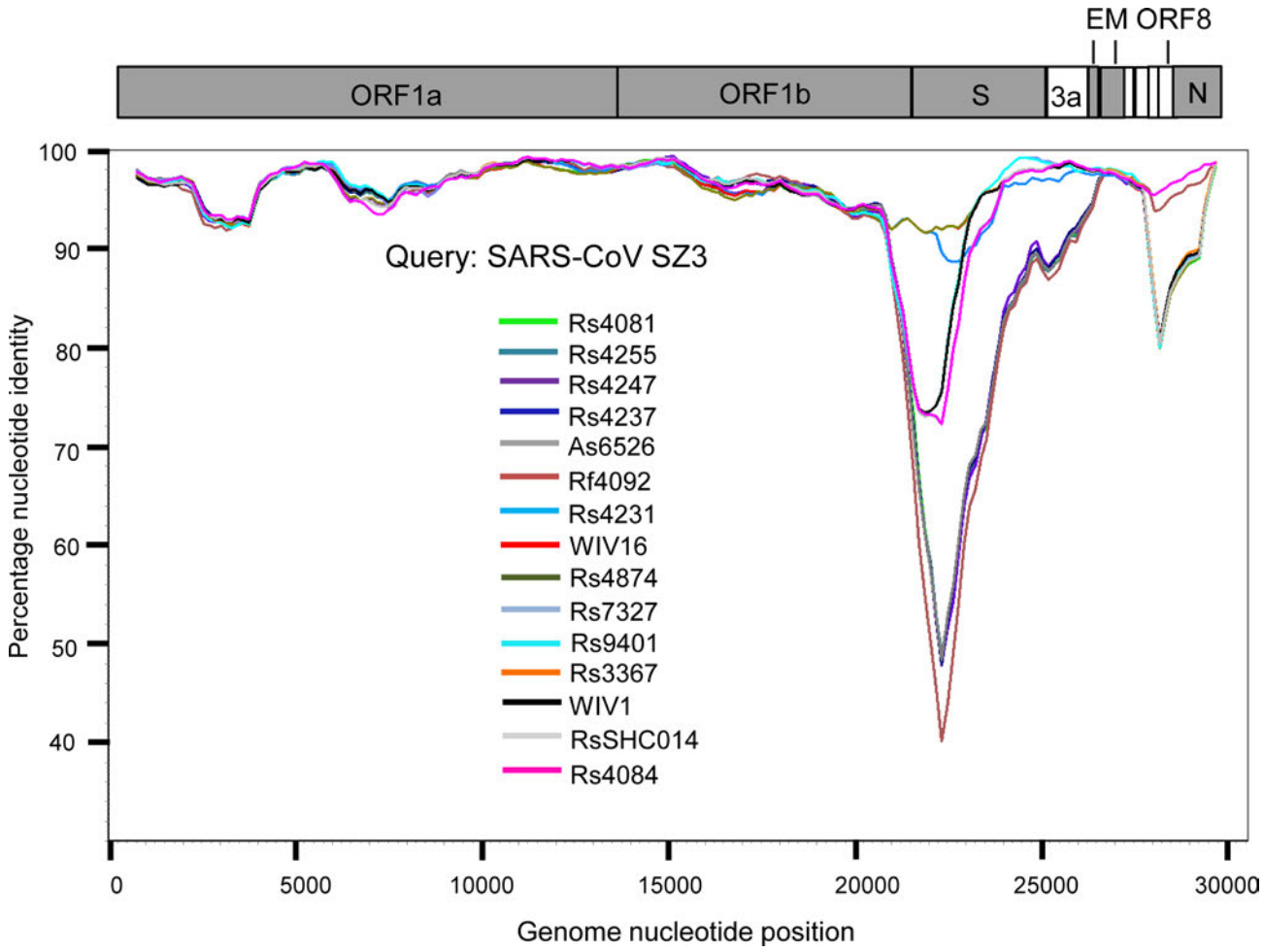

Fig 1. Similarity plot based on the full-length genome sequence of civet SARS CoV SZ3. Full-length genome sequences of all SARSr-CoV detected in bats from the cave investigated in this study were used as reference sequences. The analysis was performed with the Kimura model, a window size of 1500 base pairs and a step size of 150 base pairs.

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Genomic characterization of the novel SARSr-CoVs

Based on the diversity of RBD sequences, 11 novel SARSr-CoV strains named by abbreviation of bat species and sample ID (Rs4081, Rs4084, Rs4231, Rs4237, Rs4247, Rs4255, Rs4874, Rs7327, Rs9401, Rf4092 and As6526) were selected for full-length genomic sequencing based on sample abundance, genotype of RBD as well as sampling time. For each RBD genotype and each time of sampling, at least one representative strain was selected. The genome size of these novel SARSr-CoVs ranged from 29694 to 30291 nucleotides (nt). This gave a total of 15 full-length genomes of bat SARSr-CoVs from this single location (13 from *R.sinicus*, and one each from *R. ferrumequinum* and *A. stoliczkanus*), including our previously reported strains, Rs3367, RsSHC014, WIV1 and WIV16 [17,18]. The genomes of all 15 SARSr-CoVs circulating in this single cave shared 92.0% to 99.9% nt sequence identity. The overall nt sequence identity between these SARSr-CoVs and human and civet SARS-CoVs is 93.2% to 96%, significantly higher than that observed for bat SARSr-CoVs reported from other locations in China (88–93%) [9,10,12,14,21,22]. The genome sequence similarity among the 15 SARSr-CoVs and SARS-CoV SZ3 strain was examined by Simplot analysis (Fig 1). The 15 SARSr-CoVs are

highly conserved and share a uniformly high sequence similarity to SARS-CoV in the non-structural gene ORF1a (96.6% to 97.1% nt sequence identity, 98.0% to 98.3% aa sequence identity) and ORF1b (96.1% to 96.6% nt sequence identity, 99.0% to 99.4% aa sequence identity). In contrast, a considerable genetic diversity is shown in the S gene (corresponding to SZ3 genome position 21477 to 25244) and ORF8 (corresponding to SZ3 genome position 27764 to 28132) (Fig 1).

The 11 novel SARSr-CoVs identified from this single location generally shared similar genome organization with SARS-CoV and other bat SARSr-CoVs. In our previous study, we identified an additional ORF termed ORFx present between ORF6 and ORF7 in strain WIV1 and WIV16 [18,23]. In this study, ORFx was also found in the genomes of Rs7327 and Rs4874. Compared with that of WIV1 and WIV16, the length of ORFx in Rs7327 and Rs4874 was extended to 510 nt due to a deletion of 2 nt in a poly-T sequence that resulted in a shift of reading frame (Fig 2 and S2 Fig).

Co-circulation of different bat SARSr-CoVs with S, ORF8 and ORF3 sequences similar to those in SARS-CoV at a single location

The primary difference between SARS-CoV and most bat SARSr-CoVs is located in S gene. The S protein is functionally divided into two subunits, denoted S1 and S2, which is responsible for receptor binding and cellular membrane fusion, respectively. S1 consists of two domains, the N-terminal domain (NTD) and C-terminal domain (CTD) which is also known as the RBD in SARS-CoV [24]. SARS-CoV and bat SARSr-CoVs share high sequence identity in the S2 region in contrast to the S1 region. Among the 15 SARSr-CoVs identified from bats in the surveyed cave, six strains with deletions in their RBD regions (Rs4081, Rs4237, Rs4247, Rs4255, Rf4092 and As6526) showed 78.2% to 80.2% aa sequence identity to SARS-CoV in the S protein, while the other nine strains without deletions were much more closely related to SARS-CoV, with 90.0% (Rs4084) to 97.2% (Rs4874) aa sequence identity. These nine SARSr-CoVs can be further divided into four genotypes according to their S1 sequences (Fig 2): RsSHC014/Rs4084 showed more genetic differences from SARS-CoV in both NTD and RBD regions; The RBD sequences of SARSr-CoV Rs7327, Rs9401 and previously reported WIV1/Rs3367 closely resembled that of SARS-CoV. However, they were distinct from SARS-CoV but similar to RsSHC014 in NTD. In contrast, we found a novel SARSr-CoV, termed Rs4231, which shared highly similar NTD, but not RBD sequence with SARS-CoV (Figs 2 and 3). Its S protein showed 94.6% to 95% aa sequence identity to those of human and civet SARS-CoVs (S1 Table). Strains with both NTD and RBD highly homologous to those of SARS-CoV were also present in this cave. In addition to WIV16 which we described previously [18], Rs4874 was also found to have the S protein closest to SARS-CoV S (> 97% aa sequence identity) of all the bat SARSr-CoVs reported to date (Figs 2 and 3). In addition to the SARSr-CoVs subjected to full-length genome sequencing, we also obtained the RBD and NTD sequences from other samples collected in this cave. The sequences with high identity to SARS-CoV RBD were amplified from 10 more *R. sinicus* samples. SARSr-CoVs with this genotype of RBD were detected in different seasons throughout the five years. Strains containing the NTD similar to SARS-CoV were only found in 2013 (S2 Table).

ORF8 is another highly variable gene among different SARS-CoV and SARSr-CoV strains [25,26]. We aligned the ORF8 nt sequences of the representative SARSr-CoVs discovered in this surveillance with those of other SARSr-CoVs and SARS-CoVs (Fig 4). Though WIV16, WIV1, Rs4231 and RsSHC014 were genetically closer to SARS-CoV in S gene, they contained a single 366-nt ORF8 without the 29-nt deletion present in most human SARS-CoVs and showed only 47.1% to 51.0% nt sequence identity to human and civet SARS-CoVs. However,

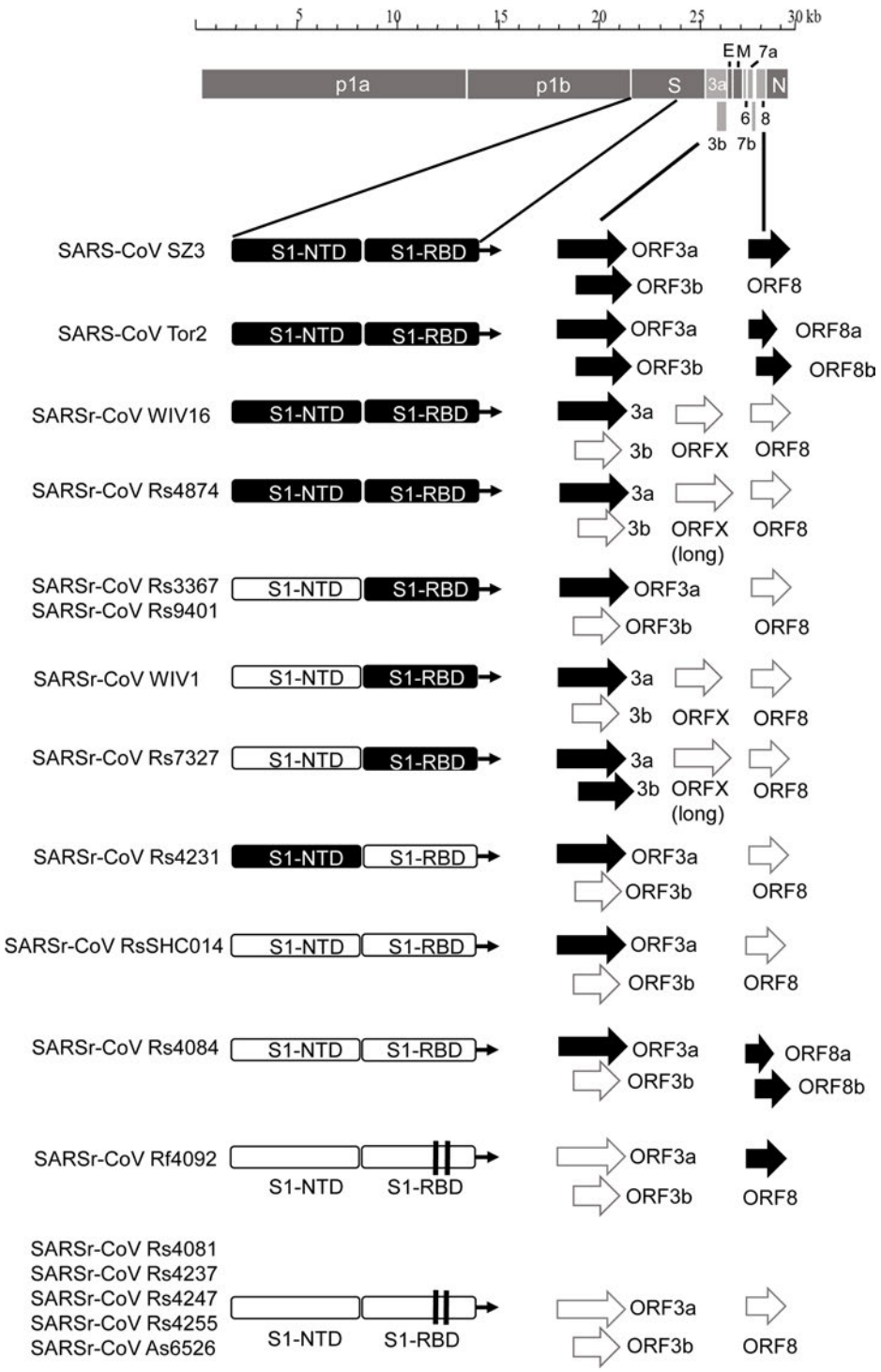

Fig 2. Schematic diagram illustrating the genomic regions or ORFs with most variation between different SARS-CoV and SARSr-CoV isolates. Coding regions of the N-terminal domain (NTD) and receptor-binding domain (RBD) of the spike protein, ORF3a/b and ORF8 (8a/b) in bat SARSr-CoV genomes highly similar to those in SARS CoV genome are indicated with black boxes or arrows while the hollow boxes or arrows represent corresponding regions with less sequence similarity to those of SARS-CoV. The deletions in the RBD of some SARSr-CoVs are indicated by two vertical lines.

https://doi.org/10.1371/journal.ppat.1006698.g002

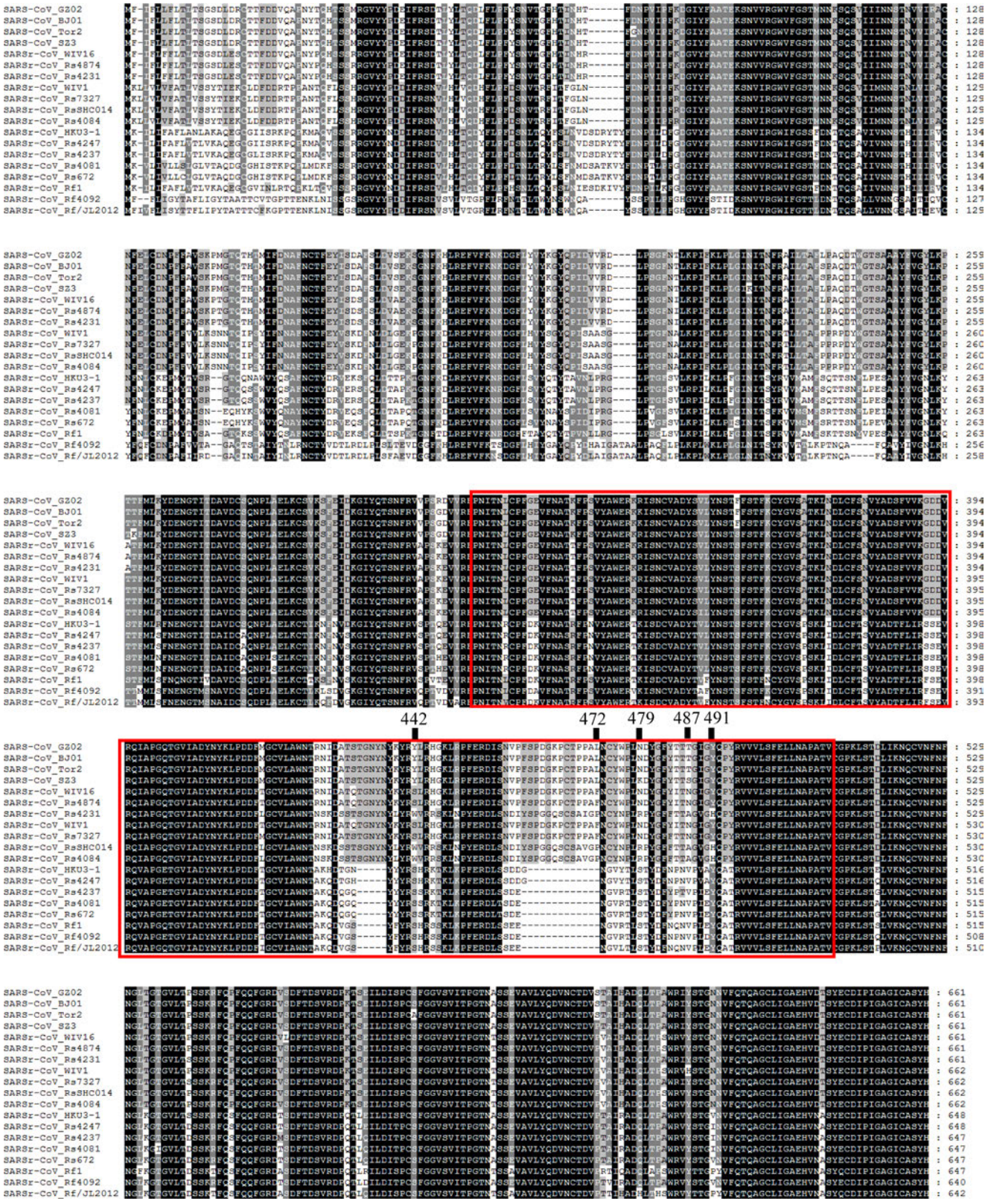

Fig 3. Amino acid sequence comparison of the S1 subunit (corresponding to aa 1–660 of the spike protein of SARS-CoV). The receptor-binding domain (aa 318–510) of SARS-CoV and the homologous region of bat SARSr-CoVs are indicated by the red box. The key aa

residues involved in the interaction with human ACE2 are numbered on top of the aligned sequences. SARS-CoV GZ02, BJ01 and Tor2 were isolated from patients in the early, middle and late phase, respectively, of the SARS outbreak in 2003. SARS-CoV SZ3 was identified from civets in 2003. SARSr-CoV Rs 672 and YN2013 were identified from *R. sinicus* collected in Guizhou and Yunnan Province, respectively. SARSr-CoV Rf1 and JL2012 were identified from *R. ferrumequinum* collected in Hubei and Jilin Province, respectively. WIV1, WIV16, RsSHC014, Rs4081, Rs4084, Rs4231, Rs4237, Rs4247, Rs7327 and Rs4874 were identified from *R.sinicus*, and Rf4092 from *R. ferrumequinum* in the cave surveyed in this study.

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the ORF8 of strain Rf4092 from *R. ferrumequinum* exhibited high similarity to that of civet SARS-CoV. It possessed a single long ORF8 of the same length (369 nt) as that of civet SARS--CoV strain SZ3, with only 10 nt mutations and 3 aa mutations detected (Fig 4). Similar ORF8 sequences were also amplified from other 7 samples collected in the cave during 2011 to 2013, from both *R. ferrumequinum* and *R. sinicus* (S2 Table). The ORF8 of Rs4084 was highly similar to Rf4092's but was split into two overlapping ORFs, ORF8a and ORF8b, due to a short 5-nt deletion (Figs 2 and 4). The position of start codons and stop codons of the two ORFs were consistent with those in most human SARS-CoV strains. Excluding the 8-aa insertion, Rs4084 and SARS-CoV strain BJ01 displayed identical aa sequence of ORF8a, and only three different

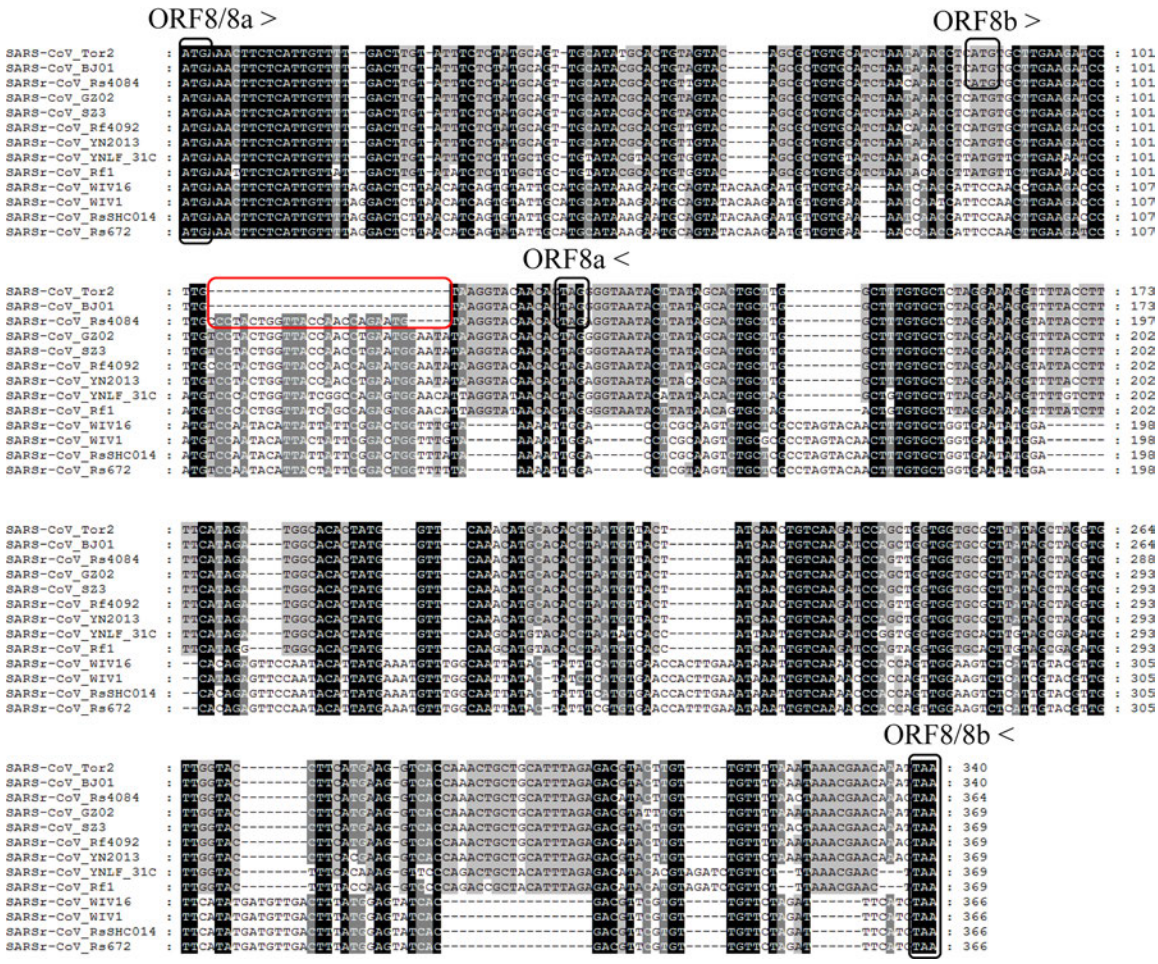


Fig 4. Alignment of nucleotide sequences of ORF8 or ORF8a/8b. The start codons and stop codons of ORF8, 8a and 8b are marked with black boxes and the forward and reverse arrows, respectively. The deletion responsible for the split ORF8a and 8b in human SARS-CoV BJ01, Tor2 and bat SARSr-CoV Rs4084 is marked with red boxes. See the legend for Fig 3 for the origin of various sequences used in this alignment.

https://doi.org/10.1371/journal.ppat.1006698.g004

aa residues were observed between their ORF8b (Fig 4). To our knowledge, Rs4084 was the first bat SARSr-CoV reported that resembled the late human SARS-CoVs in both ORF8 gene organization and sequence.

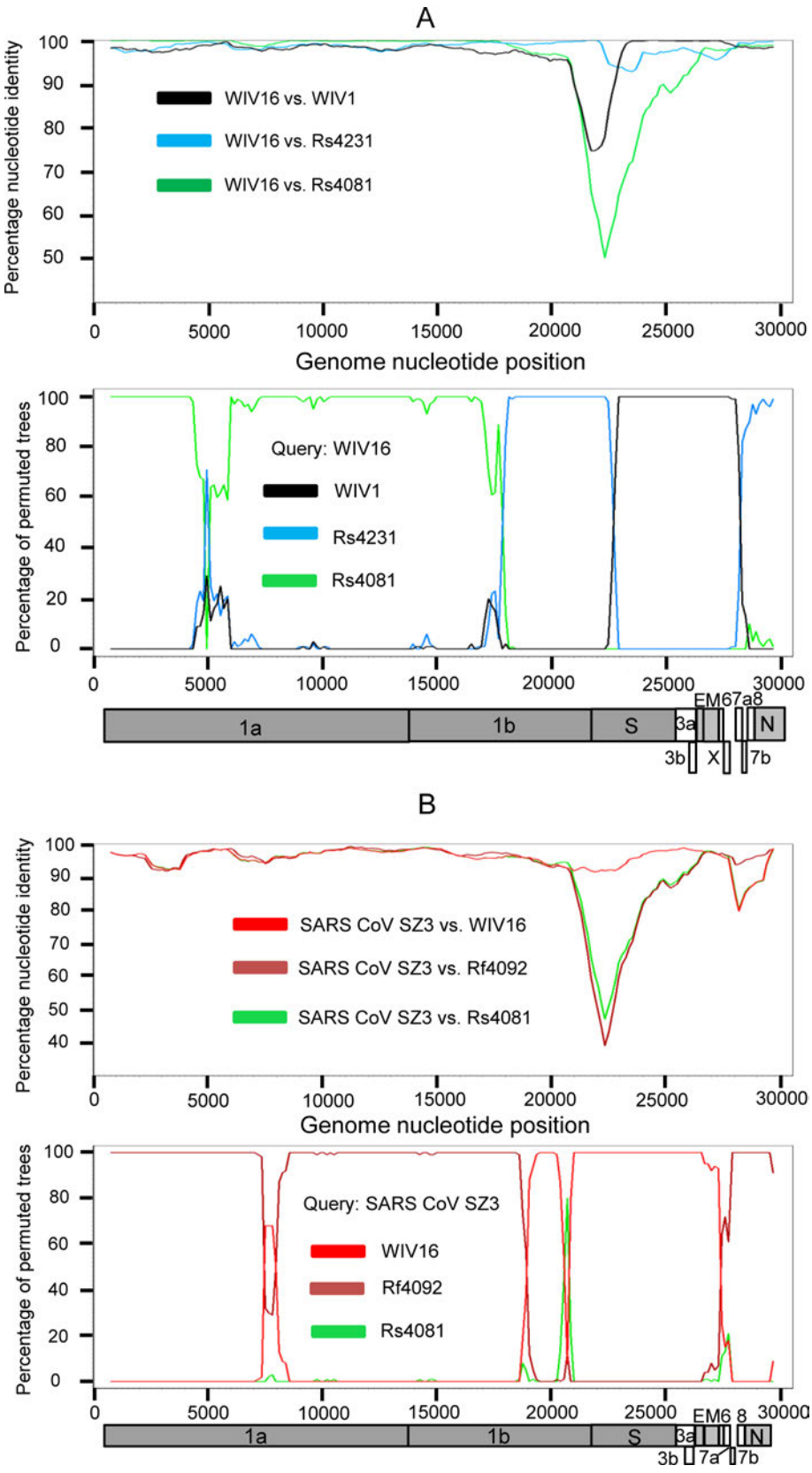
Another key difference between SARS-CoV and bat SARSr-CoV genomes is the ORF3 coding region [10,17,21]. We analyzed the ORF3a sequences amplified from 42 samples and found that most of the SARSr-CoVs closely related to SARS-CoV in the S gene shared higher ORF3a sequence similarity (96.4% to 98.9% aa identity) with SARS-CoV (S3 Fig and S2 Table). The ORF3b of SARS CoV, sharing a large part of its coding sequence with the ORF3a, encodes a 154-aa protein [27], but it is truncated to different extents at the C-terminal in previously described bat SARSr-CoVs including WIV1 and WIV16 (S4 Fig). In the current study, we identified a non-truncated ORF3b for the first time (Rs7327), which maintained the nuclear localization signal at its C-terminal. Moreover, it shared 98.1% aa sequence identity with SARS-CoV strain Tor2 with only three aa substitutions (S4 Fig). Thus, Rs7327 is the bat SARSr-CoV most similar to SARS-CoV in the ORF3 region known to date.

Recombination analysis

The full-length genome sequences of all 15 SARSr-CoVs from the surveyed cave were screened for evidence of potential recombination events. Both similarity plot and bootscan analyses revealed frequent recombination events among these SARSr-CoV strains. It was suggested that WIV16, the closest progenitor of human SARS-CoV known to date [18], was likely to be a recombinant strain from three SARSr-CoVs harbored by bats in the same cave, namely WIV1, Rs4231 and Rs4081, with strong *P* value ($<10^{-30}$). Breakpoints were identified at genome positions nt 18391, 22615 and 28160 (Fig 5A). In the genomic region between nt 22615 and 28160, which contained the region encoding the RBD and the S2 subunit of the S protein, WIV16 was highly similar to WIV1, sharing 99% sequence identity. In contrast, in the region between nt 18391 and 22615, which covered a part of ORF1b and the region encoding the NTD of the S gene, WIV16 showed substantially closer relationship to Rs4231. Meanwhile, the ORF1ab sequences upstream from nt 18391 of WIV16 displayed the highest genetic similarity (99.8% nt sequence identity) to that of Rs4081.

Evidence of recombination event was also detected in the genome of the novel SARSr-CoV Rs4084, which had a unique genome organization with split ORF8a and 8b. The previously reported strain RsSHC014 and the newly identified strain Rf4092 were suggested to be the major and minor parent of Rs4084, respectively (P value $< 10^{-80}$). The breakpoint was located at nt 26796 (S5 Fig). In the region downstream of the breakpoint including ORF8, Rs4084 showed closet genetic relationship with Rf4092, sharing 98.9% nt sequence identity, while it shared the highest nt sequence identity (99.4%) with RsSHC014 in the majority of its genome upstream from the breakpoint.

When civet SARS-CoV SZ3 was used as the query sequence in similarity plot and bootscan analysis, evidence for recombination events was also detected (Fig 5B). In the region between the two breakpoints at the genome positions nt 21161 and nt 27766, including the S gene, closer genetic relationship between SZ3 and WIV16 was observed. However, from position nt 27766 towards the 3' end of its genome, a notably close genetic relationship was observed between SZ3 and Rf4092 instead. Throughout the non-structural gene, moreover, SZ3 shared a similarly high sequence identity with WIV16 and Rf4092. It indicates that civet SARS-CoV was likely to be the descendent from a recombinant of the precursors of WIV16 and Rf4092, or that the SARSr-CoVs found in this cave, like WIV16 or Rf4092, may have been the descendants of the SARS-CoV lineage.


A
Percentage nucleotide identity
WIV16 vs. WIV1
WIV16 vs. Rs4231
WIV16 vs. Rs4081
Genome nucleotide position
Percentage of permuted trees
Query: WIV16
WIV1
Rs4231
Rs4081
1a
1b
S
3a
EM
6
7a
8
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3b
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7b
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Percentage nucleotide identity
SARS CoV SZ3 vs. WIV16
SARS CoV SZ3 vs. Rf4092
SARS CoV SZ3 vs. Rs4081
Genome nucleotide position
Percentage of permuted trees
Query: SARS CoV SZ3
WIV16
Rf4092
Rs4081
1a
1b
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3a
EM
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8
N
3b
7a
7b

Fig 5. Detection of potential recombination events by similarity plot and boot scan analysis. (A) Full-length genome sequence of SARSr-CoV WIV16 was used as query sequence and WIV1, Rs4231 and Rs4081 as reference sequences. (B) Full-length genome sequence of SARS-CoV SZ3 was used as query sequence and SARSr-CoV WIV16, Rf4092 and Rs4081 as reference sequences. All analyses were performed with a Kimura model, a window size of 1500 base pairs, and a step size of 150 base pairs. The gene map of query genome sequences are used to position breakpoints.

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Phylogenetic analysis

Phylogenetic trees were constructed using the nt sequences of nonstructural protein gene ORF1a and ORF1b. Unlike the high genetic diversity in the S gene, nearly all SARSr-CoVs from the bat cave we surveyed were closely clustered, and showed closer phylogenetic relationship to SARS-CoV than the majority of currently known bat SARSr-CoVs discovered from other locations, except YNLF 31C and 34C which were recently reported in greater horseshoe bats from another location in Yunnan [22] (Fig 6). The phylogeny of SARSr-CoVs in ORF1a and ORF1b appeared to be associated with their geographical distribution rather than with host species. Regardless of different host bat species, SARS-CoV and SARSr-CoVs detected in bats from southwestern China (Yunnan, Guizhou and Guangxi province) formed one clade, in which SARSr-CoV strains showing closer relationship to SARS-CoV were all from Yunnan. SARSr-CoVs detected in southeastern, central and northern provinces, such as Hong Kong, Hubei and Shaanxi, formed the other clade which was phylogenetically distant to human and civet SARS-CoVs (Fig 6 and S6 Fig).

Rescue of bat SARSr-CoVs and virus infectivity experiments

In the current study, we successfully cultured an additional novel SARSr-CoV Rs4874 from a single fecal sample using an optimized protocol and Vero E6 cells [17]. Its S protein shared 99.9% aa sequence identity with that of previously isolated WIV16 and it was identical to WIV16 in RBD. Using the reverse genetics technique we previously developed for WIV1 [23], we constructed a group of infectious bacterial artificial chromosome (BAC) clones with the backbone of WIV1 and variants of S genes from 8 different bat SARSr-CoVs. Only the infectious clones for Rs4231 and Rs7327 led to cytopathic effects in Vero E6 cells after transfection (S7 Fig). The other six strains with deletions in the RBD region, Rf4075, Rs4081, Rs4085, Rs4235, As6526 and Rp3 (S1 Fig) failed to be rescued, as no cytopathic effects was observed and viral replication cannot be detected by immunofluorescence assay in Vero E6 cells (S7 Fig). In contrast, when Vero E6 cells were respectively infected with the two successfully rescued chimeric SARSr-CoVs, WIV1-Rs4231S and WIV1-Rs7327S, and the newly isolated Rs4874, efficient virus replication was detected in all infections (Fig 7). To assess whether the three novel SARSr-CoVs can use human ACE2 as a cellular entry receptor, we conducted virus infectivity studies using HeLa cells with or without the expression of human ACE2. All viruses replicated efficiently in the human ACE2-expressing cells. The results were further confirmed by quantification of viral RNA using real-time RT-PCR (Fig 8).

Activation of activating transcription factor 6 (ATF6) by the ORF8 proteins of different bat SARSr-CoVs

The induction of the ATF6-dependent transcription by the ORF8s of SARS-CoV and bat SARSr-CoVs were investigated using a luciferase reporter, 5×ATF6-GL3. In HeLa cells transiently transfected with the expression plasmids of the ORF8s of bat SARSr-CoV Rf1, Rf4092 and WIV1, the relative luciferase activities of the 5×ATF6-GL3 reporter was enhanced by 5.56 to 9.26 folds compared with cells transfected with the pCAGGS empty vector, while it was

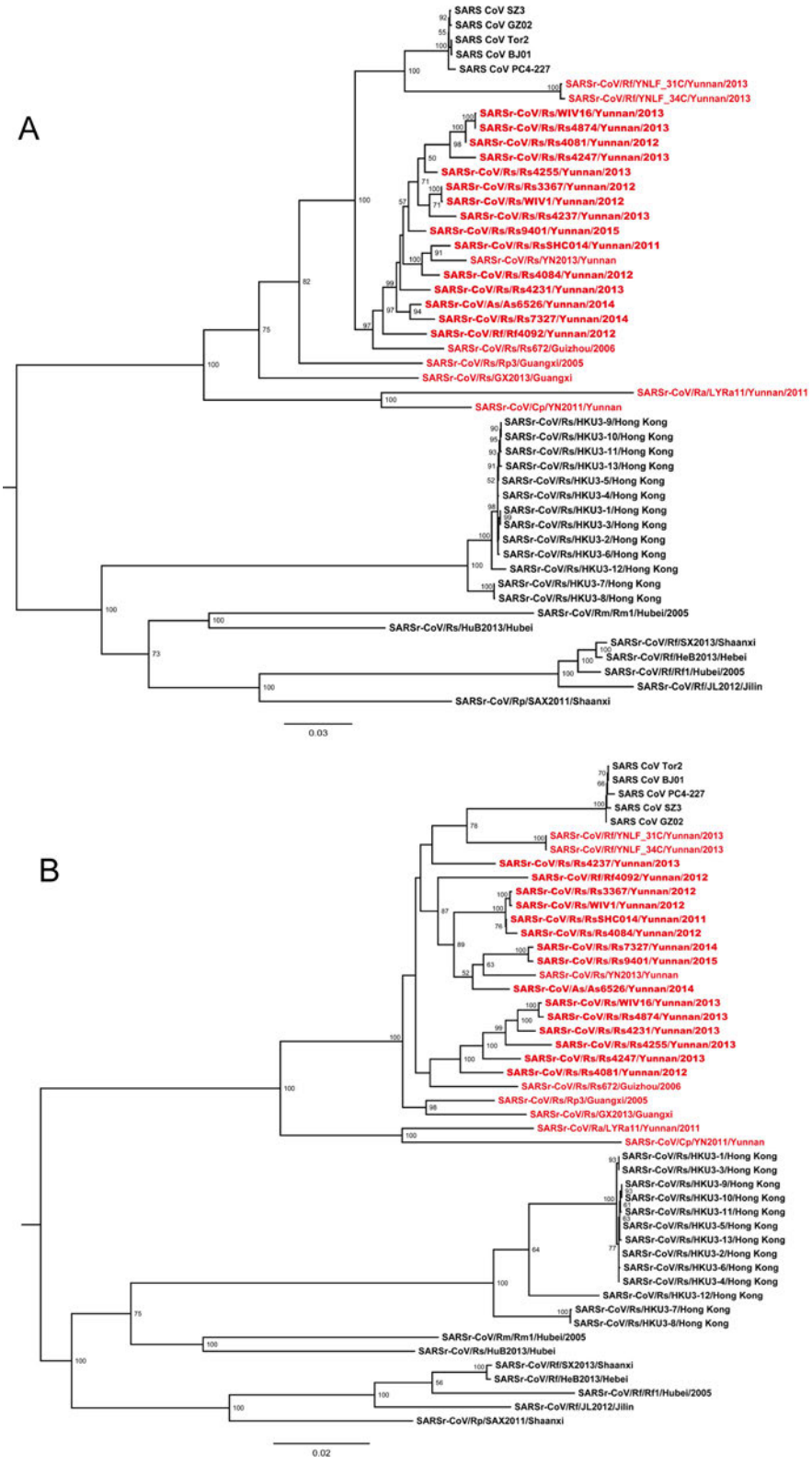

Fig 6. Phylogenetic trees based on nucleotide sequences of ORF1a (A) and ORF1b (B). The trees were constructed by the maximum likelihood method using the LG model with bootstrap values determined by 1000 replicates. Only bootstraps > 50% are shown. The scale bars represent 0.03 (A) and 0.02 (B) substitutions per

nucleotide position. Rs, *Rhinolophus sinicus*; Rf, *Rhinolophus ferremequinum*; Rm, *Rhinolophus macrotis*; Ra, *Rhinolophus affinis*; Rp, *Rhinolophus pusillus*; As, *Aselliscus stoliczkanus*; Cp, *Chaerephon plicata*. SARSr-CoVs detected in bats from the single cave surveyed in this study are in bold. Sequences detected in southwestern China are indicated in red.

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increased by 4.42 fold by the SARS-CoV GZ02 ORF8. As a control, the treatment with tunicamyxin (TM) stimulated the transcription by about 11 folds (Fig 9A). The results suggests that various ORF8 proteins of bat SARSr-CoVs can activate ATF6, and those of some strains have a stronger effect than the SARS-CoV ORF8.

Induction of apoptosis by the ORF8a of the newly identified bat SARSr-CoV

We conducted transient transfection to examine whether the ORF8a of SARSr-CoV Rs4084 triggered apoptosis. As shown in Fig 9B, 11.76% and 9.40% of the 293T cells transfected with the SARSr-CoV Rs4084-ORF8a and SARS-CoV Tor2-ORF8a expression plasmid underwent apoptosis, respectively. In contrast, transfection with the empty vector resulted in apoptosis in only 2.79% of the cells. The results indicate that Rs4084 ORF8a has an apoptosis induction activity similar to that of SARS-CoV [28].

Discussion

Genetically diverse SARSr-CoVs have been detected in various horseshoe bat species across a wide geographic range in China in the past decade [9–12,14,29]. However, most bat SARSr-CoVs show considerable genetic distance to SARS-CoV, particularly in the highly variable S1, ORF8 and ORF3 regions [10,25]. Recently, several novel SARSr-CoVs have been described to be more closely related to SARS-CoV, either in the S gene or in ORF8. The S proteins of RsSHC014, Rs3367, WIV1 and WIV16, which were reported in our previous studies, shared 90% to 97% aa sequence identities to those of human/civet SARS-CoVs [17,18]. Another strain from *Rhinolophus affinis* in Yunnan termed LYRa11 showed 90% aa sequence identity to SARS-CoV in the S gene [13]. In addition, two studies have described 4 novel SARSr-CoVs (YNLF_31C/34C and GX2013/YN2013) which possessed a full-length ORF8 with substantially higher similarity to that of SARS-CoV [22,30]. These findings provide strong genetic evidence for the bat origin of SARS-CoV with regard to the S gene or ORF8. However, all of these SARSr-CoVs were distinct from SARS-CoV in at least one other gene, suggesting that none of them was the immediate progenitor of SARS-CoV. Moreover, these SARSr-CoVs were discovered in bat populations from physically distinct locations. The site of origin of the true progenitor of SARS-CoV and the evolutionary origin of SARS-CoV have until now remained elusive. In the current study, we have identified a bat habitat potentially important for SARSr-CoV evolution where a series of recombination events have likely occurred among different SARSr-CoV strains, which provides new insights into the origin of SARS-CoV.

SARS first emerged in Guangdong province in late 2002 [7]. However, SARSr-CoVs discovered in bats from neighboring areas of Guangdong to date have shown phylogenetic disparity from SARS-CoV especially in the S gene [9,10,14], suggesting SARS-CoV may have originated from another region. Our analysis of the phylogeny of SARS-CoVs and all known bat SARSr-CoVs using the nt sequence of their non-structural ORF1a and ORF1b genes, which constitute the majority of the genome, shows that SARSr-CoV evolution is strongly correlated with their geographical origin, but not host species. It is noteworthy that SARSr-CoVs detected in Yunnan are more closely related to SARS-CoV than strains from other regions in China. This finding implies that Yunnan, or southwestern China, is more likely to be the geographical source

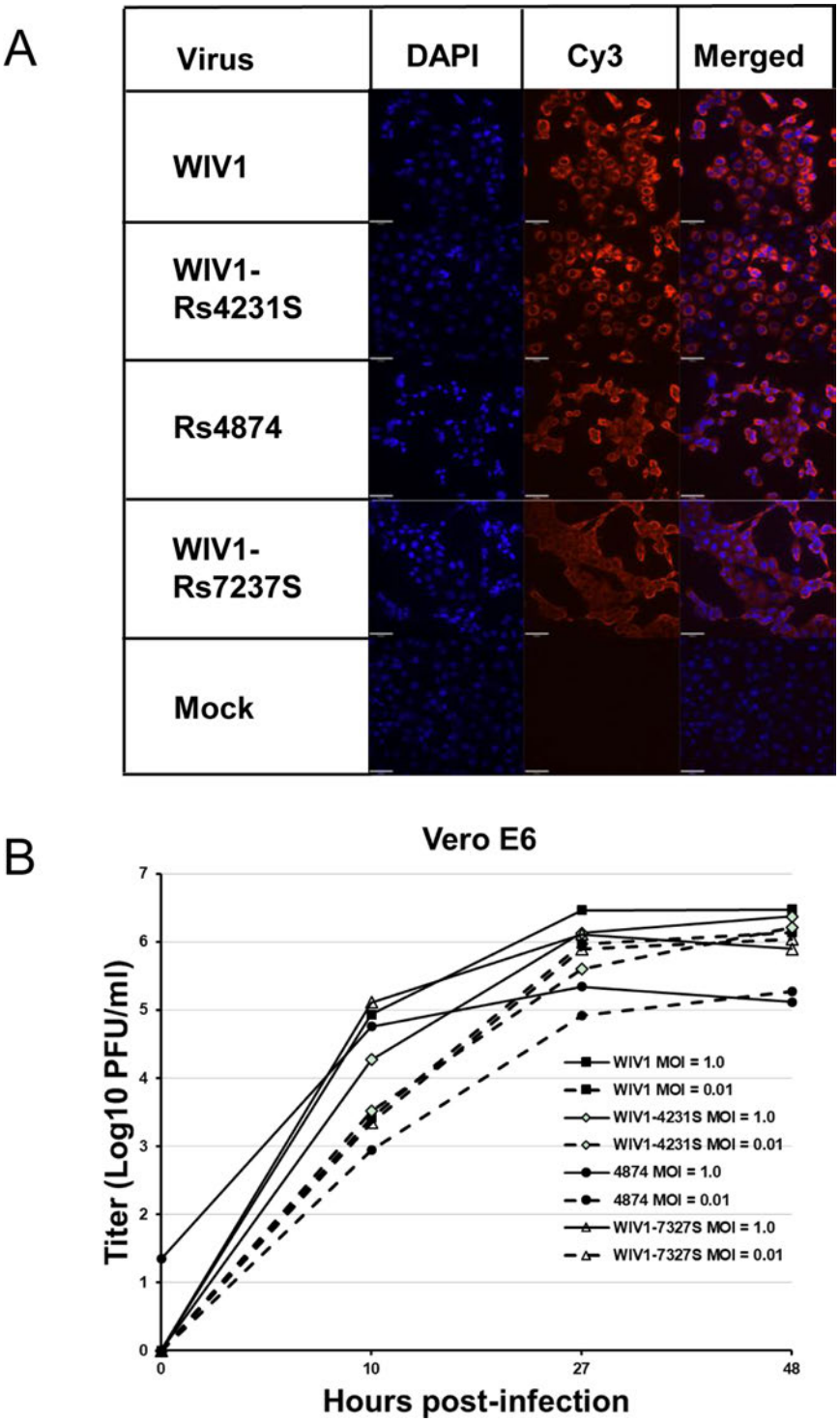

Fig 7. Infection of Vero E6 cells by bat SARSr-CoV WIV1, Rs4874, WIV1-Rs4231S and WIV1-Rs7327S. (A) The successful infection was confirmed by immunofluorescent antibody staining using rabbit antibody against the SARSr-CoV Rp3 nucleocapsid protein. The columns (from left to right) show staining of nuclei (blue), virus replication (red), and both nuclei and virus replication (merged double-stain images). (B) The growth curves in Vero E6 cells with a MOI of 1.0 and 0.01.

https://doi.org/10.1371/journal.ppat.1006698.g007

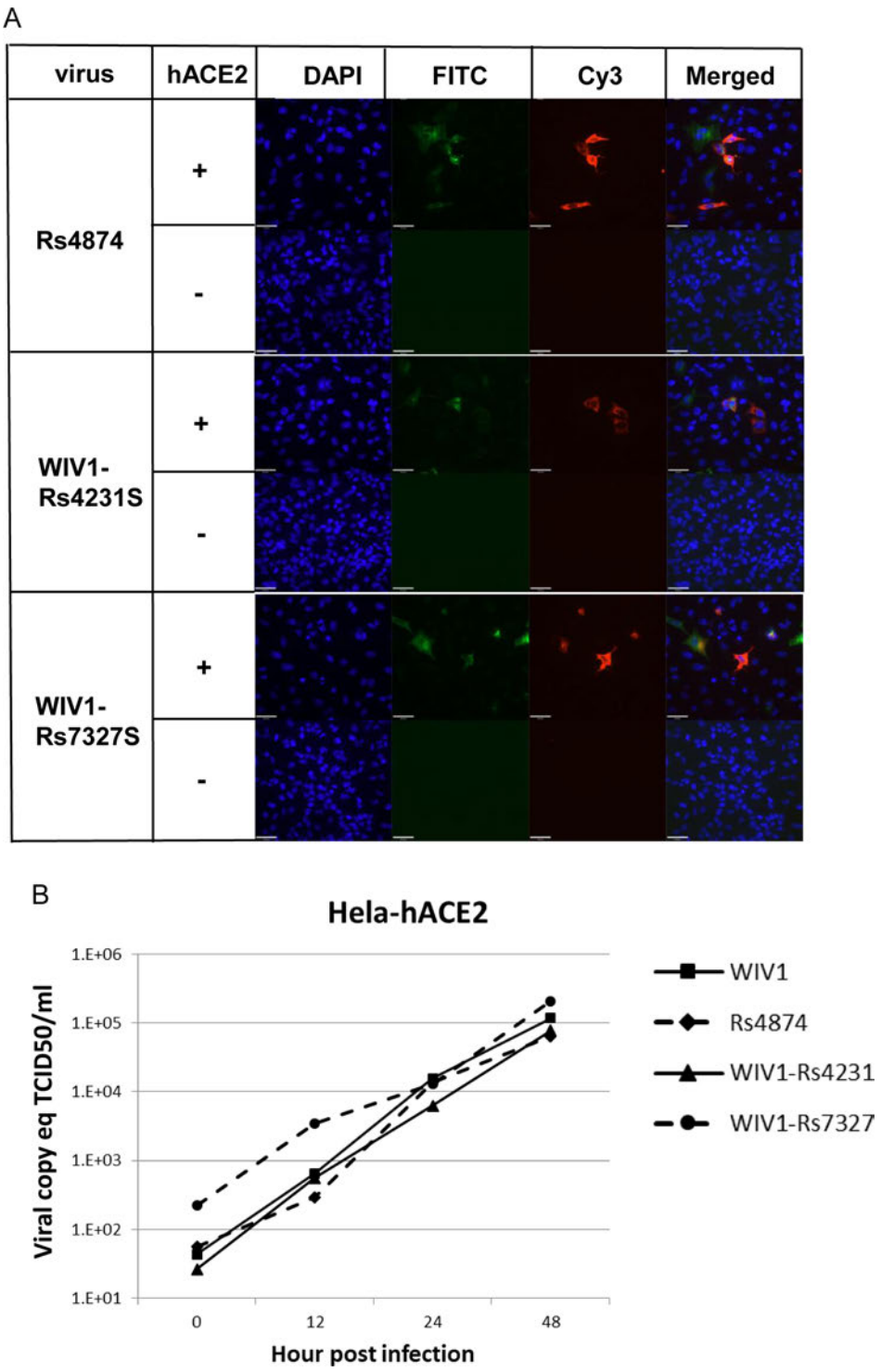

Fig 8. Analysis of receptor usage by immunofluorescence assay (A) and real-time PCR (B). Virus infectivity of Rs4874, WIV1-Rs4231S and WIV1-Rs7327S was determined in HeLa cells with and without the expression of human ACE2. ACE2 expression was detected with goat anti-human ACE2 antibody followed by fluorescein isothiocyanate (FITC)-conjugated donkey anti-goat IgG. Virus replication was detected with rabbit antibody against the SARSr-CoV Rp3 nucleocapsid protein followed by cyanine 3 (Cy3)-conjugated mouse anti-rabbit IgG. Nuclei were stained with DAPI (49,6-diamidino-2-phenylindole).The columns (from left to right) show staining of nuclei (blue), ACE2 expression (green), virus replication (red) and the merged triple-stained images, respectively.

https://doi.org/10.1371/journal.ppat.1006698.g008

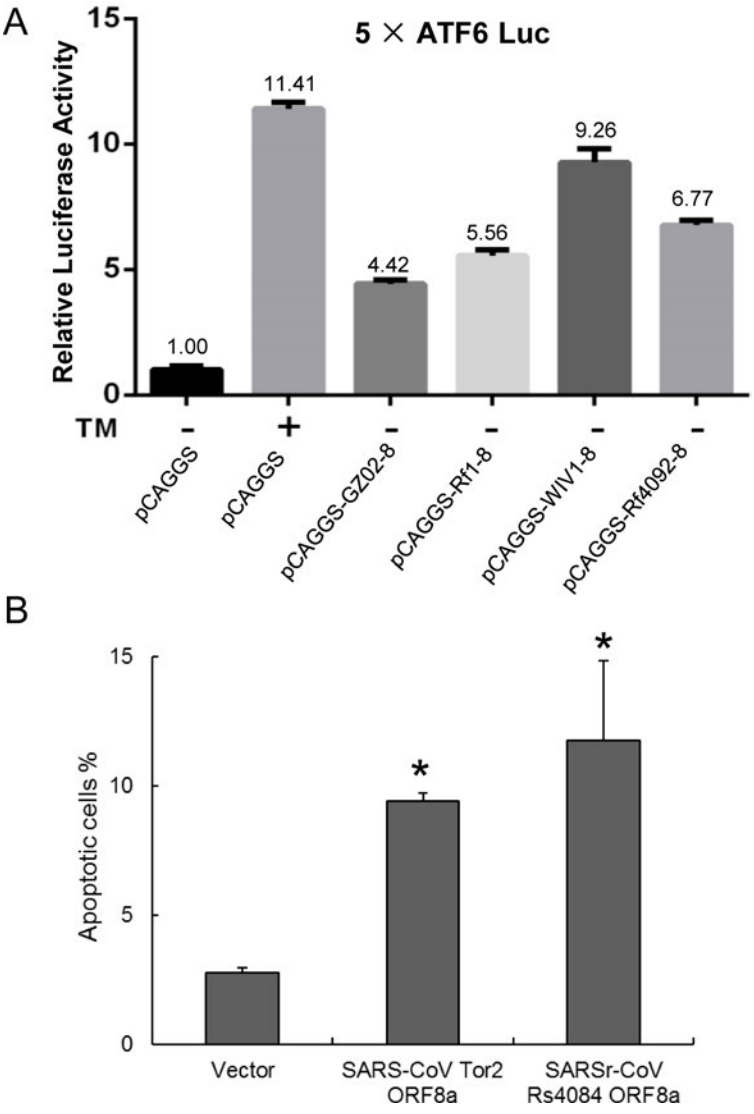

Fig 9. Functional characterization of diverse ORF8 and ORF8a proteins of bat SARSr-CoVs. (A) The ORF8 proteins of SARS-CoV and bat SARSr-CoVs induces the ATF6-dependent transcriptional activity. HeLa cells were transiently transfected with the pcAGGS expression plasmids of the ORF8 of SARS-CoV GZ02, bat SARSr-CoV Rf1, WIV1 and Rf4092 and the reporter plasmid 5×ATF6-GL3 for 40h. Control cells were co-transfected with the reporter plasmid and the empty pCAGGS vector for 24h, and treated with or without TM (2μg/ml) for an additional 16h. The cell lysates were harvested for dual luciferase assay and data are shown as the average values from triplicate wells. (B) The ORF8a proteins of SARS-CoV and bat SARSr-CoV triggered apoptosis. 293T cells were transfected with the expression plasmids of the ORF8a of SARS-CoV Tor2 and bat SARSr-CoV Rs4084 and a pcAGGS vector control for 24h. Apoptosis was analyzed by flow cytometry after annexin V staining and the percentage of apoptotic cells were calculated. Data are shown as the average values from triplicate cells. Error bars indicate SDs. * $P<0.05$.

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of SARS-CoV than other regions in China, but data from more extensive surveillance are yet needed to support this inference.

In our longitudinal surveillance of SARSr-CoVs in a single cave in Yunnan where we discovered Rs3367, RsSHC014, WIV1 and WIV16, the CoV prevalence in fecal samples varied among different sampling time. Generally, a higher prevalence was observed in autumn (September and October) than in spring and early summer (April and May). This may be due to

the establishment of a susceptible subpopulation of newborn bats which had not developed their own immunity after the parturition period [31]. Another factor may be the changes in the composition of bat species in the cave at different sampling dates. For example, in September 2012 when the CoV prevalence reached 51.3%, the majority of samples were from *R. sinicus*, but in May 2015 when only 3 out of the 145 samples tested positive, *Aselliscus stoliczkanus* was the predominant bat species in the cave. We failed to amplify the RBD sequences from 15 of the 64 SARSr-CoV positive samples. Most of these samples had comparatively low viral concentration ($< 10^7$ copies/g) (S8 Fig), as revealed by our previous quantitative studies [32]. The unsuccessful amplification of RBD in some samples with high viral concentration was probably because of the more divergent sequences in this region of these SARSr-CoV genomes.

In this cave, we have now obtained full-length genome sequences of additional 11 novel SARSr-CoVs from bats. Our findings suggest the co-circulation of different bat SARSr-CoVs highly similar to SARS-CoV in the most variable S1 (NTD and RBD), ORF8 and ORF3 regions, respectively, in this single location. In the ORF1a, ORF1b, E, M and N genes, the SARSr-CoVs circulating in this cave also shared > 98% aa sequence identities with human/civet SARS-CoVs. Thus, all of the building blocks of the SARS-CoV genome were present in SARSr-CoVs from this single location in Yunnan during our sampling period. Furthermore, strains closely related to different representative bat SARSr-CoVs from other provinces (e.g. Rs672, HKU3 and Rf1) in the RBD region were also detected there. Therefore, this cave could be regarded as a rich gene pool of bat SARSr-CoVs, wherein concurrent circulation of a high diversity of SARSr-CoV strains has led to an unusually diverse assemblage of SARSr-CoVs.

During our 5-year surveillance in this single cave, we first reported Rs3367 and WIV1 in 2013, with RBD sequence closely resembling that of SARS-CoV [17]. More recently, we discovered WIV16 which had an RBD almost identical to WIV1's but shared much higher similarity with SARS-CoV than WIV1 in the NTD region of S1, making it the closest SARSr-CoV to the epidemic strains identified to date [18]. In this study, we found a novel strain Rs4231 from the same location sharing almost identical NTD sequence with WIV16 but distinct from it in the RBD, with evidence of a recombination event. Our recombination analysis indicated that a recombination event may have taken place at the junction between the coding region of NTD and RBD in the Rs4231 and WIV1 genomes and resulted in WIV16. Recombination at this genomic position also happened among other SARSr-CoVs relatively distant to SARS-CoV found in this location (e.g. Rs4081 and Rs4247, S5 Fig). The frequent recombination at this hotspot in the S gene increased the genetic diversity of SARSr-CoVs harbored in these bat populations and might have been responsible for the generation of the S gene of the direct progenitor strain of SARS-CoV.

The genomes of SARS-CoVs from patients during the early epidemic phase and civet SARS-CoVs all contained a single full-length ORF8 [3,7]. We have found that a number of bat SARSr-CoVs from this cave possessed a complete ORF8 highly similar to that of early human/civet SARS-CoV (>97% nt sequence identity), represented by strain Rf4092 (S3C Fig). This provided further evidence for the source of human SARS-CoV ORF8 in bats [22,30]. In contrast, the ORF8 was split into overlapping ORF8a and ORF8b in most human SARS-CoV strains from later-phase patients due to the acquisition of a 29-nt deletion [8,26]. In this study, we have discovered for the first time a bat SARSr-CoV with ORF8a and ORF8b highly similar to the later-phase human SARS-CoVs, though the split of ORF8 in the bat SARSr-CoV and that in human SARS-CoV were two independent events. Our recombination analysis suggests that this strain, Rs4084, likely acquired its ORF8 from Rf4092 through recombination, followed by the development of the 5-nt deletion which led to the splitting. It suggests that ORF8 region in bat SARSr-CoV genomes is prone to deletions as in human SARS-CoV [3,25]. Finally, the recombination analysis suggests that an ancestral strain of SARS-CoV SZ3 would have been generated if the recombination around ORF8 had occurred between the lineages that led to WIV16 and Rf4092.

Taken together, the evidence of recombination events among SARSr-CoVs harbored by bats in this single location suggests that the direct progenitor of SARS-CoV may have originated as a result of a series of recombination within the S gene and around ORF8. This could have been followed by the spillover from bats to civets and people either in the region, or during movement of infected animals through the wildlife trade. However, given the paucity of data on animal trade prior to the SARS outbreak, the likely high geographical sampling bias in bat surveillance for SARSr-CoVs in southern China, and the possibility that other caves harbor similar bat species assemblages and a rich diversity of SARSr-CoVs, a definite conclusion about the geographical origin of SARS-CoV cannot be drawn at this point.

R. sinicus are regarded as the primary natural host of SARS-CoV, as all SARSr-CoVs highly homologous to SARS-CoV in the S gene were predominantly found in this species. However, it is noted that two SARSr-CoVs previously reported from *R. ferrumequinum* showed the closest phylogenetic position to SARS-CoV in the ORF1a/1b trees. These strains were discovered in another location in Yunnan 80 km from the cave surveyed in the current study [22]. This information also supports the speculation that SARS-CoV may have originated from this region. Nonetheless, since the correlation between the host species and the phylogeny of SARSr-CoV ORF1ab seems limited, more SARSr-CoV sequences need to be obtained from different *Rhinolophus* bat species in both locations in Yunnan, and from other locations in southern China. In particular, it will be important to assess whether *R. ferrumequinum* played a more important role in the evolution of SARS-CoV ORF1ab.

The cave we studied is located approximately 60 km from the city of Kunming. Beside a number of rhinolophid and hipposiderid species from which SARSr-CoVs have been detected, other bats like myotis were also present there. The temperature in the cave is around 22–25˚C and the humidity around 85%-90%. The physical nature of the cave is not unique, but it does appear to host a particularly dense population of bats in the reproductive season. Similar caves co-inhabited by bat populations of different species are not rare in other areas in Yunnan. We propose that efforts to study the ecology, host species diversity, and viral strain populations of these caves may provide critical information on what drives SARSr-CoV evolution.

Our previous studies demonstrated the capacity of both WIV1 and WIV16 to use ACE2 orthologs for cell entry and to efficiently replicate in human cells [17,18]. In this study, we confirmed the use of human ACE2 as receptor of two novel SARSr-CoVs by using chimeric viruses with the WIV1 backbone replaced with the S gene of the newly identified SARSr-CoVs. Rs7327's S protein varied from that of WIV1 and WIV16 at three aa residues in the receptor-binding motif, including one contact residue (aa 484) with human ACE2. This difference did not seem to affect its entry and replication efficiency in human ACE2-expressing cells. A previous study using the SARS-CoV infectious clone showed that the RsSHC014 S protein could efficiently utilize human ACE2 [33], despite being distinct from SARS-CoV and WIV1 in the RBD (S1 Fig). We examined the infectivity of Rs4231, which shared similar RBD sequence with RsSHC014 but had a distinct NTD sequence, and found the chimeric virus WIV1-Rs4231S also readily replicated in HeLa cells expressing human ACE2 molecule. The novel live SARSr-CoV we isolated in the current study (Rs4874) has an S gene almost identical to that of WIV16. As expected, it is also capable of utilizing human ACE2. These results indicate that diverse variants of SARSr-CoV S protein without deletions in their RBD are able to use human ACE2. In contrast, our previous study revealed that the S protein of a *R. sinicus* SARSr-CoV with deletions (Rp3) failed to use human, civet and bat ACE2 for cell entry [34]. In this study, in addition to Rs4231 and Rs7327, we also constructed infectious clones with the S gene of Rs4081, Rf4075, Rs4085, Rs4235 and As6526, which all contained the deletions in their RBD. These 7 strains, plus Rs4874 and the previously studied WIV1 and RsSHC014, could represent all types of S variants of SARSr-CoVs in this location (S3A Fig). However, none of the strains

with deletions in the RBD could be rescued from Vero E6 cells. Therefore, the two distinct clades of SARSr-CoV S gene may represent the usage of different receptors in their bat hosts.

The full-length ORF8 protein of SARS-CoV is a luminal endoplasmic reticulum (ER) membrane-associated protein that induces the activation of ATF6, an ER stress-regulated transcription factor that activates the transcription of ER chaperones involved in protein folding [35]. We amplified the ORF8 genes of Rf1, Rf4092 and WIV1, which represent three different genotypes of bat SARSr-CoV ORF8 (S3C Fig), and constructed the expression plasmids. All of the three ORF8 proteins transiently expressed in HeLa cells can stimulate the ATF6-dependent transcription. Among them, the WIV1 ORF8, which is highly divergent from the SARS-CoV ORF8, exhibited the strongest activation. The results indicate that the variants of bat SARSr-CoV ORF8 proteins may play a role in modulating ER stress by activating the ATF6 pathway. In addition, the ORF8a protein of SARS-CoV from the later phase has been demonstrated to induce apoptosis [28]. In this study, we have found that the ORF8a protein of the newly identified SARSr-CoV Rs4084, which contained an 8-aa insertion compared with the SARS-CoV ORF8a, significantly triggered apoptosis in 293T cells as well.

Compared with the 154-aa ORF3b of SARS-CoV, the ORF3b proteins of all previously identified bat SARSr-CoVs were smaller in size due to the early translation termination. However, for the first time, we discovered an ORF3b without the C-terminal truncation in a bat SARSr-CoV, Rs7327, which differed from the ORF 3b of SARS-CoV GZ02 strain at only one aa residue. The SARS-CoV ORF3b antagonizes interferon function by modulating the activity of IFN regulatory factor 3 (IRF3) [27]. As previous studies suggested, the nuclear localization signal-containing C-terminal may not be required for the IFN antagonist activity of ORF3b [36]. Our previous studies also demonstrated that the ORF3b protein of a bat SARSr-CoV, termed Rm1, which was C-terminally truncated to 56 aa and shared 62% aa sequence identity with SARS-CoV, still displayed the IFN antagonist activity [37]. It is very interesting to investigate in further studies whether Rs7327's ORF3b and other versions of truncated ORF3b such as WIV1 and WIV16 also show IFN antagonism profiles.

As a whole, our findings from a 5-year longitudinal study conclusively demonstrate that all building blocks of the pandemic SARS-CoV genome are present in bat SARSr-CoVs from a single location in Yunnan. The data show that frequent recombination events have happened among those SARSr-CoVs in the same cave. While we cannot rule out the possibility that similar gene pools of SARSr-CoVs exist elsewhere, we have provided sufficient evidence to conclude that SARS-CoV most likely originated from horseshoe bats via recombination events among existing SARSr-CoVs. In addition, we have also revealed that various SARSr-CoVs capable of using human ACE2 are still circulating among bats in this region. Thus, the risk of spillover into people and emergence of a disease similar to SARS is possible. This is particularly important given that the nearest village to the bat cave we surveyed is only 1.1 km away, which indicates a potential risk of exposure to bats for the local residents. Thus, we propose that monitoring of SARSr-CoV evolution at this and other sites should continue, as well as examination of human behavioral risk for infection and serological surveys of people, to determine if spillover is already occurring at these sites and to design intervention strategies to avoid future disease emergence.

Materials and methods

Ethics statement

All sampling procedures were performed by veterinarians with approval from Animal Ethics Committee of the Wuhan Institute of Virology (WIVH05210201). The study was conducted in accordance with the Guide for the Care and Use of Wild Mammals in Research of the People's Republic of China.

Sampling

Bat samplings were conducted ten times from April 2011 to October 2015 at different seasons in their natural habitat at a single location (cave) in Kunming, Yunnan Province, China. All members of field teams wore appropriate personal protective equipment, including N95 masks, tear-resistant gloves, disposable outerwear, and safety glasses. Bats were trapped and fecal swab samples were collected as described previously [9]. Clean plastic sheets measuring 2.0 by 2.0 m were placed under known bat roosting sites at about 18:00 h each evening for collection of fecal samples. Fresh fecal pellets were collected from sheets early in the next morning. Each sample (approximately 1 gram of fecal pellet) was collected in 1ml of viral transport medium composed of Hank's balanced salt solution at pH7.4 containing BSA (1%), amphotericin (15 μg/ml), penicillin G (100 units/ml), and streptomycin (50 μg/ml), and were stored at -80˚C until processing. Bats trapped for this study were released back into their habitat.

RNA extraction, PCR screening and sequencing

Fecal swab or pellet samples were vortexed for 1 min, and 140 μl of supernatant was collected from each sample after centrifuge at 3000 rpm under 4˚C for 1min. Viral RNA was extracted with Viral RNA Mini Kit (Qiagen) following the manufacturer's instructions. RNA was eluted in 60 μl of buffer AVE (RNase-free water with 0.04% sodium azide, Qiagen), aliquoted, and stored at -80˚C. One-step hemi-nested RT-PCR (Invitrogen) was employed to detect the presence of coronavirus sequences as described previously using a set of primers that target a 440-nt fragment in the RNA-dependent RNA polymerase gene (*RdRp*) of all known alpha- and betacoronaviruses [20]. For the first round PCR, the 25 μl reaction mix contained 12.5 μl PCR 2 × reaction mix buffer, 10 pmol of each primer, 2.5 mM $MgSO_4$, 20 U RNase inhibitor, 1 μl SuperScript III/Platinum Taq Enzyme Mix and 5 μl RNA template. The amplification was performed as follows: 50˚C for 30 min, 94˚C for 2 min, followed by 40 cycles consisting of 94˚C for 15 sec, 52˚C for 30 sec, 68˚C for 40 sec, and a final extension of 68˚C for 5 min. For the second round PCR, the 25 μl reaction mix contained 2.5 μl PCR reaction buffer, 5 pmol of each primer, 50 mM $MgCl_2$, 0.5mM dNTP, 0.1 μl Platinum Taq Enzyme (Invitrogen) and 1 μl product of the first round PCR. The amplification was performed as follows: 94˚C for 3 min followed by 35 cycles consisting of 94˚C for 30 sec, 52˚C for 30 sec, 72˚C for 40 sec, and a final extension of 72˚C for 7 min. The RBD region was amplified using the one-step nested RT-PCR method previously described [17].

PCR products were gel purified and sequenced with an ABI Prism 3730 DNA analyzer (Applied Biosystems, USA). PCR products with low concentration or generating heterogeneity in the sequencing chromatograms were cloned into pGEM-T Easy Vector (Promega) for sequencing. The positive samples in this study were termed using the abbreviated name of bat species plus the sample ID number (e.g. Rs4081). To confirm the bat species of individual sample, PCR amplification of cytochrome b (*Cytob*) or NADH dehydrogenase subunit 1 (*ND1*) gene was performed using DNA extracted from the feces or swabs [38,39].

Sequencing of full-length genomes

Full genomic sequences of 11 SARSr-CoVs were determined by One-step PCR (Invitrogen) amplification of overlapping genomic fragments with degenerate primers designed by multiple alignment of available SARS-CoV and bat SARSr- CoV sequences deposited in GenBank, and additional specific primers designed from the results of previous rounds of sequencing in this study. Primer sequences are available upon request. Sequences of the 5' and 3' genomic ends were obtained by 5' and 3' RACE (Roche), respectively. PCR products with expected size were gel-purified and subjected directly to sequencing. Each fragment was sequenced at least twice.

The sequencing chromatogram of each product was thoroughly examined and sequence heterogeneity was not observed. For some fragments with low concentration of amplicons, the PCR products were cloned into pGEM-T Easy Vector (Promega) for sequencing. At least five independent clones were sequenced to obtain a consensus sequence. Co-presence of sequences of distinct SARSr-CoVs was not found in any of the amplicons. The sequences of overlapping genomic fragments were assembled to obtain the full-length genome sequences, with each overlapping sequence longer than 100 bp.

Evolution analysis

Full-length genome sequences of the 15 SARSr-CoVs detected from bats in the cave surveyed in this study were aligned with those of selected SARS-CoVs using MUSCLE [40]. The aligned sequences were scanned for recombination events by Recombination Detection Program (RDP) [41]. The potential recombination events suggested by strong *P* values ($<10^{-20}$) were further confirmed using similarity plot and bootscan analyses implemented in Simplot 3.5.1 [42]. Phylogenetic trees based on nucleotide sequences were constructed using the Maximum Likelihood algorithm under the LG model with bootstrap values determined by 1000 replicates in the PhyML (version 3.0) software package [43].

Virus isolation

The Vero E6 cell line was kindly provided by Australian Animal Health Laboratory, CSIRO (Geelong, Australia). Vero E6 monolayer was maintained in DMEM medium supplemented with 10% fetal calf serum (FCS). Fecal samples (in 200 μl buffer) were gradient centrifuged at 3,000–12,000 g, and the supernatant was diluted 1:10 in DMEM before being added to Vero E6 cells. After incubation at 37˚C for 1 h, the inoculum was removed and replaced with fresh DMEM medium with 2% FCS. The cells were incubated at 37˚C and checked daily for cytopathic effect. All tissue culture media were supplemented with triple antibiotics penicillin/streptomycin/amphotericin (Gibco) (penicillin 200 IU/ml, streptomycin 0.2 mg/ml, amphotericin 0.5 μg/ml). Three blind passages were carried out for each sample. After each passage, both the culture supernatant and cell pellet were examined for presence of SARSr-CoV by RT-PCR using specific primers targeting the RdRp or S gene. The viruses which caused obvious cytopathic effect and could be detected in three blind passages by RT-PCR were further confirmed by electron microscopy.

Construction of recombinant viruses

Recombinant viruses with the S gene of the novel bat SARSr-CoVs and the backbone of the infectious clone of SARSr-CoV WIV1 were constructed using the reverse genetic system described previously [23] (S9 Fig). The fragments E and F were re-amplified with primer pairs (FE, 5'-AGGGCCCACCTGGCACTGGTAAGAGTCATTTTGC-3', R-EsBsaI, 5'-ACTGGTCTCTTCGTTTAGTTATTAACTAAAATATCACTAGACACC-3') and (F-FsBsaI, 5'-TGAGGTCTCCGAACTTATGGATTTGTTTATGAG-3', RF, 5'-AGGTAGGCCTCTAGGGCAGCTAAC-3'), respectively. The products were named as fragment Es and Fs, which leave the spike gene coding region as an independent fragment. BsaI sites (5'-GGTCTCN|NNNN-3') were introduced into the 3' terminal of the Es fragment and the 5' terminal of the Fs fragment, respectively. The spike sequence of Rs4231 was amplified with the primer pair (F-Rs4231-BsmBI, 5'-AGTCGTCTCAACGAACATGTTTATTTTCTTATTCTTTCTCACTCTCAC-3' and R-Rs4231-BsmBI, 5'-TCACGTCTCAGTTCGTTTATGTGTAATGTAATTTGACACCCTTG-3'). The S gene sequence of Rs7327 was amplified with primer pair (F-Rs7327-BsaI, 5'-AGTGGTCTCAACGAACATGAAATTGTTAGTTTTAGTTTTTGCTAC-3' and R-

Rs7327-BsaI, 5'- TCAGGTCTCAGTTCGTTTATGTGTAATGTAATTTAACACCCTTG-3'). The fragment Es and Fs were both digested with BglI (NEB) and BsaI (NEB). The Rs4231 S gene was digested with BsmBI. The Rs7327 S gene was digested with BsaI. The other fragments and bacterial artificial chromosome (BAC) were prepared as described previously. Then the two prepared spike DNA fragments were separately inserted into BAC with Es, Fs and other fragments. The correct infectious BAC clones were screened. The chimeric viruses were rescued as described previously [23].

Determination of virus infectivity by immunofluorescence assay

The HeLa cell line was kindly provided by Australian Animal Health Laboratory, CSIRO (Geelong, Australia). HeLa cells expressing human ACE2 were constructed as described previously [17]. HeLa cells expressing human ACE2 and Vero E6 cells were cultured on coverslips in 24-well plates (Corning) incubated with the newly isolated or recombinant bat SARSr-CoVs at a multiplicity of infection (MOI) = 1.0 for 1h. The inoculum was removed and the cells were washed twice with PBS and supplemented with medium. Vero E6 cells without virus inoculation and HeLa cells without ACE2 were used as negative control. Twenty-four hours after infection, cells were rinsed with PBS and fixed with 4% formaldehyde in PBS (pH7.4) at 4˚C for 20 min. ACE2 expression was detected by using goat anti-human ACE2 immunoglobulin followed by FITC-labelled donkey anti-goat immunoglobulin (PTGLab). Virus replication was detected by using rabbit antibody against the nucleocapsid protein of bat SARSr-CoV Rp3 followed by Cy3-conjugated mouse anti-rabbit IgG. Nuclei were stained with DAPI. Staining patterns were observed under an FV1200 confocal microscope (Olympus).

Determination of virus replication in Vero E6 cells by plaque assay

Vero E6 cells were infected with WIV1, Rs4874, WIV1-Rs4231S, and WIV1-Rs7327S at an MOI of 1.0 and 0.01. After incubation for an hour, the cells were washed with DHanks for three times and supplied with DMEM containing 2% FCS. Samples were collected at 0, 10, 27, and 48 h post infection. The viral titers were determined by plaque assay.

Determination of virus replication in HeLa cells expressing human ACE2 by quantitative RT-PCR

HeLa cells expressing human ACE2 were inoculated with WIV1, Rs4874, WIV1-Rs4231S, and WIV1-Rs7327S at an MOI of 1.0, and were incubated for 1h at 37˚C. After the inoculum was removed, the cells were supplemented with medium containing 1% FBS. Supernatants were collected at 0, 12, 24 and 48h. Virus titers were determined using quantitative RT-PCR targeting the partial N gene with a standard curve which expresses the correlation between Ct value and virus titer (shown as TCID50/ml). The standard curve was made using RNA dilutions from the purified Rs4874 virus stock (with a titer of 2.15×10^6 TCID50/ml). For qPCR, RNA was extracted from 140 μl of each supernatant with Viral RNA Mini Kit (Qiagen) following manufacturer's instructions and eluted in 60 μl AVE buffer. The PCR was performed with the TaqMan AgPath-ID One-Step RT–PCR Kit (Applied Biosystems) in a 25 μl reaction mix containing 4 μl RNA, 1 × RT–PCR enzyme mix, 1 × RT–PCR buffer, 40 pmol forward primer (5'-GTGGTGGTGACGGCA AAATG-3'), 40 pmol reverse primer (5'-AAGTGAAGCTTCTGG GCCAG-3') and 12 pmol probe (5'-FAM-AAAGAGCTCAGCCCCAGATG-BHQ1-3'). The amplification was performed as follows: 50˚C for 10 min, 95˚C for 10 min followed by 50 cycles consisting of 95˚C for 15 sec and 60˚C for 20 sec.

Plasmids

The ORF8 genes of bat SARSr-CoV WIV1 and Rf4092 and the ORF8a gene of bat SARSr-CoV Rs4084 were amplified by PCR from the viral RNA extracted from the isolated virus or fecal samples. The ORF8 gene of SARS-CoV GZ02 and bat SARSr-CoV Rf1, and the ORF8a gene of SARS-CoV Tor2 were synthesized by Tsingke Biological Technology Co., Ltd (Wuhan, China). All genes were cloned into the pCAGGS vector constructed with a C-terminal HA tag. Expression of the proteins was confirmed by Western blotting using a mAb against the HA tag. Five tandem copies of the ATF6 consensus binding sites were synthesized and inserted into the pGL3-Basic vector to construct the luciferase reporter plasmid 5×ATF6-GL3, in which the luciferase gene is under the control of the c-*fos* minimal promoter and the ATF6 consensus binding sites.

Luciferase reporter assay

HeLa cells in 24-well plates were transfected using Lipofectamine 3000 reagent (Life Technologies) following the manufacturer's instruction. Cells per well were co-transfected with 600ng of the 5×ATF6-GL3 reporter plasmid, with 300ng of each expression plasmid of SARS-CoV and SARSr-CoV ORF8 or empty vector and 20ng of pRL-TK (Promega) which served as an internal control. The cells were incubated for 24h, and were treated with or without 2μg/ml tunicamycin for 16h. Cells were harvested and lysed. Luciferase activity was determined using a dual-luciferase assay system (Promega). The experiment was performed in triplicate wells.

Quantification of apoptotic cells

293T cells in 12-well plates were transfected using Lipofectamine 3000 reagent (Life Technologies) following the manufacturer's instruction. Cells per well were transfected with 3μg of the expression plasmid of SARS-CoV Tor2 or SARSr-CoV Rs4084 ORF8a, or the empty vector. 24h post transfection, apoptotic cells were quantified by using the Annexin V-fluorescein isothiocyanate (FITC)/PI Apoptosis Detection Kit (Yeasen Biotech, Shanghai) in accordance with the manufacturer's instruction. Apoptosis was analyzed by flow cytometry. The experiment was performed in triplicate wells.

Accession numbers

The complete genome sequences of bat SARS-related coronavirus strains As6526, Rs4081, Rs4084, Rf4092, Rs4231, Rs4237, Rs4247, Rs4255, Rs4874, Rs7327 and Rs9401 have been deposited in the GenBank database with the accession numbers from KY417142 to KY417152, respectively.

Supporting information

S1 Fig. Alignment of amino acid sequences of the receptor-binding motif (corresponding to aa 424–495 of SARS-CoV S protein). Two clades of the SARSr-CoVs identified from bats in the studied cave are indicated with vertical lines on the left.
(PPTX)

S2 Fig. Alignment of nucleotide sequences of a genomic region covering ORF6 to ORF7a. ORFX is located between ORF6 and ORF7a in the genomes of WIV1, WIV16, Rs7327 and Rs4874. The start codon and stop codon of ORFX are marked with red boxes. The deletion responsible for the long ORFX in Rs7327 and Rs4874 is marked with the blue box.
(PPTX)

S3 Fig. Phylogenetic analyses based on nucleotide sequences of the S gene (A), ORF3a (B) and ORF8 (C). The trees were constructed by the maximum likelihood method using the LG model with bootstrap values determined by 1000 replicates. Only bootstraps > 50% are shown. Rs, *Rhinolophus sinicus*; Rf, *Rhinolophus ferremequinum*; Rm, *Rhinolophus macrotis*; Ra, *Rhinolophus affinis*; Rp, *Rhinolophus pusillus*; As, *Aselliscus stoliczkanus*; Cp, *Chaerephon plicata*. SARSr-CoVs detected in bats from the single cave surveyed in this study are in bold.
(PPTX)

S4 Fig. Alignment of amino acid sequences of ORF3b protein.
(PPTX)

S5 Fig. Detection of potential recombination events by similarity plot and boot scan analysis. (A) Full-length genome sequence of SARSr-CoV Rs4084 was used as query sequence and RsSHC014, Rf4092 and Rs4081 as reference sequences. (B) Full-length genome sequence of SARSr-CoV Rs4237 was used as query sequence and SARSr-CoV Rs4247, Rs4081 and Rs3367 as reference sequences. All analyses were performed with a Kimura model, a window size of 1500 base pairs, and a step size of 150 base pairs.
(PPTX)

S6 Fig. Chinese provinces where bat SARSr-CoVs have been detected.
(PPTX)

S7 Fig. The successful or failed rescue of the chimeric SARSr-CoVs. (A) Cytopathic effects in Vero E6 cells transfected with the infectious BAC clones constructed with the backbone of WIV1 and various S genes of different bat SARSr-CoV strains. Microphotographs were taken 24 hours post transfection. (B) The culture media supernatant collected from the cells transfected with the infectious BAC clones was used to infect Vero E6 cells. Immunofluorescent assay (IFA) was performed to detect infection and viral replication. Cells were fixed 24 hours post infection, and stained using rabbit antibody against the SARSr-CoV Rp3 nucleocapsid protein and a Cy3-conjugated anti-rabbit IgG.
(PPTX)

S8 Fig. Quantification of SARSr-CoV in individual bat fecal samples. The number of genome copies of SARSr-CoV per gram of bat feces was determined by quantitative real-time PCR targeting the RdRp gene. Samples from which the SARSr-CoV RBD sequences were successfully amplified are indicated in red.
(PPTX)

S9 Fig. Spike substitution strategy. The original fragments E and F were shortened to leave spike gene as an independent fragment. The new fragments were designated as Es and Fs. BsaI or BsmBI sites were introduced into the junctions of Es/Spike and Spike/Fs. Then any spike could be substituted into the genome of SARSr-CoV WIV1 through this strategy.
(TIF)

S1 Table. Comparison of the novel bat SARSr-CoVs identified in this study with human/civet SARS-CoVs and previously described bat SARSr-CoVs.
(DOCX)

S2 Table. Distribution of SARSr-CoVs highly similar to SARS-CoV in the variable S, ORF3 and ORF8 genes in the single cave.
(DOCX)

S1 Dataset. Full-length genome sequences of bat SARSr-CoVs newly identified in this study.
(FAS)

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Author Contributions

Conceptualization: Lin-Fa Wang, Jie Cui, Zheng-Li Shi.

Data curation: Ben Hu.

Formal analysis: Ben Hu, Xing-Yi Ge, Jie Cui.

Funding acquisition: Peter Daszak, Lin-Fa Wang, Jie Cui, Zheng-Li Shi.

Investigation: Ben Hu, Lei-Ping Zeng, Xing-Lou Yang, Wei Zhang, Bei Li, Jia-Zheng Xie, Xu-Rui Shen, Ning Wang, Dong-Sheng Luo, Xiao-Shuang Zheng.

Methodology: Lei-Ping Zeng, Zheng-Li Shi.

Project administration: Zheng-Li Shi.

Resources: Xing-Lou Yang, Xing-Yi Ge, Yun-Zhi Zhang, Dong-Sheng Luo, Mei-Niang Wang.

Software: Jie Cui.

Supervision: Zheng-Li Shi.

Validation: Ben Hu.

Visualization: Ben Hu, Zheng-Li Shi.

Writing – original draft: Ben Hu.

Writing – review & editing: Peter Daszak, Lin-Fa Wang, Jie Cui, Zheng-Li Shi.

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From: (b) (6)
To: Collins, Francis (NIH/OD) [E]; Tabak, Lawrence (NIH/OD) [E]; Wolinetz, Carrie (NIH/OD) [E]; Lauer, Michael (NIH/OD) [E]; McManus, Ayanna (NIH/OD) [E]
Subject: ECCO Health Discussion
Attachments: NIH Response to EcoHealth Response to Suspension_10_23_20.pdf
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Francis Collins is inviting you to a scheduled ZoomGov meeting.

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DEPARTMENT OF HEALTH & HUMAN SERVICES

Public Health Service

National Institutes of Health
National Institute of Allergy
and Infectious Diseases
Bethesda, Maryland 20892

23 October 2020

Drs. Aleksei Chmura and Peter Daszak
EcoHealth Alliance, Inc.
460 W 34th St
Suite 1701
New York, NY 10001

Re: NIH Grant R01AI110964

Dear Drs. Chmura and Daszak:

I am following up on Mr. Krinsky's August 13, 2020, letter on behalf of EcoHealth Alliance, Inc. ("EcoHealth") responding to NIH's suspension of grant R01AI110964, which funds the project *Understanding the Risk of Bat Coronavirus Emergence* (the "Project"). Per my letter of July 8, 2020, NIH reinstated the grant but suspended all award activities because we have concerns that the Wuhan Institute of Virology (WIV), which previously served as a subrecipient of the Project, had not satisfied safety requirements that applied to its subawards with EcoHealth, and that EcoHealth had not satisfied its obligations to monitor the activities of its subrecipient to ensure compliance. EcoHealth objected to the suspension on the grounds that WIV has no *current* connection to the Project or EcoHealth's research, and EcoHealth had not issued any subawards in connection with the Grant *at the time of the suspension*.

The fact that EcoHealth does not currently have a subrecipient relationship with WIV and had not issued subawards to WIV at the time of suspension does not absolve EcoHealth of any past non-compliance with the terms and conditions of award for grant R01AI110964. While EcoHealth did not issue a subaward to WIV for year 6 of the grant, WIV served as a subrecipient for years 1 through 5. NIH awarded EcoHealth grant R01AI110964 in 2014, with a project period of June 1, 2014, through June 30, 2024, as renewed. In EcoHealth's grant application, EcoHealth listed Drs. Zheng Li Shi and Xing Yi Ge of WIV as co-investigators and senior/key personnel. It stated that "Drs. Shi, Zhang, and Daszak have collaborated together since 2002 and have been involved in running joint conferences, and shipping samples into and out of China." EcoHealth listed WIV as a Project/Performance Site Location. In describing WIV's facilities, EcoHealth described WIV as China's premier institute for virological research" and touted WIV's "fully equipped biosafety level 3 laboratory" and "a newly opened BLS-4 laboratory." In support of the application, Dr. Zheng Li Shi's personal statement indicated that "My lab will be responsible for diagnosis, genomics and isolation of coronavirus from wild and domestic animals in Southern China and for analyzing their receptor binding domains." The application stated that "Wuhan Institute of Virology and the Wuhan University Center for Animal Experiment BSL-3

lab have an Internal Biosafety Committee and are accredited BSL-2 and BSL 3 laboratories. All experimental work using infectious material will be conducted under appropriate biosafety standards. Disposal of hazardous materials will be conducted according to the institutional biosafety regulations."

EcoHealth requested funding specifically for activities to be carried out by WIV. NIH awarded EcoHealth a total of $749,976 for WIV's work in the following annual amounts for years 1 through 5:

	-Yr 1	-Yr 2	-Yr 3	-Yr 4	-Yr 5
Total Direct Costs	$123,699	$128,718	$147,335	$147,335	$147,335
F&A Costs @ 8%	$9,896	$10,297	$11,787	$11,787	$11,787
TOTAL COSTS	$133,595	$139,015	$159,122	$159,122	$159,122

As stated in the Notices of Award for each budget period of the grant, the awards were subject to terms and conditions, which include the NIH Grants Policy Statement (GPS) and applicable HHS grant regulations. As I indicated in my letter of July 8, 2020, as a term and condition of award EcoHealth was required to "monitor the activities of the subrecipient as necessary to ensure that the subaward is used for authorized purposes, in compliance with Federal statutes, regulations, and the terms and conditions of the subaward . . ." 45 C.F.R. § 75.352(d). See also, 45 C.F.R. § 75.342(a) ("The non-Federal entity is responsible for oversight of the operations of the Federal award supported activities."). Moreover, EcoHealth was required to "Establish and maintain effective internal control over the Federal award that provides reasonable assurance that the non-Federal entity is managing the Federal award in compliance with Federal statutes, regulations, and the terms and conditions of the Federal award[.]" 45 C.F.R. § 75.303(a). The Notice of Award stated that as a term and condition of award, "Research funded under this grant must adhere to the [CDC/NIH Biosafety in Microbiological and Biomedical Laboratories (BMBL)]." Moreover, the NIH GPS provides that NIH grant recipients are expected to provide safe working conditions for their employees and foster work environments conducive to high-quality research. NIH GPS, Section 4. The terms and conditions of the grant award flow down to subawards to subrecipients, so these terms applied to WIV. 45 C.F.R. § 75.101.

As I stated, NIH has concerns of non-compliance with terms and conditions of award—namely, that WIV had not satisfied safety requirements under the award and that EcoHealth Alliance had not satisfied its obligations to monitor the activities of its subrecipient to ensure compliance. Accordingly, NIH suspended all activities related to R01AI110964, pursuant to 45 C.F.R. § 75.371, Remedies for Noncompliance, which permits suspension of award activities in cases of non-compliance, and the NIH GPS, Section 8.5.2, which permits NIH to take immediate action to suspend a grant when necessary to protect the public health and welfare.

In my letter of July 8, 2020, I provided EcoHealth with the opportunity to object and to provide information and documentation challenging the suspension. Specifically, I sought information and materials that speak to WIV's lab safety and EcoHealth's oversight of its subrecipient, and an inspection of WIV's laboratory records and facilities. I indicated that as a specific condition of award, during the period of suspension, EcoHealth Alliance may not allow research under this

project to be conducted and that no funds from grant R01AI110964 may be provided to or expended by EcoHealth Alliance or any subrecipients.

EcoHealth objected to the requests on the grounds that "NIAID is not authorized under 45 CFR§§ 75.371, 75.205, and 75.207, entitled *Specific Award Conditions*, to impose, *inter alia*, conditions that consist of demands for information regarding entities that are neither subrecipients of grant funds nor project affiliates."

These provisions are irrelevant to NIH's requests. NIH is required to permit the opportunity for recipients to object and provide information and documentation challenging a suspension, 45 C.F.R. § 75.374, so we specifically gave EcoHealth the opportunity to provide information that speaks to NIH's concerns. Moreover, as a granting agency, NIH is required to "manage and administer the Federal award in a manner so as to ensure that Federal funding is expended and associated programs are implemented in full accordance with U.S. statutory and public policy requirements: Including, but not limited to, those protecting public welfare [and] the environment[.]" 45 C.F.R. § 75.300(a). In addition to seeking information that speaks to compliance with terms and conditions of award, NIH is entitled to "make site visits as warranted by program needs." 45 C.F.R. § 75.342. As a term and condition of award, NIH "must have the right of access to any documents, papers, or other records of the non-Federal entity which are pertinent to the Federal award, in order to make audits, examinations, excerpts, and transcripts" (45 C.F.R. § 75.364); and must have "timely and reasonable access to the non-Federal entity's personnel for the purpose of interview and discussion related to such documents" (id.). These requirements flow down to subawards to subrecipients. 45 C.F.R. § 75.101. "Non-Federal entities must comply with requirements in [45 C.F.R. Part 75] regardless of whether the non-Federal entity is a recipient or subrecipient of a Federal award." 45 C.F.R. 75.101. As the grantee, EcoHealth was required to have in place, "A requirement that the subrecipient permit the pass-through entity and auditors to have access to the subrecipient's records and financial statements as necessary for the pass-through entity to meet the requirements of this part." 45 C.F.R. § 75.352(a)(5). For each of these reasons, NIH is justified in seeking the materials, information, and a site visit specified in my letter of July 8, 2020.

In addition to objecting to NIH's authority to seek the materials, information, and a site visit, EcoHealth has responded that it lacks knowledge or information regarding the requests; that it is not in possession, custody, or control of the specified items; and that it has no authority to grant NIAID and the U.S. National Academy of Sciences access to WIV's facility to conduct an inspection. EcoHealth's responses have not satisfied NIH's concerns that EcoHealth had failed to adequately monitor the compliance of its subrecipient, and that the subrecipient, WIV, had failed to comply with safety requirements.

Notwithstanding this, NIH is providing an additional opportunity for EcoHealth to provide information and documentation challenging these concerns of non-compliance. Accordingly, in addition to reiterating our prior requests (1) through (6) per our letter of July 8, 2020, NIH requests the following information and materials, which must be complete and accurate:

1. Provide copies of all EcoHealth Alliance – WIV subrecipient agreements as well as any other documents and information describing how EcoHealth Alliance monitored WIV's compliance with the terms and conditions of award, including with respect to biosafety.
2. Describe EcoHealth's efforts to evaluate WIV's risk of noncompliance with Federal statutes, regulations, and the terms and conditions of the subaward.
3. Provide copies of all WIV biosafety reports from June 1, 2014 through May 31, 2019.

During the ongoing period of suspension, NIH will continue to review the activities under this award, taking into consideration information provided by EcoHealth Alliance, to further assess whether EcoHealth Alliance and WIV complied with the terms and conditions of award, including compliance with other terms and conditions of award that may be implicated. We remind you that during the period of suspension, EcoHealth Alliance may not allow research under this project to be conducted. Further, no funds from grant R01AI110964 may be provided to or expended by EcoHealth Alliance or any subrecipients; all such charges are unallowable. It is EcoHealth Alliance's responsibility as the recipient of this grant award to ensure that the terms of this suspension are communicated to and understood by all subrecipients. EcoHealth Alliance must provide adequate oversight to ensure compliance with the terms of the suspension. Any noncompliance of the terms of this suspension must be immediately reported to NIH. EcoHealth Alliance will receive a revised Notice of Award from NIAID indicating the continued suspension of these research activities and funding restrictions as a specific condition of award.

Please note that this action does not preclude NIH from taking additional corrective or enforcement actions pursuant to 45 C.F.R. Part 75, including, but not limited to, terminating the grant award or disallowing costs. NIH may also take other remedies that may be legally available if NIH discovers other violations of terms and conditions of award on the part of EcoHealth Alliance or WIV.

Sincerely,

Michael S Lauer, MD
NIH Deputy Director for Extramural Research
Email: (b) (6)

cc: Dr. Erik Stemmy (NIAID)
Ms. Emily Linde (NIAID)

DEPARTMENT OF HEALTH & HUMAN SERVICES

Public Health Service

National Institutes of Health
National Institute of Allergy
and Infectious Diseases
Bethesda, Maryland 20892

8 July 2020

Drs. Aleksei Chmura and Peter Daszak
EcoHealth Alliance, Inc.
460 W 34th St
Suite 1701
New York, NY 10001

Re: NIH Grant R01AI110964

Dear Drs. Chmura and Daszak:

In follow-up to my previous letter of April 24, 2020, I am writing to notify you that the National Institute of Allergy and Infectious Diseases (NIAID), an Institute within the National Institutes of Health (NIH), under the Department of Health and Human Services (HHS), has withdrawn its termination of grant R01AI110964, which supports the project *Understanding the Risk of Bat Coronavirus Emergence*. Accordingly, the grant is reinstated.

However, as you are aware, the NIH has received reports that the Wuhan Institute of Virology (WIV), a subrecipient of EcoHealth Alliance under R01AI110964, has been conducting research at its facilities in China that pose serious bio-safety concerns and, as a result, create health and welfare threats to the public in China and other countries, including the United States. Grant award R01AI110964 is subject to biosafety requirements set forth in the NIH Grants Policy Statement (e.g., NIH GPS, Section 4.1.24 "Public Health Security") and the Notice of Award (e.g., requiring that "Research funded under this grant must adhere to the [CDC/NIH Biosafety in Microbiological and Biomedical Laboratories (BMBL)]."). Moreover, NIH grant recipients are expected to provide safe working conditions for their employees and foster work environments conducive to high-quality research. NIH GPS, Section 4. The terms and conditions of the grant award flow down to subawards to subrecipients. 45 C.F.R. § 75.101.

As the grantee, EcoHealth Alliance was required to "monitor the activities of the subrecipient as necessary to ensure that the subaward is used for authorized purposes, in compliance with Federal statutes, regulations, and the terms and conditions of the subaward . . ." 45 C.F.R. § 75.352(d). We have concerns that WIV has not satisfied safety requirements under the award, and that EcoHealth Alliance has not satisfied its obligations to monitor the activities of its subrecipient to ensure compliance.

Moreover, as we have informed you through prior Notices of Award, this award is subject to the Transparency Act subaward and executive compensation reporting requirement of 2 C.F.R. Part

170. To date you have not reported any subawards in the Federal Subaward Reporting System.

Therefore, effective the date of this letter, July 8, 2020, NIH is suspending all activities related to R01AI110964, until such time as these concerns have been addressed to NIH's satisfaction. This suspension is taken in accordance with 45 C.F.R. § 75.371, Remedies for Noncompliance, which permits suspension of award activities in cases of non-compliance, and the NIH GPS, Section 8.5.2, which permits NIH to take immediate action to suspend a grant when necessary to protect the public health and welfare. This action is not appealable in accordance with 42 C.F.R. § 50.404 and the NIH GPS Section 8.7, Grant Appeals Procedures. However, EcoHealth Alliance has the opportunity to provide information and documentation demonstrating that WIV and EcoHealth Alliance have satisfied the above-mentioned requirements.

Specifically, to address the NIH's concerns, EcoHealth must provide the NIH with the following information and materials, which must be complete and accurate:

1. Provide an aliquot of the actual SARS-CoV-2 virus that WIV used to determine the viral sequence.
2. Explain the apparent disappearance of Huang Yanling, a scientist / technician who worked in the WIV lab but whose lab web presence has been deleted.
3. Provide the NIH with WIV's responses to the 2018 U.S. Department of State cables regarding safety concerns.
4. Disclose and explain out-of-ordinary restrictions on laboratory facilities, as suggested, for example, by diminished cell-phone traffic in October 2019, and the evidence that there may have been roadblocks surrounding the facility from October 14-19, 2019.
5. Explain why WIV failed to note that the RaTG13 virus, the bat-derived coronavirus in its collection with the greatest similarity to SARS-CoV-2, was actually isolated from an abandoned mine where three men died in 2012 with an illness remarkably similar to COVID-19, and explain why this was not followed up.
6. Additionally, EcoHealth Alliance must arrange for WIV to submit to an outside inspection team charged to review the lab facilities and lab records, with specific attention to addressing the question of whether WIV staff had SARS-CoV-2 in their possession prior to December 2019. The inspection team should be granted full access to review the processes and safety of procedures of all of the WIV field work (including but not limited to collection of animals and biospecimens in caves, abandoned man-made underground cavities, or outdoor sites). The inspection team could be organized by NIAID, or, if preferred, by the U.S. National Academy of Sciences.
7. Lastly, EcoHealth Alliance must ensure that all of its subawards are fully reported in the Federal Subaward Reporting System

During this period of suspension, NIH will continue to review the activities under this award, taking into consideration information provided by EcoHealth Alliance, to further asses compliance by EcoHealth Alliance and WIV, including compliance with other terms and conditions of award that may be implicated. Additionally, during the period of suspension, EcoHealth Alliance may not allow research under this project to be conducted. Further, no funds from grant R01AI110964 may be provided to or expended by EcoHealth Alliance or any subrecipients; all such charges are unallowable. It is EcoHealth Alliance's responsibility as the

recipient of this grant award to ensure that the terms of this suspension are communicated to and understood by all subrecipients. EcoHealth Alliance must provide adequate oversight to ensure compliance with the terms of the suspension. Any noncompliance of the terms of this suspension must be immediately reported to NIH. Once the original award is reinstated, NIH will take additional steps to restrict all funding in the HHS Payment Management System in the amount of $369,819. EcoHealth Alliance will receive a revised Notice of Award from NIAID indicating the suspension of these research activities and funding restrictions as a specific condition of award.

Please note that this action does not preclude NIH from taking additional corrective or enforcement actions pursuant to 45 CFR Part 75, including, but not limited to, terminating the grant award. NIH may also take other remedies that may be legally available if NIH discovers other violations of terms and conditions of award on the part of EcoHealth Alliance or WIV.

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Sincerely,

Michael S Lauer, MD
NIH Deputy Director for Extramural Research
Email: (b) (6)

cc: Dr. Erik Stemmy
Ms. Emily Linde

The Lab-Leak Hypothesis

Nicholson Baker Jan. 4, 2021

For decades, scientists have been hot-wiring viruses in hopes of preventing a pandemic, not causing one. But what if ...?

By

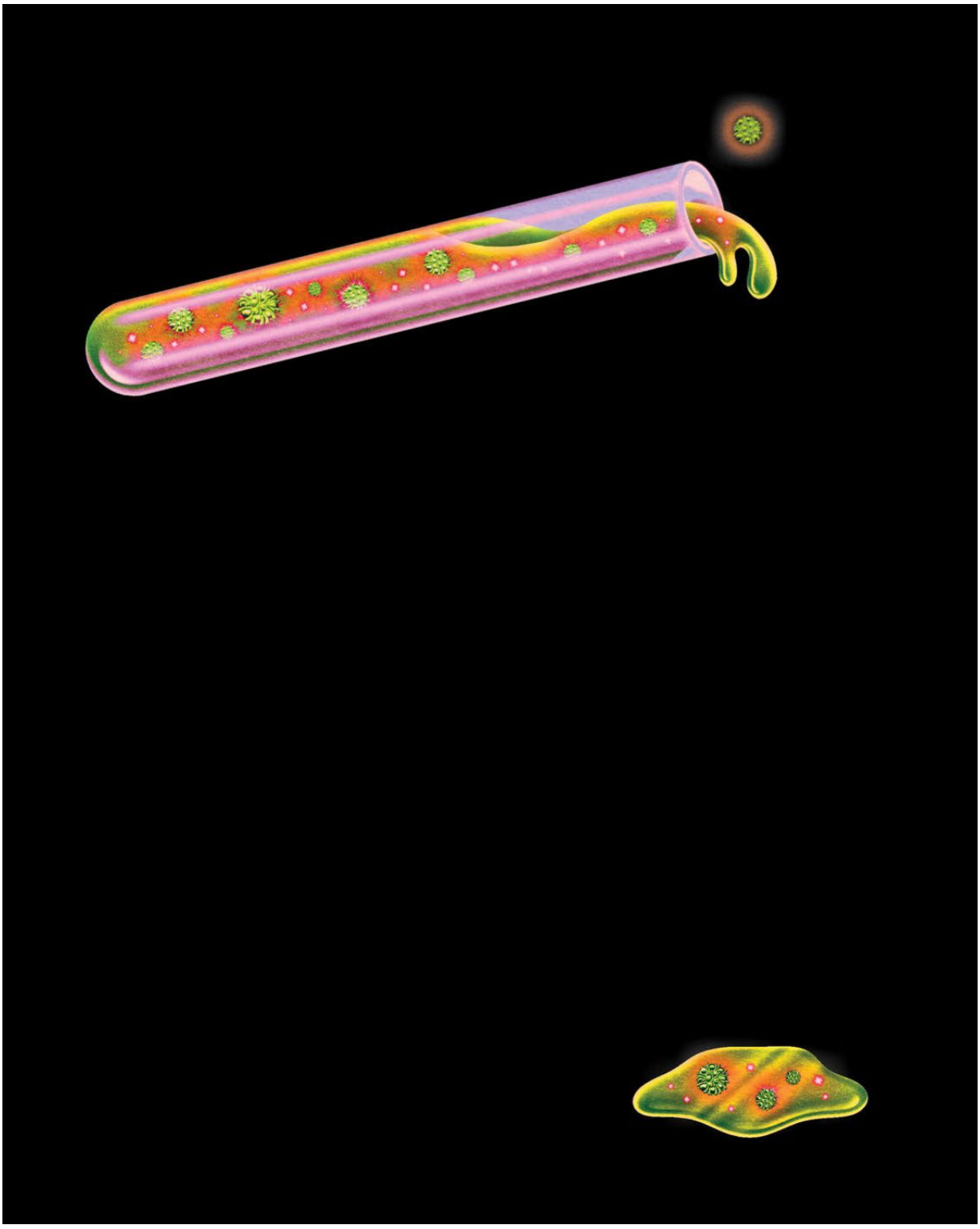

Illustration: Illustration by Robert Beatty for New York Magazine

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I.

Flask Monsters

What happened was fairly simple, I've come to believe. It was an accident. A virus spent some time in a laboratory, and eventually it got out. SARS-CoV-2, the virus that causes COVID-19, began its existence inside a bat, then it learned how to infect people in a claustrophobic mine shaft, and then it was made more infectious in one or more laboratories, perhaps as part of a scientist's well-intentioned but risky effort to create a broad-spectrum vaccine. SARS-2 was not designed as a biological weapon. But it was, I think, designed. Many thoughtful people dismiss this notion, and they may be right. They sincerely believe that the coronavirus arose naturally, "zoonotically," from animals, without having been previously studied, or hybridized, or sluiced through cell cultures, or otherwise worked on by trained professionals. They hold that a bat, carrying a coronavirus, infected some other creature, perhaps a pangolin, and that the pangolin may have already been sick with a different coronavirus disease, and out of the conjunction and commingling of those two diseases within the pangolin, a new disease, highly infectious to humans, evolved. Or they hypothesize that two coronaviruses recombined in a bat, and this new virus spread to other bats, and then the bats infected a person directly — in a rural setting, perhaps — and that this person caused a simmering undetected outbreak of respiratory disease, which over a period of months or years evolved to become virulent and highly transmissible but was not noticed until it appeared in Wuhan.

There is no direct evidence for these zoonotic possibilities, just as there is no direct evidence for an experimental mishap — no written confession, no incriminating notebook, no official accident report. Certainty craves detail, and detail requires an investigation. It has been a full year, 80 million people

have been infected, and, surprisingly, no public investigation has taken place. We still know very little about the origins of this disease.

Nevertheless, I think it's worth offering some historical context for our yearlong medical nightmare. We need to hear from the people who for years have contended that certain types of virus experimentation might lead to a disastrous pandemic like this one. And we need to stop hunting for new exotic diseases in the wild, shipping them back to laboratories, and hot-wiring their genomes to prove how dangerous to human life they might become.

Over the past few decades, scientists have developed ingenious methods of evolutionary acceleration and recombination, and they've learned how to trick viruses, coronaviruses in particular, those spiky hairballs of protein we now know so well, into moving quickly from one species of animal to another or from one type of cell culture to another. They've made machines that mix and mingle the viral code for bat diseases with the code for human diseases — diseases like SARS, severe acute respiratory syndrome, for example, which arose in China in 2003, and MERS, Middle East respiratory syndrome, which broke out a decade later and has to do with bats and camels. Some of the experiments — "gain of function" experiments — aimed to create new, more virulent, or more infectious strains of diseases in an effort to predict and therefore defend against threats that might conceivably arise in nature. The term *gain of function* is itself a euphemism; the Obama White House more accurately described this work as "experiments that may be reasonably anticipated to confer attributes to influenza, MERS, or SARS viruses such that the virus would have enhanced pathogenicity and/or transmissibility in mammals via the respiratory route." The virologists who carried out these experiments have accomplished amazing feats of genetic transmutation, no question, and there have been very few publicized accidents over the years. But there have been some.

And we were warned, repeatedly. The intentional creation of new microbes that combine virulence with heightened transmissibility "poses extraordinary risks to the public," wrote infectious-disease experts Marc Lipsitch and Thomas Inglesby in 2014. "A rigorous and transparent risk-assessment process for this work has not yet been established." That's still true today. In 2012, in *Bulletin of the Atomic Scientists*, Lynn Klotz warned that there was an 80 percent chance, given how many laboratories were then handling virulent viro-varietals, that a leak of a potential pandemic pathogen would occur sometime in the next 12 years.

A lab accident — a dropped flask, a needle prick, a mouse bite, an illegibly labeled bottle — is apolitical. Proposing that something unfortunate happened during a scientific experiment in Wuhan — where COVID-19 was first diagnosed and where there are three high-security virology labs, one of which held in its freezers the most comprehensive inventory of sampled bat viruses in the world — isn't a conspiracy theory. It's just a theory. It merits attention, I believe, alongside other reasoned attempts to explain the source of our current catastrophe.

II.

"A Reasonable Chance"

Seeking Ebola strains in Sierra Leone's wild-animal population for USAID's Predict project in 2018. Photo: Simon Townsley

From early 2020, the world was brooding over the origins of COVID-19. People were reading research papers, talking about what kinds of live animals were or were not sold at the Wuhan seafood market — wondering where the new virus had come from.

Meanwhile, things got strange all over the world. The Chinese government shut down transportation and built hospitals at high speed. There were video clips of people who'd suddenly dropped unconscious in the street. A doctor on YouTube told us how we were supposed to scrub down our produce when we got back from the supermarket. A scientist named Shi Zhengli of the Wuhan Institute of Virology published a paper saying that the novel coronavirus was 96 percent identical to a bat virus, RaTG13, found in

Yunnan province in southern China. On March 13, I wrote in my journal that there seemed to be something oddly artificial about the disease: "It's too airborne — too catching — it's something that has been selected for infectivity. That's what I suspect. No way to know so no reason to waste time thinking about it."

This was just a note to self — at the time, I hadn't interviewed scientists about SARS-2 or read their research papers. But I did know something about pathogens and laboratory accidents; I published a book last year, *Baseless*, that talks about some of them. The book is named after a Pentagon program, Project Baseless, whose goal, as of 1951, was to achieve "an Air Force–wide combat capability in biological and chemical warfare at the earliest possible date."

A vast treasure was spent by the U.S. on the amplification and aerial delivery of diseases — some well known, others obscure and stealthy. America's biological-weapons program in the '50s had A1-priority status, as high as nuclear weapons. In preparation for a total war with a numerically superior communist foe, scientists bred germs to be resistant to antibiotics and other drug therapies, and they infected lab animals with them, using a technique called "serial passaging," in order to make the germs more virulent and more catching.

And along the way, there were laboratory accidents. By 1960, hundreds of American scientists and technicians had been hospitalized, victims of the diseases they were trying to weaponize. Charles Armstrong, of the National Institutes of Health, one of the consulting founders of the American germ-warfare program, investigated Q fever three times, and all three times, scientists and staffers got sick. In the anthrax pilot plant at Camp Detrick, Maryland, in 1951, a microbiologist, attempting to perfect the "foaming process" of high-volume production, developed a fever and died. In 1964,

veterinary worker Albert Nickel fell ill after being bitten by a lab animal. His wife wasn't told that he had Machupo virus, or Bolivian hemorrhagic fever. "I watched him die through a little window to his quarantine room at the Detrick infirmary," she said.

In 1977, a worldwide epidemic of influenza A began in Russia and China; it was eventually traced to a sample of an American strain of flu preserved in a laboratory freezer since 1950. In 1978, a hybrid strain of smallpox killed a medical photographer at a lab in Birmingham, England; in 2007, live foot-and-mouth disease leaked from a faulty drainpipe at the Institute for Animal Health in Surrey. In the U.S., "more than 1,100 laboratory incidents involving bacteria, viruses and toxins that pose significant or bioterror risks to people and agriculture were reported to federal regulators during 2008 through 2012," reported *USA Today* in an exposé published in 2014.
In 2015, the Department of Defense discovered that workers at a germ-warfare testing center in Utah had mistakenly sent close to 200 shipments of live anthrax to laboratories throughout the United States and also to Australia, Germany, Japan, South Korea, and several other countries over the past 12 years. In 2019, laboratories at Fort Detrick — where "defensive" research involves the creation of potential pathogens to defend against — were shut down for several months by the Centers for Disease Control and Prevention for "breaches of containment." They reopened in December 2019.

High-containment laboratories have a whispered history of near misses. Scientists are people, and people have clumsy moments and poke themselves and get bitten by the enraged animals they are trying to nasally inoculate. Machines can create invisible aerosols, and cell solutions can become contaminated. Waste systems don't always work properly. Things can go wrong in a hundred different ways.

Hold that human fallibility in your mind. And then consider the cautious words of Alina Chan, a scientist who works at the Broad Institute of MIT and Harvard. "There is a reasonable chance that what we are dealing with is the result of a lab accident," Chan told me in July of last year. There was also, she added, a reasonable chance that the disease had evolved naturally — both were scientific possibilities. "I don't know if we will ever find a smoking gun, especially if it was a lab accident. The stakes are so high now. It would be terrifying to be blamed for millions of cases of COVID-19 and possibly up to a million deaths by year end, if the pandemic continues to grow out of control. The Chinese government has also restricted their own scholars and scientists from looking into the origins of SARS-CoV-2. At this rate, the origin of SARS-CoV-2 may just be buried by the passage of time."

I asked Jonathan A. King, a molecular biologist and biosafety advocate from MIT, whether he'd thought *lab accident* when he first heard about the epidemic. "Absolutely, absolutely," King answered. Other scientists he knew were concerned as well. But scientists, he said, in general were cautious about speaking out. There were "very intense, very subtle pressures" on them not to push on issues of laboratory biohazards. Collecting lots of bat viruses, and passaging those viruses repeatedly through cell cultures, and making bat-human viral hybrids, King believes, "generates new threats and desperately needs to be reined in."

"All possibilities should be on the table, including a lab leak," a scientist from the NIH, Philip Murphy — chief of the Laboratory of Molecular Immunology — wrote me recently. Nikolai Petrovsky, a professor of endocrinology at Flinders University College of Medicine in Adelaide, Australia, said in an email, "There are indeed many unexplained features of this virus that are hard if not impossible to explain based on a completely natural origin." Richard Ebright, a molecular biologist at Rutgers University, wrote that he'd been concerned for some years about the Wuhan laboratory and about the

work being done there to create "chimeric" (i.e., hybrid) SARS-related bat coronaviruses "with enhanced human infectivity." Ebright said, "In this context, the news of a novel coronavirus in Wuhan ***screamed*** lab release."

III.

"No Credible Evidence"

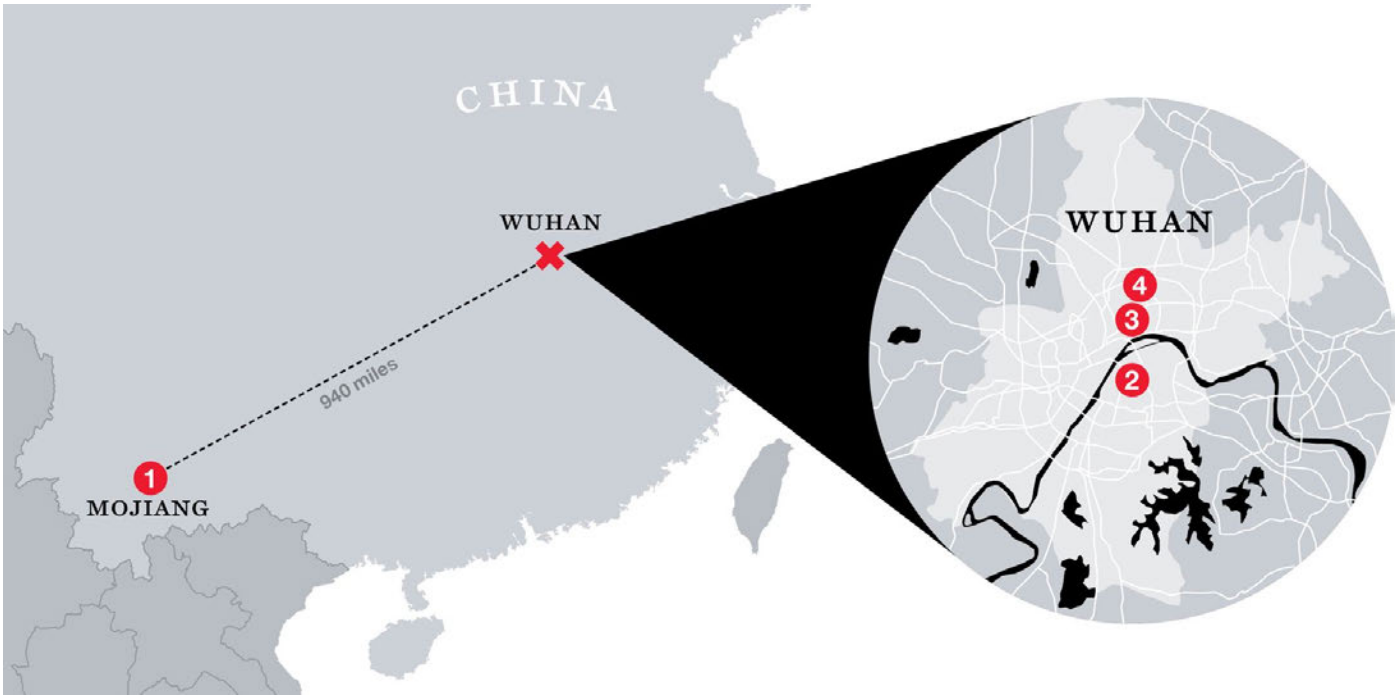
The new disease, as soon as it appeared, was intercepted — stolen and politicized by people with ulterior motives. The basic and extremely interesting scientific question of what happened was sucked up into an ideological sharknado.

Some Americans boycotted Chinese restaurants; others bullied and harassed Asian Americans. Steve Bannon, broadcasting from his living room, in a YouTube series called *War Room*, said that the Chinese Communist Party had made a biological weapon and intentionally released it. He called it the "CCP virus." And his billionaire friend and backer, Miles Guo, a devoted Trump supporter, told a right-wing website that the communists' goal was to "use the virus to infect selective people in Hong Kong, so that the Chinese Communist Party could use it as an excuse to impose martial law there and ultimately crush the Hong Kong pro-democracy movement. But it backfired terribly."

In *The Lancet*, in February, a powerful counterstatement appeared, signed by 27 scientists. "We stand together to strongly condemn conspiracy theories suggesting that COVID-19 does not have a natural origin," the statement said. "Scientists from multiple countries have published and analyzed genomes of the causative agent, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), and they overwhelmingly conclude

that this coronavirus originated in wildlife, as have so many other emerging pathogens."

The behind-the-scenes organizer of this *Lancet* statement, Peter Daszak, is a zoologist and bat-virus sample collector and the head of a New York nonprofit called EcoHealth Alliance — a group that (as veteran science journalist Fred Guterl explained later in *Newsweek*) has channeled money from the National Institutes of Health to Shi Zhengli's laboratory in Wuhan, allowing the lab to carry on recombinant research into diseases of bats and humans. "We have a choice whether to stand up and support colleagues who are being attacked and threatened daily by conspiracy theorists or to just turn a blind eye," Daszak said in February in *Science* magazine.



How Did It Get Out? 1. The Tongguan Mine Shaft in Mojiang, Yunnan, where, in 2013, fragments of RaTG13, the closest known relative of SARSCoV-2, were recovered and transported to the Wuhan Institute of Virology; **2. The Wuhan Institute of Virology,** where Shi Zhengli's team brought the RaTG13 sample, sequenced its genome, then took it out of the freezer several times in recent years; **3. The Wuhan Center for Disease Control and Prevention,** which first reported signs of the novel coronavirus in hospital patients; **4. The Huanan Seafood Wholesale Market,** an early suspected origin of the pandemic, where the first major outbreak occurred. Illustration: Map by Jason Lee

Vincent Racaniello, a professor at Columbia and a co-host of a podcast called *This Week in Virology*, said on February 9 that the idea of an accident in Wuhan was "complete bunk." The coronavirus was 96 percent similar to a bat virus found in 2013, Racaniello said. "It's not a man-made virus. It wasn't released from a lab."

Racaniello's dismissal was seconded by a group of scientists from Ohio State, the University of Pennsylvania, and the University of North Carolina, who put out a paper in *Emerging Microbes and Infections* to quiet the "speculations, rumors, and conspiracy theories that SARS-CoV-2 is of laboratory origin." There was "currently no credible evidence" that SARS-2 leaked from a lab, these scientists said, using a somewhat different argument from Racaniello's. "Some people have alleged that the human SARS-CoV-2 was leaked directly from a laboratory in Wuhan where a bat CoV (RaTG13) was recently reported," they said. But RaTG13 could not be the source because it differed from the human SARS-2 virus by more than a thousand nucleotides. One of the paper's authors, Susan Weiss, told the Raleigh *News & Observer*, "The conspiracy theory is ridiculous."

The most influential natural-origin paper, "The Proximal Origin of SARS-CoV-2," by a group of biologists that included Kristian Andersen of Scripps Research, appeared online in a preliminary version in mid-February. "We do not believe any type of laboratory-based scenario is plausible," the scientists said. Why? Because molecular-modeling software predicted that if you wanted to optimize an existing bat virus so that it would replicate well in human cells, you would arrange things a different way than how the SARS-2 virus actually does it — even though the SARS-2 virus does an extraordinarily good job of replicating in human cells. The laboratory-based scenario was implausible, the paper said, because, although it was true that the virus could conceivably have developed its unusual genetic features in a laboratory, a stronger and "more parsimonious" explanation was that the

features came about through some kind of natural mutation or recombination. "What we think," explained one of the authors, Robert F. Garry of Tulane University, on YouTube, "is that this virus is a recombinant. It probably came from a bat virus, plus perhaps one of these viruses from the pangolin." Journalists, for the most part, echoed the authoritative pronouncements of Daszak, Racaniello, Weiss, Andersen, and other prominent natural-originists. "The balance of the scientific evidence strongly supports the conclusion that the new coronavirus emerged from nature — be it the Wuhan market or somewhere else," said the Washington *Post*'s "Fact Checker" column. "Dr. Fauci Again Dismisses Wuhan Lab As Source of Coronavirus," said CBS News, posting a video interview of Anthony Fauci by *National Geographic*. "If you look at the evolution of the virus in bats, and what's out there now," Fauci said, "it's very, very strongly leaning toward 'This could not have been artificially or deliberately manipulated' — the way the mutations have naturally evolved."

Everyone took sides; everyone thought of the new disease as one more episode in an ongoing partisan struggle. Think of Mike Pompeo, that landmass of Cold War truculence; think of Donald Trump himself. They stood at their microphones saying, in a winking, I-know-something-you-don't-know sort of way, that this disease escaped from a Chinese laboratory. Whatever they were saying must be wrong. It became impermissible, almost taboo, to admit that, of course, SARS-2 could have come from a lab accident. "The administration's claim that the virus spread from a Wuhan lab has made the notion politically toxic, even among scientists who say it could have happened," wrote science journalist Mara Hvistendahl in the Intercept.

IV.

"Is It a Complete Coincidence?"

Even so, in January and February of 2020, there were thoughtful people who were speaking up, formulating their perplexities.

One person was Sam Husseini, an independent journalist. He went to a CDC press conference at the National Press Club on February 11, 2020. By then, 42,000 people had gotten sick in China and more than a thousand had died. But there were only 13 confirmed cases in the U.S. Halfway through the Q&A period, Husseini went to the microphone and asked the CDC's representative, Anne Schuchat, where the virus had come from. His head was spinning, he told me later.

"Obviously the main concern is how to stop the virus," Husseini said; nonetheless, he wanted to know more about its source. "Is it the CDC's contention," he asked, "that there's absolutely no relation to the BSL-4 lab in Wuhan? It's my understanding that this is the only place in China with a BSL-4 lab. We in the United States have, I think, two dozen or so, and there have been problems and incidents." (A BSL-4 laboratory is a maximum-security biosafety-level-four facility, used to house research on the most dangerous known pathogens. *New York* has confirmed there are at least 11 BSL-4 facilities currently operating in the U.S.) Husseini hastened to say that he wasn't implying that what happened in Wuhan was in any way intentional. "I'm just asking, Is it a complete coincidence that this outbreak happened in the one city in China with a BSL-4 lab?"

Schuchat thanked Husseini for his questions and comments. Everything she'd seen was quite consistent with a natural, zoonotic origin for the disease, she said.

That same month, a group of French scientists from Aix-Marseille University posted a paper describing their investigation of a small insertion in the genome of the new SARS-2 virus. The virus's spike protein contained a

sequence of amino acids that formed what Etienne Decroly and colleagues called a "peculiar furin-like cleavage site" — a chemically sensitive region on the lobster claw of the spike protein that would react in the presence of an enzyme called furin, which is a type of protein found everywhere within the human body, but especially in the lungs. When the spike senses human furin, it shudders, chemically speaking, and the enzyme opens the protein, commencing the tiny morbid ballet whereby the virus burns a hole in a host cell's outer membrane and finds its way inside.

The code for this particular molecular feature — not found in SARS or any SARS-like bat viruses, but present in a slightly different form in the more lethal MERS virus — is easy to remember because it's a roar: "R-R-A-R." The letter code stands for amino acids: arginine, arginine, alanine, and arginine. Its presence, so Decroly and his colleagues observed, may heighten the "pathogenicity" — that is, the god-awfulness — of a disease.

Botao Xiao, a professor at the South China University of Technology, posted a short paper on a preprint server titled "The Possible Origins of 2019-nCoV Coronavirus." Two laboratories, the Wuhan Center for Disease Control and Prevention (WHCDC) and the Wuhan Institute of Virology, were not far from the seafood market, which was where the disease was said to have originated, Xiao wrote — in fact, the WHCDC was only a few hundred yards away from the market — whereas the horseshoe bats that hosted the disease were hundreds of miles to the south. (No bats were sold in the market, he pointed out.) It was unlikely, he wrote, that a bat would have flown to a densely populated metropolitan area of 15 million people. "The killer coronavirus probably originated from a laboratory in Wuhan," Xiao believed. He urged the relocation of "biohazardous laboratories" away from densely populated places. His article disappeared from the server.

And late in the month, a professor at National Taiwan University, Fang Chi-

tai, gave a lecture on the coronavirus in which he described the anomalous R-R-A-R furin cleavage site. The virus was "unlikely to have four amino acids added all at once," Fang said — natural mutations were smaller and more haphazard, he argued. "From an academic point of view, it is indeed possible that the amino acids were added to COVID-19 in the lab by humans." When the Taiwan *News* published an article about Fang's talk, Fang disavowed his own comments, and the video copy of the talk disappeared from the website of the Taiwan Public Health Association. "It has been taken down for a certain reason," the association explained. "Thank you for your understanding."

V.

"A Serious Shortage of Appropriately Trained Technicians"

In the spring, I did some reading on coronavirus history. Beginning in the 1970s, dogs, cows, and pigs were diagnosed with coronavirus infections; dog shows were canceled in 1978 after 25 collies died in Louisville, Kentucky. New varieties of coronaviruses didn't start killing humans, though, until 2003 — that's when restaurant chefs, food handlers, and people who lived near a live-animal market got sick in Guangzhou, in southern China, where the shredded meat of a short-legged raccoonlike creature, the palm civet, was served in a regional dish called "dragon-tiger-phoenix soup." The new disease, SARS, spread alarmingly in hospitals, and it reached 30 countries and territories. More than 800 people died; the civet-borne virus was eventually traced to horseshoe bats.

Later, smaller outbreaks of SARS in Taiwan, Singapore, and China's National Institute of Virology in Beijing were all caused by laboratory accidents. Of the Beijing Virology Institute, the World Health Organization's safety

investigators wrote, in May 2004, that they had "serious concerns about biosafety procedures." By one account, a SARS storage room in the Beijing lab was so crowded that the refrigerator holding live virus was moved out to the hallway. "Scientists still do not fully understand exactly where or how SARS emerged 18 months ago," wrote Washington *Post* reporter David Brown in June 2004. "But it is clear now that the most threatening source of the deadly virus today may be places they know intimately — their own laboratories."

I'm just asking, Is it a complete coincidence that this outbreak happened in the one city in China with a BSL-4 lab?

MERS arose in 2012, possibly spread by camels that had contracted the disease from bats or bat guano, then passed it to human drinkers of raw camel milk and butchers of camel meat. It was an acute sickness, with a high fatality rate, mostly confined to Saudi Arabia. Like SARS, MERS ebbed quickly — it all but disappeared outside the Middle East, except for an outbreak in 2015 at the Samsung Medical Center in South Korea, where a single case of MERS led to more than 180 infections, many involving hospital workers.

In January 2015, the brand-new BSL-4 lab in Wuhan, built by a French contractor, celebrated its opening, but full safety certification came slowly. According to State Department cables from 2018 leaked to the Washington *Post*, the new BSL-4 lab had some start-up problems, including "a serious shortage of appropriately trained technicians and investigators needed to safely operate this high-containment laboratory." The staff had gotten some training at a BSL-4 lab in Galveston, Texas, but they were doing potentially dangerous work with SARS-like viruses, the memo said, and they needed more help from the U.S.

In November or December of 2019, the novel coronavirus began to spread. Chinese scientists initially named it "Wuhan seafood market pneumonia virus," but soon that idea went away. The market, closed and decontaminated by Chinese officials on January 1, 2020, was an amplifying hub, not the source of the outbreak, according to several studies by Chinese scientists. Forty-five percent of the earliest SARS-2 patients had no link with the market.

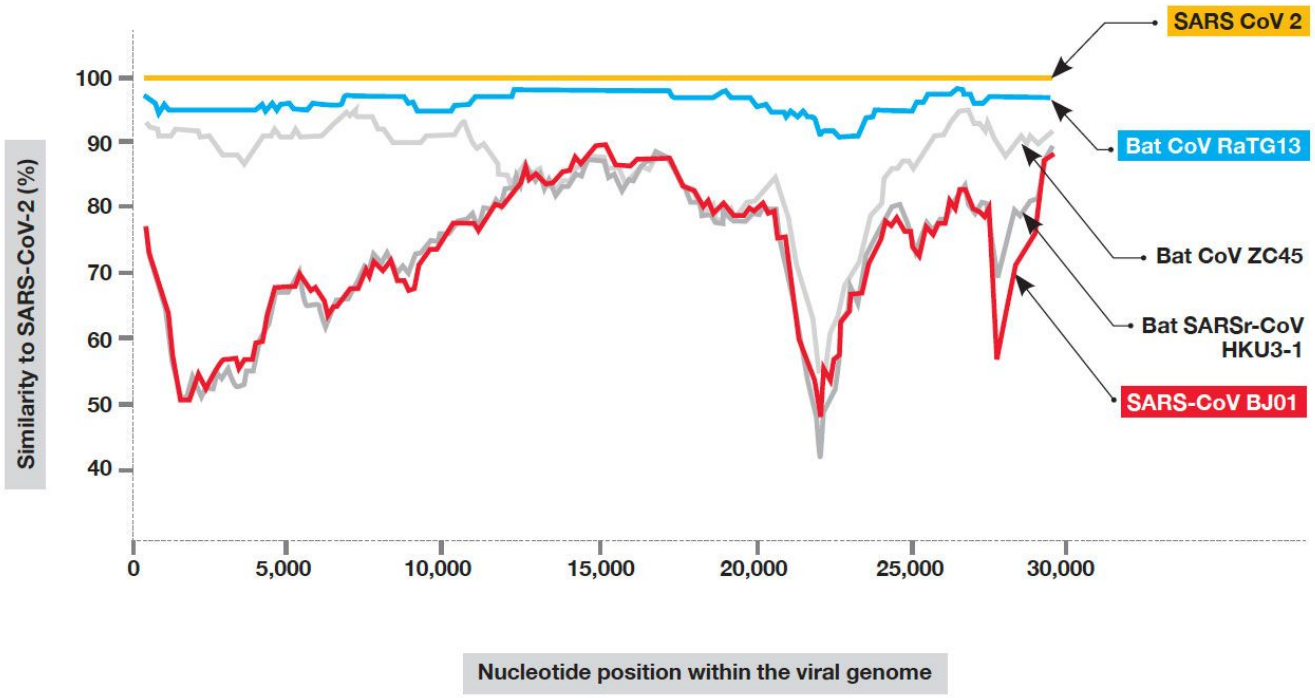
VI.

Emergence

Now let's take a step back. AIDS, fatal and terrifying and politically charged, brought on a new era in government-guided vaccine research, under the guidance of Anthony Fauci. A virologist at Rockefeller University, Stephen S. Morse, began giving talks on "emerging viruses" — other plagues that might be in the process of coming out of nature's woodwork. In 1992, Richard Preston wrote a horrific account of one emergent virus, Ebola, in *The New Yorker*, which became a best-selling book in 1994; Laurie Garrett's *The Coming Plague: Newly Emerging Diseases in a World Out of Balance* appeared that same year and was also a best seller. The idea seemed to be everywhere: We were on the verge of a wave of zoonotic, emergent plagues.

This new, useful term, *emerging*, began to glow in the research papers of some coronavirologists, who were out of the spotlight, working on common colds and livestock diseases. The term was useful because it was fluid. An emerging disease could be real and terrifying, as AIDS was — something that had just arrived on the medical scene and was confounding our efforts to combat it — or it could be a disease that hadn't arrived, and might never arrive, but could be shown in a laboratory to be waiting in the wings, just a

few mutations away from a human epidemic. It was real and unreal at the same time — a quality that was helpful when applying for research grants.



Where Did It Come From? This chart measures the genetic similarity of known viruses to the novel coronavirus (which appears in yellow). By far the closest is the bat virus RaTG13, which appears in blue, and which was recovered in 2013 and brought to the Wuhan Institute of Virology. The first SARS, marked in red, is a much more distant relative. Graphic: Zhou, P., Yang, XL., Wang, XG. et al. A pneumonia outbreak associated with a new coronavirus of probable bat origin. Nature 579, 270–273 (2020)

Take, for instance, this paper from 1995: "High Recombination and Mutation Rates in Mouse Hepatitis Viruses Suggest That Coronaviruses May Be Potentially Important Emerging Viruses." It was written by Dr. Ralph Baric and his bench scientist, Boyd Yount, at the University of North Carolina. Baric, a gravelly voiced former swim champion, described in this early paper how his lab was able to train a coronavirus, MHV, which causes hepatitis in mice, to jump species, so that it could reliably infect BHK (baby-hamster kidney) cell cultures. They did it using serial passaging: repeatedly dosing a mixed solution of mouse cells and hamster cells with mouse-hepatitis virus,

while each time decreasing the number of mouse cells and upping the concentration of hamster cells. At first, predictably, the mouse-hepatitis virus couldn't do much with the hamster cells, which were left almost free of infection, floating in their world of fetal-calf serum. But by the end of the experiment, after dozens of passages through cell cultures, the virus had mutated: It had mastered the trick of parasitizing an unfamiliar rodent. A scourge of mice was transformed into a scourge of hamsters. And there was more: "It is clear that MHV can rapidly alter its species specificity and infect rats and primates," Baric said. "The resulting virus variants are associated with demyelinating diseases in these alternative species." (A demyelinating disease is a disease that damages nerve sheaths.) With steady prodding from laboratory science, along with some rhetorical exaggeration, a lowly mouse ailment was morphed into an emergent threat that might potentially cause nerve damage in primates. That is, nerve damage in us.

A few years later, in a further round of "interspecies transfer" experimentation, Baric's scientists introduced their mouse coronavirus into flasks that held a suspension of African-green-monkey cells, human cells, and pig-testicle cells. Then, in 2002, they announced something even more impressive: They'd found a way to create a full-length infectious clone of the entire mouse-hepatitis genome. Their "infectious construct" replicated itself just like the real thing, they wrote.

Not only that, but they'd figured out how to perform their assembly seamlessly, without any signs of human handiwork. Nobody would know if the virus had been fabricated in a laboratory or grown in nature. Baric called this the "no-see'm method," and he asserted that it had "broad and largely unappreciated molecular biology applications." The method was named, he wrote, after a "very small biting insect that is occasionally found on North Carolina beaches."

In 2006, Baric, Yount, and two other scientists were granted a patent for their invisible method of fabricating a full-length infectious clone using the seamless, no-see'm method. But this time, it wasn't a clone of the mouse-hepatitis virus — it was a clone of the entire deadly human SARS virus, the one that had emerged from Chinese bats, via civets, in 2002. The Baric Lab came to be known by some scientists as "the Wild Wild West." In 2007, Baric said that we had entered "the golden age of coronavirus genetics."

"I would be afraid to look in their freezers," one virologist told me.

Baric and Shi Zhengli of the Wuhan Institute of Virology, the two top experts on the genetic interplay between bat and human coronaviruses, began collaborating in 2015.

VII.

"I Had Not Slept a Wink"

Virologist Shi Zhengli at the Wuhan Institute of Virology in 2017. Photo: Feature China / Barcroft Studios / Future Publishing / Getty Images

Early in the pandemic, *Scientific American* profiled Shi Zhengli, known in China as the "bat woman." Shi trapped hundreds of bats in nets at the mouths of caves in southern China, sampled their saliva and their blood, swabbed their anuses, and gathered up their fecal pellets. Several times, she visited and sampled bats in a mine in Mojiang, in southern China, where, in 2012, six men set to work shoveling bat guano were sickened by a severe lung disease, three of them fatally. Shi's team took the samples back to Wuhan and analyzed whatever fragments of bat virus she could find. In some cases, when she found a sequence that seemed particularly significant, she experimented with it in order to understand how it might potentially infect humans. Some of her work was funded by the National Institutes of Health and some of it by the U.S. Defense Threat Reduction

Agency of the Department of Defense via Peter Daszak's EcoHealth Alliance.

As Shi explained to *Scientific American*, late in December 2019, she heard from the director of the Wuhan Institute that there was an outbreak of a new disease in the city. Medical samples taken from hospital patients arrived at her lab for analysis. Shi determined that the new virus was related to SARS but even more closely related to a bat disease that her own team had found on a virus-hunting trip: the now-famous RaTG13. Shi was surprised that the outbreak was local, she said: "I had never expected this kind of thing to happen in Wuhan, in central China." The bat hiding places that she'd been visiting were, after all, as far away as Orlando, Florida, is from New York City. Could this new virus, she wondered, have come from her own laboratory? She checked her records and found no exact matches. "That really took a load off my mind," she said. "I had not slept a wink for days."

If one of the first thoughts that goes through the head of a lab director at the Wuhan Institute of Virology is that the new coronavirus could have come from her lab, then we are obliged to entertain the scientific possibility that it could indeed have come from her lab. Right then, there should have been a comprehensive, pockets-inside-out, fully public investigation of the Virology Institute, along with the other important virus labs in Wuhan, including the one close by the seafood market, headquarters of the Wuhan CDC. There should have been interviews with scientists, interviews with biosafety teams, close parsings of laboratory notebooks, freezer and plumbing and decontamination systems checks — everything. It didn't happen. The Wuhan Institute of Virology closed down its databases of viral genomes, and the Chinese Ministry of Education sent out a directive: "Any paper that traces the origin of the virus must be strictly and tightly managed."

Shi made some WeChat posts early in 2020. "The novel 2019 coronavirus is nature punishing the human race for keeping uncivilized living habits," she wrote. "I, Shi Zhengli, swear on my life that it has nothing to do with our laboratory." She advised those who believed rumors, and gave credence to unreliable scientific papers, to "shut their stinking mouths."

VIII.

" 'Bug to Drug' in 24 Hours"

It wasn't only AIDS that changed the way the NIH funded research. The War on Terror also influenced which diseases got the most attention. In the late '90s, under Bill Clinton and then George W. Bush, biodefense specialists became interested — again — in anthrax. The Defense Threat Reduction Agency built a small anthrax factory in Nevada, using simulants, to demonstrate how easy it would be for a terrorist to build a small anthrax factory. And in the first year of the Bush presidency, the Defense Intelligence Agency wrote up plans to create a vaccine-resistant form of anthrax using state-of-the-art gene-splicery. A front-page article describing these initiatives, "U.S. Germ Warfare Research Pushes Treaty Limits," appeared in the New York *Times* on September 4, 2001, one week before 9/11. "Pentagon Says Projects Are Defense, Is Pressing Ahead," was the subtitle.

After the 9/11 attacks, and the mysterious anthrax mailings that began a week later (which said, "TAKE PENACILIN [*sic*] NOW / DEATH TO AMERICA / DEATH TO ISRAEL / ALLAH IS GREAT"), the desire for biopreparedness became all consuming. Now there were emerging biothreats from humans as well as from the evolving natural world. Fauci's anti-terror budget went from $53 million in 2001 to $1.7 billion in 2003. Setting aside his work toward an AIDS vaccine, which was taking longer than he'd foreseen, Fauci

said he would be going all out to defend against a suite of known Cold War agents, all of which had been bred and perfected in American weapons programs many years before — brucellosis, anthrax, tularemia, and plague, for instance. "We are making this the highest priority," Fauci said. "We are really marshaling all available resources."

> *I would be afraid to look in their freezers.*

Vaccine development had to progress much faster, Fauci believed; he wanted to set up "vaccine systems" and "vaccine platforms," which could be quickly tailored to defend against a particular emergent strain some terrorist with an advanced biochemistry degree might have thrown together in a laboratory. "Our goal within the next 20 years is 'bug to drug' in 24 hours," Fauci said. "This would specifically meet the challenge of genetically engineered bioagents." The first Project BioShield contract Fauci awarded was to VaxGen, a California pharmaceutical company, for $878 million worth of shots of anthrax vaccine.

By 2005, so much money was going toward biothreat reduction and preparedness that more than 750 scientists sent a protest letter to the NIH. Their claim was that grants to study canonical biowar diseases — anthrax, plague, brucellosis, and tularemia, all exceptionally rare in the U.S. — had increased by a factor of 15 since 2001, whereas funds for the study of widespread "normal" diseases, of high public-health importance, had decreased.

Fauci was firm in his reply: "The United States through its leaders made the decision that this money was going to be spent on biodefense," he said. "We disagree with the notion that biodefense concerns are of 'low public-health significance.' "

In 2010, by one count, there were 249 BSL-3 laboratories and seven BSL-4 laboratories in the U.S., and more than 11,000 scientists and staffers were authorized to handle the ultralethal germs on the government's select pathogen list. And yet the sole bioterrorist in living memory who actually killed American citizens, according to the FBI — the man who sent the anthrax letters — turned out to be one of the government's own researchers. Bruce Ivins, an eccentric, suicidal laboratory scientist from Ohio who worked in vaccine development at Fort Detrick, allegedly wanted to boost the fear level so as to persuade the government to buy more of the patented, genetically engineered anthrax VaxGen vaccine, of which he was a co-inventor. (See David Willman's fascinating biography of Ivins, *Mirage Man*.) Fauci's staff at NIH funded Ivins's vaccine laboratory and gave $100 million to VaxGen to accelerate vaccine production. (The NIH's $878 million contract with VaxGen, however, was quietly canceled in 2006; Ivins, who was never charged, killed himself in 2008.)

"The whole incident amounted to a snake eating its own tail," wrote Wendy Orent in an August 2008 piece titled "Our Own Worst Bioenemy" in the Los Angeles *Times*. "No ingenious biowarrior from Al Qaeda sent the lethal envelopes through the U.S. postal system. An American scientist did." What confirmed Ivins's guilt, according to the FBI, was that there was a genetic match between the anthrax used in the killings and the strain held at Fort Detrick.

IX.

"Weapons of Mass Disruption"

After SARS appeared in 2003, Ralph Baric's laboratory moved up the NIH funding ladder. SARS was a "dual use" organism — a security threat and a zoonotic threat at the same time. In 2006, Baric wrote a long, fairly creepy

paper on the threat of "weaponizable" viruses. Synthetic biology had made possible new kinds of viral "weapons of mass disruption," he wrote, involving, for example, "rapid production of numerous candidate bioweapons that can be simultaneously released," a scattershot terror tactic Baric called the " 'survival of the fittest' approach."

Baric hoped to find a SARS vaccine, but he couldn't; he kept looking for it, year after year, supported by the NIH, long after the disease itself had been contained. It wasn't really gone, Baric believed. Like other epidemics that pop up and then disappear, as he told a university audience some years later, "they don't go extinct. They are waiting to return." What do you do if you run a well-funded laboratory, an NIH "center of excellence," and your emergent virus is no longer actually making people sick? You start squeezing it and twisting it into different shapes. Making it stand on its hind legs and quack like a duck, or a bat. Or breathe like a person.

Baric's safety record is good — although there was a minor mouse-bite incident in 2016, uncovered by ProPublica — and his motives are beyond reproach: "Safe, universal, vaccine platforms are needed that can be tailored to new pathogens as they emerge, quickly tested for safety, and then strategically used to control new disease outbreaks in human populations," he wrote in a paper on public health. But the pioneering work he did over the past 15 years — generating tiny eager single-stranded flask monsters and pitting them against human cells, or bat cells, or gene-spliced somewhat-human cells, or monkey cells, or humanized mice — was not without risk, and it may have led others astray.

In 2006, for instance, Baric and his colleagues, hoping to come up with a "vaccine strategy" for SARS, produced noninfectious virus replicon particles (or VRPs) using the Venezuelan-equine-encephalitis virus (another American germ-warfare agent), which they fitted with various SARS spike

proteins. Then, wearing Tyvek suits and two pairs of gloves each, and working in a biological safety cabinet in a BSL-3-certified laboratory, they cloned and grew recombinant versions of the original SARS virus in an incubator in a medium that held African-green-monkey cells. When they had grown enough virus, the scientists swapped out one kind of spike protein for a carefully chosen mutant, and they challenged their prototype vaccine with it in mice.

The scientists also tried their infectious SARS clones in something called an air-liquid interface, using a relatively new type of cell culture developed by Raymond Pickles of the University of North Carolina's Cystic Fibrosis Center. Pickles had perfected a method of emulating the traits of human airway tissue by cultivating cells taken from lung-disease patients — nurturing the culture over four to six weeks in such a way that the cells differentiated and developed a crop of tiny moving hairs, or cilia, on top and goblet cells within that produced real human mucus. In fact, before infecting these HAE (human airway epithelial) cells with a virus, the lab worker must sometimes rinse off some of the accumulated mucus, as if helping the lab-grown tissue to clear its throat. So Baric was exposing and adapting his engineered viruses to an extraordinarily true-to-life environment — the juicy, sticky, hairy inner surface of our breathing apparatus.

SARS-2 seems almost perfectly calibrated to grab and ransack our breathing cells and choke the life out of them. "By the time SARS-CoV-2 was first detected in late 2019, it was already pre-adapted to human transmission," Alina Chan and her co-authors have written, whereas SARS, when it first appeared in 2003, underwent "numerous adaptive mutations" before settling down. Perhaps viral nature hit a bull's-eye of airborne infectivity, with almost no mutational drift, no period of accommodation and adjustment, or perhaps some lab worker somewhere, inspired by Baric's

work with human airway tissue, took a spike protein that was specially groomed to colonize and thrive deep in the ciliated, mucosal tunnels of our inner core and cloned it onto some existing viral bat backbone. It could have happened in Wuhan, but — because anyone can now "print out" a fully infectious clone of any sequenced disease — it could also have happened at Fort Detrick, or in Texas, or in Italy, or in Rotterdam, or in Wisconsin, or in some other citadel of coronaviral inquiry. No conspiracy — just scientific ambition, and the urge to take exciting risks and make new things, and the fear of terrorism, and the fear of getting sick. Plus a whole lot of government money.

X.

"Risky Areas for Spillover"

Project Bioshield began to fade by the end of the Bush administration, although the expensive high-containment laboratories, controversial preservers and incubators of past and future epidemics, remain. By 2010, some BioShield projects had dissolved into Obama's Predict program, which paid for laboratories and staff in 60 "risky areas for spillover" around the world. Jonna Mazet, a veterinary scientist from the University of California, Davis, was in charge of Predict, which was a component of USAID's "Emerging Pandemic Threats" program. Her far-flung teams collected samples from 164,000 animals and humans and claimed to have found "almost 1,200 potentially zoonotic viruses, among them 160 novel coronaviruses, including multiple SARS- and MERS-like coronaviruses." The fruits of Predict's exotic harvest were studied and circulated in laboratories worldwide, and their genetic sequences became part of GenBank, the NIH's genome database, where any curious RNA wrangler anywhere could quickly synthesize snippets of code and test out a new disease on human cells.

Baric, Jonna Mazet, and Peter Daszak of EcoHealth worked together for years — and Daszak also routed Predict money to Shi Zhengli's bat-surveillance team in Wuhan through his nonprofit, mingling it with NIH money and money from the U.S. Defense Threat Reduction Agency. In 2013, Mazet announced that Shi Zhengli's virus hunters, with Predict's support, had, for the first time, isolated and cultured a live SARS-like virus from bats and demonstrated that this virus could bind to the human ACE2, or "angiotensin-converting enzyme 2," receptor, which Baric's laboratory had determined to be the sine qua non of human infectivity. "This work shows that these viruses can directly infect humans and validates our assumption that we should be searching for viruses of pandemic potential before they spill over to people," Mazet said.

Daszak, for his part, seems to have viewed his bat quests as part of an epic, quasi-religious death match. In a paper from 2008, Daszak and a co-author described Bruegel's painting *The Fall of the Rebel Angels* and compared it to the contemporary human biological condition. The fallen angels could be seen as pathogenic organisms that had descended "through an evolutionary (not spiritual) pathway that takes them to a netherworld where they can feed only on our genes, our cells, our flesh," Daszak wrote. "Will we succumb to the multitudinous horde? Are we to be cast downward into chthonic chaos represented here by the heaped up gibbering phantasmagory against which we rail and struggle?"

XI.

"Lab-Made?"

There are, in fact, some helpful points of agreement between zoonoticists — those who believe in a natural origin of the SARS-2 virus — and those who believe that it probably came from a laboratory. Both sides agree, when

pressed, that a lab origin can't be conclusively ruled out and a natural origin can't be ruled out either — because nature, after all, is capable of improbable, teleological-seeming achievements. Both sides also agree, for the most part, that the spillover event that began the human outbreak probably happened only once, or a few times, quite recently, and not many times over a longer period. They agree that bat virus RaTG13 (named for the *Rinolophus affinus* bat, from Tongguan, in 2013) is the closest match to the human virus that has yet been found, and that although the two viruses are very similar, the spike protein of the bat virus lacks the features the human spike protein possesses that enable it to work efficiently with human tissue.

Zoonoticists hold that SARS-2's crucial features — the furin cleavage site and the ACE2 receptor — are the result of a recombinant event involving a bat coronavirus (perhaps RaTG13 or a virus closely related to it) and another, unknown virus. Early on, researchers proposed that it could be a snake sold at the seafood market — a Chinese cobra or a banded krait — but no: Snakes don't typically carry coronaviruses. Then there was a thought that the disease came from sick smuggled pangolins, because there existed a certain pangolin coronavirus that was, inexplicably, almost identical in its spike protein to the human coronavirus — but then, no: There turned out to be questions about the reliability of the genetic information in that diseased-pangolin data set, on top of which there were no pangolins for sale at the Wuhan market. Then a group from China's government veterinary laboratory at Harbin tried infecting beagles, pigs, chickens, ducks, ferrets, and cats with SARS-2 to see if they could be carriers. (Cats and ferrets got sick; pigs, ducks, and most dogs did not.)

In September, some scientists at the University of Michigan, led by Yang Zhang, reported that they had created a "computational pipeline" to screen nearly a hundred possible intermediate hosts, including the Sumatran orangutan, the Western gorilla, the Olive baboon, the crab-eating macaque,

and the bonobo. All these primates were “permissive” to the SARS-2 coronavirus and should undergo “further experimentational investigation,” the scientists proposed.

Despite this wide-ranging effort, there is at the moment no animal host that zoonoticists can point to as the missing link. There’s also no single, agreed-upon hypothesis to explain how the disease may have traveled from the bat reservoirs of Yunnan all the way to Wuhan, seven hours by train, without leaving any sick people behind and without infecting anyone along the way.

The zoonoticists say that we shouldn’t find it troubling that virologists have been inserting and deleting furin cleavage sites and ACE2-receptor-binding domains in experimental viral spike proteins for years: The fact that virologists have been doing these things in laboratories, in advance of the pandemic, is to be taken as a sign of their prescience, not of their folly. But I keep returning to the basic, puzzling fact: This patchwork pathogen, which allegedly has evolved without human meddling, first came to notice in the only city in the world with a laboratory that was paid for years by the U.S. government to perform experiments on certain obscure and heretofore unpublicized strains of bat viruses — which bat viruses then turned out to be, out of all the organisms on the planet, the ones that are most closely related to the disease. What are the odds?

In July, I discovered a number of volunteer analysts who were doing a new kind of forensic, samizdat science, hunched over the letter code of the SARS-2 genome like scholars deciphering the cuneiform impressions in Linear B tablets. There were the anonymous authors of Project Evidence, on GitHub, who “disavow all racism and violent attacks, including those which are aimed at Asian or Chinese people,” and there was Yuri Deigin, a biotech entrepreneur from Canada, who wrote a massive, lucid paper on Medium, “Lab-Made?,” which illumined the mysteries of the spike protein. Jonathan

Latham of the Bioscience Resource Project, with his co-author Allison Wilson, wrote two important papers: one a calm, unsparing overview of laboratory accidents and rash research and the other a close look at the small outbreak of an unexplained viral pneumonia in a bat-infested copper mine in 2012. I corresponded with Alina Chan (now the subject of a nicely turned piece in *Boston* magazine by Rowan Jacobsen) and with the pseudonymous Billy Bostickson, a tireless researcher whose Twitter photo is a cartoon of an injured experimental monkey, and Monali Rahalkar, of the Agharkar Research Institute in Pune, India, who wrote a paper with her husband, Rahul Bahulikar, that also sheds light on the story of the bat-guano-shoveling men whose virus was remarkably like SARS-2, except that it was not nearly as catching. I talked to Rossana Segreto, a molecular biologist at the University of Innsbruck, whose paper, "Is Considering a Genetic-Manipulation Origin for SARS-CoV-2 a Conspiracy Theory That Must Be Censored?," co-authored with Yuri Deigin, was finally published in November under a milder title; it argued that SARS-2's most notable features, the furin site and the human ACE2-binding domain, were unlikely to have arisen simultaneously and "might be the result of lab manipulation techniques such as site directed mutagenesis." Segreto is also the person who first established that a bat-virus fragment named BtCoV/4991, identified in 2013, was 100 percent identical to the closest known cousin to SARS-CoV-2, the bat virus RaTG13, thereby proving that the virus closest to the SARS-2-pandemic virus was linked back not to a bat cave but to a mine shaft, and that this same virus had been stored and worked on in the Wuhan Institute for years. This made possible the first big investigative piece on SARS-2's origins, in the *Times* of London, in July: "Nobody can deny the bravery of scientists who risked their lives harvesting the highly infectious virus," the *Times* authors write. "But did their courageous detective work lead inadvertently to a global disaster?"

XII.

"A New, Non-Natural Risk"

In 2011, a tall, confident Dutch scientist, Ron Fouchier, using grant money from Fauci's group at NIH, created a mutant form of highly pathogenic avian influenza, H5N1, and passaged it ten times through ferrets in order to prove that he could "force" (his word) this potentially fatal disease to infect mammals, including humans, "via aerosols or respiratory droplets." Fouchier said his findings indicated that these avian influenza viruses, thus forced, "pose a risk of becoming pandemic in humans."

This experiment was too much for some scientists: Why, out of a desire to prove that something extremely infectious could happen, would you make it happen? And why would the U.S. government feel compelled to pay for it to happen? Late in 2011, Marc Lipsitch of the Harvard School of Public Health got together with several other dismayed onlookers to ring the gong for caution. On January 8, 2012, the New York *Times* published a scorcher of an editorial, "An Engineered Doomsday." "We cannot say there would be no benefits at all from studying the virus," the *Times* said. "But the consequences, should the virus escape, are too devastating to risk."

These gain-of-function experiments were an important part of the NIH's approach to vaccine development, and Anthony Fauci was reluctant to stop funding them. He and Francis Collins, director of the National Institutes of Health, along with Gary Nabel, NIAID director of vaccine research, published an opinion piece in the Washington *Post* in which they contended that the ferret flu experiments, and others like them, were "a risk worth taking." "Important information and insights can come from generating a potentially dangerous virus in the laboratory," they wrote; the work can "help delineate the principles of virus transmission between species." The

work was safe because the viruses were stored in a high-security lab, they believed, and the work was necessary because nature was always coming up with new threats. “Nature is the worst bioterrorist,” Fauci told a reporter. “We know that through history.”

Soon afterward, there followed some distressing screwups in secure federal laboratories involving live anthrax, live smallpox, and live avian influenza. These got attention in the science press. Then Lipsitch’s activists (calling themselves the Cambridge Working Group) sent around a strong statement on the perils of research with “Potential Pandemic Pathogens,” signed by more than a hundred scientists. The work might “trigger outbreaks that would be difficult or impossible to control,” the signers said. Fauci reconsidered, and the White House in 2014 announced that there would be a “pause” in the funding of new influenza, SARS, and MERS gain-of-function research.

Baric, in North Carolina, was not happy. He had a number of gain-of-function experiments with pathogenic viruses in progress. “It took me ten seconds to realize that most of them were going to be affected,” he told NPR. Baric and a former colleague from Vanderbilt University wrote a long letter to an NIH review board expressing their “profound concerns.” “This decision will significantly inhibit our capacity to respond quickly and effectively to future outbreaks of SARS-like or MERS-like coronaviruses, which continue to circulate in bat populations and camels,” they wrote. The funding ban was itself dangerous, they argued. “Emerging coronaviruses in nature do not observe a mandated pause.”

Hoping to smooth over controversy by showing due diligence, the National Science Advisory Board for Biosecurity, founded in the BioShield era under President Bush, paid a consulting firm, Gryphon Scientific, to write a report on gain-of-function research, which by now was simply referred to as GoF.

In chapter six of this thousand-page dissertation, published in April 2016, the consultants take up the question of coronaviruses. “Increasing the transmissibility of the coronaviruses could significantly increase the chance of a global pandemic due to a laboratory accident,” they wrote.

The Cambridge Working Group continued to write letters of protest and plead for restraint and sanity. Steven Salzberg, a professor of biomedical engineering at Johns Hopkins, said, “We have enough problems simply keeping up with the current flu outbreaks — and now with Ebola — without scientists creating incredibly deadly new viruses that might accidentally escape their labs.” David Relman of Stanford Medical School said, “It is unethical to place so many members of the public at risk and then consult only scientists — or, even worse, just a small subset of scientists — and exclude others from the decision-making and oversight process.” Richard Ebright wrote that creating and evaluating new threats very seldom increases security: “Doing so in biology — where the number of potential threats is nearly infinite, and where the asymmetry between the ease of creating threats and the difficulty of addressing threats is nearly absolute — is especially counterproductive.” Lynn Klotz wrote, “Awful as a pandemic brought on by the escape of a variant H5N1 virus might be, it is SARS that now presents the greatest risk. The worry is less about recurrence of a natural SARS outbreak than of yet another escape from a laboratory researching it to help protect against a natural outbreak.” Marc Lipsitch argued that gain-of-function experiments can mislead, “resulting in worse not better decisions,” and that the entire gain-of-function debate as overseen by the NIH was heavily weighted in favor of scientific insiders and “distinctly unwelcoming of public participation.”

Nariyoshi Shinomiya, a professor of physiology and nano-medicine at the National Defense Medical College in Japan, offered this warning: “Similar to nuclear or chemical weapons there is no going back once we get a thing in

our hands."

But in the end, Baric was allowed to proceed with his experiments, and the research papers that resulted, showered with money, became a sort of *Anarchist's Cookbook* for the rest of the scientific world. In November 2015, Baric and colleagues published a collaboration paper with Shi Zhengli titled "A SARS-like Cluster of Circulating Bat Coronaviruses Shows Potential for Human Emergence." Into a human SARS virus that they had adapted so that it would work in mice, Baric and Shi et al. inserted the spike protein of a bat virus, SHC014, discovered by Shi in southern China. They dabbed the mice nasally with virus and waited, looking for signs of sickness: "hunching, ruffled fur." They also infected human airway cells with the mouse-adapted bat-spike-in-a-human-virus backbone. In both mice and human airway cells, the chimeric virus caused a "robust infection."

This proved, Baric and Shi believed, that you did not need civets or other intermediate hosts in order for bats to cause an epidemic in humans and that therefore all the SARS-like viruses circulating in bat populations "may pose a future threat." Peter Daszak, who had used Predict funds to pay Shi for her work on the paper, was impressed by this conclusion; the findings, he said, "move this virus from a candidate emerging pathogen to a clear and present danger."

Richard Ebright was trenchantly unenthusiastic. "The only impact of this work," he said, "is the creation, in a lab, of a new, non-natural risk."

Early in 2016, Baric and Shi again collaborated. Shi sent Baric a fresh bat virus spike protein, and Baric inserted it into the backbone of a human SARS virus and then used that infectious clone to attack human airway cells. "The virus readily and efficiently replicated in cultured human airway tissues, suggesting an ability to potentially jump directly to humans,"

reported the UNC's website. This time, they also used the bat-human hybrid virus to infect transgenic humanized mice that grew human ACE2 protein. The mice, young and old, lost weight and died, proving, again, that this particular bat virus was potentially "poised to emerge in human populations." It was "an ongoing threat," Baric wrote. But was it? Civets and camels that are exposed to a lot of bat-guano dust may be an ongoing threat and a manageable one. But the bats themselves just want to hang in their caves and not be bothered by frowning sightseers in spacesuits who want to poke Q-tips in their bottoms. This 2016 "poised for human emergence" paper was supported by eight different NIH grants. In 2015, Baric's lab received $8.3 million from the NIH; in 2016, it received $10.5 million.

Gain-of-function research came roaring back under Trump and Fauci. "The National Institutes of Health will again fund research that makes viruses more dangerous," said an article in *Nature* in December 2017. Carrie Wolinetz of the NIH's office of science policy defended the decision. "These experiments will help us get ahead of viruses that are already out there and pose a real and present danger to human health," she told *The Lancet*. The NIH, Wolinetz said, was committed to a leadership role with gain-of-function research internationally. "If we are pursuing this research in an active way, we will be much better positioned to develop protection and countermeasures should something bad happen in another country."

A reporter asked Marc Lipsitch what he thought of the resumption of NIH funding. Gain-of-function experiments "have done almost nothing to improve our preparedness for pandemics," he said, "yet they risked creating an accidental pandemic."

XIII.

"Proximity Is a Problem"

In April, four months into the coronavirus emergency, a deputy director at the NIH wrote an email to EcoHealth Alliance. "You are instructed to cease providing any funds to Wuhan Institute of Virology," it said. In response, Daszak and the chief scientific officer of New England Biolabs (a company that sells seamless gene-splicing products to laboratories, among other things) got 77 Nobel Prize winners to sign a statement saying that the cancellation deprived the "nation and the world of highly regarded science that could help control one of the greatest health crises in modern history and those that may arise in the future." Later, as a condition of further funding, the NIH wrote to say it wanted Daszak to arrange an outside inspection of the Wuhan lab and to procure from Wuhan's scientists a sample of whatever they'd used to sequence the SARS-2 virus. Daszak was outraged ("I am not trained as a private detective"), and again he fought back. He was reluctant to give up his own secrets, too. "Conspiracy-theory outlets and politically motivated organizations have made Freedom of Information Act requests on our grants and all of our letters and emails to the NIH," he told *Nature.* "We don't think it's fair that we should have to reveal everything we do."

But Daszak has survived — even prospered. Recently, *The Lancet* made him the lead investigator in its inquiry into the origins of the pandemic, and the World Health Organization named him to its ten-person origins investigation. ("We're still close enough to the origin to really find out more details about where it has come from," Daszak told *Nature*.)

The NIH has also set up an ambitious new international program, called CREID, which stands for Centers for Research in Emerging Infectious Diseases, and it has put Daszak's EcoHealth in charge of trapping animals and looking for obscure bat viruses in Singapore, Malaysia, and Thailand.

Baric is one of Daszak's partners in CREID. The virus hunting and collecting, which Richard Ebright likens to "looking for a gas leak with a lighted match," will continue and widen with U.S. funding. "We're going to work in remote parts of Malaysia and Thailand to get to the front line of where the next pandemic is going to start," Daszak told NPR.

In May, an interviewer from the People's Pharmacy website asked Baric if he had any thoughts on whether the coronavirus began with a natural bat-to-human transfer. "Or was there something a little bit more, perhaps, insidious involved?"

"Well, of course the answers to those questions are in China," Baric replied. "Exactly how they work in that facility is something that would be very difficult for a Westerner to know," he said. "The main problems that the Institute of Virology has is that the outbreak occurred in close proximity to that Institute. That Institute has in essence the best collection of virologists in the world that have gone out and sought out, and isolated, and sampled bat species throughout Southeast Asia. So they have a very large collection of viruses in their laboratory. And so it's — you know — proximity is a problem. It's a problem."

Over the course of the fall, and especially after the election muffled Donald Trump's influence over the country's public-health apparatus, that proximity problem — and the uncomfortable questions of origins it raised — began to grow somewhat more discussable. The BBC, *Le Monde*, and Italy's RAI have all recently taken seriously the scientific possibility of a lab leak. In late October, the World Health Organization convened the first meeting of its second inquiry into the origins of the disease. The WHO's effort is perhaps the world's best chance to satisfy its curiosity about goings-on at the Wuhan Institute of Virology and at the Wuhan CDC's virus lab near the Wuhan seafood market. But, as the New York *Times* has reported, the

WHO's information gathering has been hindered by Chinese secretiveness since February, when an initial investigative team sent to Beijing was told its members' access to scientists would be restricted and that it couldn't visit the seafood market, then considered a hub of the pandemic.

When a BBC video team tried to inspect the Yunnan mine shaft, they found the road to the mine blocked by a strategically parked truck that had "broken down" shortly before they arrived. Reporter John Sudworth asked Daszak, one of the ten members of the second WHO investigative team, whether he would push for access to the Wuhan Institute of Virology. "That's not my job to do that," Daszak replied.

In November, David Relman, the Stanford microbiologist, one of the most thoughtful of the voices warning against gain-of-function research, published a paper in *Proceedings of the National Academy of Sciences* on the urgent need to unravel the origins of COVID-19. "If SARS-CoV-2 escaped from a lab to cause the pandemic," he wrote, "it will become critical to understand the chain of events and prevent this from happening again." Conflicts of interest by researchers and administrators will need to be addressed, Relman wrote; to reach the truth, the investigation must be transparent, international, and, as much as possible, unpolitical. "A more complete understanding of the origins of COVID-19 clearly serves the interests of every person in every country on this planet."

"The world is sitting on a precedent-setting decision right now," wrote Alina Chan on December 8. "It is unclear if SARS2 is 100 percent natural or emerged due to lab/research activities. If we walk away from this, demonstrating that we cannot effectively investigate its origins, it will pave the way for future COVIDS."

Just before this issue of *New York* went to press, I reached Ralph Baric by

phone and asked him where he now believed SARS-2 came from. (Anthony Fauci, Shi Zhengli, and Peter Daszak didn't respond to emails, and Kristian Andersen said he was busy with other things.) Baric said he still thought the virus came from bats in southern China, perhaps directly, or possibly via an intermediate host, although the smuggled pangolins, in his view, were a red herring. The disease evolved in humans over time without being noticed, he suspected, becoming gradually more infectious, and eventually a person carried it to Wuhan "and the pandemic took off." Then he said, "Can you rule out a laboratory escape? The answer in this case is probably not."

XIV.

Transmission

So how did we actually get this disease?

Here's what I think happened. In April 2012, in a copper mine in Mojiang, China, three men were given an awful job — they were told to shovel bat guano out of a mine shaft. They went to work and shoveled guano for seven hours a day in the confined, insufficiently ventilated space of the mine shaft, and by the end of the week, they were sick with a viral pneumonia of unknown etiology. Three more, younger shovelers were hired to replace the ones who were out sick.

The viral load in their lungs was so huge, because of all the guano dust, that their lungs became a kind of accelerated laboratory passaging experiment, as Jonathan Latham and Allison Wilson have written, forcing the virus to switch its allegiance from bats to humans. SARS experts were consulted, and the disease was judged to be SARS-like but not SARS. It was something new. (Shi Zhengli told *Scientific American* that the guano shovelers had died of a fungal disease, but, as Monali Rahalkar pointed out,

they were treated with antivirals, and their symptoms were consistent with viral pneumonia with attendant secondary fungal infections.)

Although it was a severe disease, and in the end three of the shovelers died, there was no resultant epidemic. It was actually a case of industrial overexposure to an infectious substance — what we might call a massive OSHA violation. The bat disease that the men encountered wasn't necessarily all that dangerous except in an environment of immunosuppressive overload.

Peter Daszak and Shi Zhengli were interested, of course, because this unidentified coronavirus disease involved bats and people. Of the fragmentary bits of virus Shi retrieved from the mine shaft, one was SARS-like, and Shi sequenced it and called it BtCoV/4991 and published a paper about it. Several times — in 2016 and 2018 and 2019 — this most interesting sample, a portion of what we now know as RaTG13, was taken out of the freezers in Shi's lab and worked on in undisclosed ways. (Peter Daszak claims that these samples have disintegrated and can't be validated or studied.) Samples of the nameless human disease also traveled back to the Wuhan Institute of Virology — few specifics about these valuable specimens have been released by Chinese sources, however.

This is the period in the story that demands a very close investigation, when chimeric assemblages may have been created and serially passaged, using BtCoV/4991, a.k.a. RaTG13, and other bat viruses, perhaps along with forms of the human virus. It's when Shi and Baric both published papers that were about what happened when you hot-swapped mutant spike proteins between bat viruses and human viruses.

The link, via the renamed sample BtCoV/4991, to the copper mine is of exceptional importance because of the one huge difference between the

unnamed guano shovelers' virus and the SARS-2 virus that is now ravaging, for example, California: transmissibility. Airborne human-to-human transmissibility — the kind of thing that gain-of-functioneers like Ron Fouchier and Ralph Baric were aiming at, in order to demonstrate what Baric called "lurking threats" — is COVID-19's crucial distinguishing feature. If six men had gotten extremely sick with COVID-19 back in 2012 in southern China, doctors and nurses in the hospital where they lay dying would likely have gotten sick as well. There might have been hundreds or thousands of cases. Instead, only the shovelers themselves, who had breathed a heavy concentration of guano dust for days, got it.

The existence of bat virus RaTG13 is therefore not necessarily evidence of a natural bat origin. In fact, it seems to me to imply the opposite: New functional components may have been overlaid onto or inserted into the RaTG13 genome, new Tinkertoy intermolecular manipulations, especially to its spike protein, which have the effect of making it unprecedentedly infectious in human airways.

This is where the uniquely peculiar furin insert and/or the human-tuned ACE2-receptor-binding domain may come in — although it's also possible that either of these elements could have evolved as part of some multistep zoonotic process. But in the climate of gonzo laboratory experimentation, at a time when all sorts of tweaked variants and amped-up substitutions were being tested on cell cultures and in the lungs of humanized mice and other experimental animals, isn't it possible that somebody in Wuhan took the virus that had been isolated from human samples, or the RaTG13 bat virus sequence, or both (or other viruses from that same mine shaft that Shi Zhengli has recently mentioned in passing), and used them to create a challenge disease for vaccine research — a chopped-and-channeled version of RaTG13 or the miners' virus that included elements that would make it thrive and even rampage in people? And then what if, during an

experiment one afternoon, this new, virulent, human-infecting, furin-ready virus got out?

For more than 15 years, coronavirologists strove to prove that the threat of SARS was ever present and must be defended against, and they proved it by showing how they could doctor the viruses they stored in order to force them to jump species and go directly from bats to humans. More and more bat viruses came in from the field teams, and they were sequenced and synthesized and "rewired," to use a term that Baric likes. In this international potluck supper of genetic cookery, hundreds of new variant diseases were invented and stored. And then one day, perhaps, somebody messed up. It's at least a reasonable, "parsimonious" explanation of what might have happened.

This may be the great scientific meta-experiment of the 21st century. Could a world full of scientists do all kinds of reckless recombinant things with viral diseases for many years and successfully avoid a serious outbreak? The hypothesis was that, yes, it was doable. The risk was worth taking. There would be no pandemic.

I hope the vaccine works.

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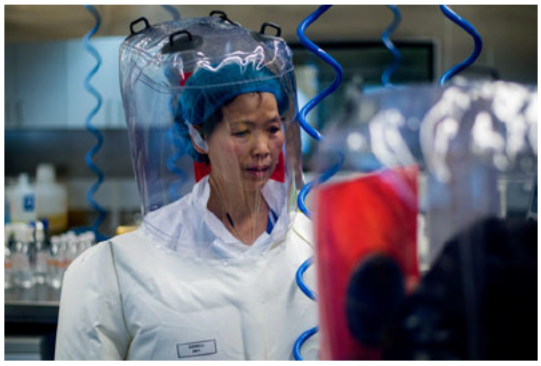
https://www.wsj.com/articles/the-world-needs-a-real-investigation-into-the-origins-of-covid-19-11610728316

LIFE & ARTS | IDEAS | ESSAY

The World Needs a Real Investigation Into the Origins of Covid-19

A team of WHO researchers has arrived in China but won't investigate the possibility that the coronavirus originated in a lab.



Dr. Shi Zhingli, whose lab at the Wuhan Institute of Virology has been a suspected source of the coronavirus, in 2017.
PHOTO: JOHANNES EISELE/AFP/GETTY IMAGES

By Alina Chan and Matt Ridley
Jan. 15, 2021 11:31 am ET

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In the first week of January, scientists representing the World Health Organization (WHO) were due to arrive in China to trace the origins of Covid-19. The team membership and terms of reference were preapproved by the Chinese government, yet at the last minute Beijing denied entry to the investigators. This prompted WHO to take the rare step of criticizing China, which relented and allowed the group to enter the country this week.

The brief standoff highlights a more serious problem: the inadequacy of WHO's current investigative framework for exploring all plausible origins of Covid-19. The world needs an inquiry that considers not just natural origins but the possibility that SARS-CoV-2, the virus that causes Covid-19, escaped from a laboratory. The WHO team, however, plans to build on reports by Chinese scientists rather than mount an independent investigation. Given that Chinese authorities have been slow to release information, penalized scientists and doctors who shared clinical and genomic details of the novel coronavirus, and have since demonstrated a keen interest in controlling the narrative of how the virus emerged, this is not a promising foundation for WHO's investigation.

The WHO team includes experts who traced the origins of Ebola and MERS outbreaks, but critics are concerned that it doesn't have the expertise for an investigation that would examine possible lab origins. Dr. David Relman of Stanford University, who raised the possibility early on that the virus might have leaked from a lab, told us: "Based on the scant information that has been shared publicly about the WHO investigation, it doesn't appear that WHO has adequately represented the range of views and perspectives of key stakeholders or incorporated all needed forms of expertise." Responding to whether the

Critics are concerned that the WHO team doesn't have the expertise for an investigation that would examine possible lab origins of the coronavirus.

WHO team will investigate lab origins, Dr. Peter Ben Embarek, the leader of the team, told us, "If our studies point to a possible lab accident, then other international mechanisms would be involved to document such an event. It would take time and additional types of expertise."

Tedros Adhanom Ghebreyesus, director-general of the World Health Organization, at a press conference in March 2020.

PHOTO: SALVATORE DI NOLFI/ASSOCIATED PRESS

Could the virus have escaped from a laboratory? Then-deputy U.S. national security adviser Matthew Pottinger told international leaders late last year that the latest intelligence points to SARS-CoV-2 having originated from the Wuhan Institute of Virology (WIV). This intelligence has not been made public, and China has denied that the virus came from a lab. Dr. Shi Zhengli, whose lab at WIV has been a suspected source of the virus, told Scientific American last March that "none of the [early SARS-CoV-2] sequences matched those of the viruses her team had sampled from bat caves."

The hypothesis that SARS-CoV-2 originated in a lab remains controversial. Last March, in the journal Nature Medicine, Dr. Kristian Andersen of the Scripps Research Institute and colleagues asserted that "SARS-CoV-2 is not a laboratory construct or a purposefully manipulated virus." They said there was no evidence to support lab-based origins and that the available data was consistent with natural evolution. Dr. David Robertson of the University of Glasgow told us that "SARS-CoV-2 is just too different to the [viruses] we were aware of prior to its emergence."

The ability to build coronavirus genomes without leaving traces of manipulation has existed for years.

In November, however, in the journal PNAS, Dr. Relman wrote that Dr. Andersen's argument didn't acknowledge that unpublished viruses closely related to SARS-CoV-2 could have been studied in a laboratory. For more than a decade, Dr. Shi has been publishing experiments on "chimera" coronaviruses, built by inserting parts of newly found viruses into better known viruses to understand how novel viruses could infect human cells. These were used to assess the risk that such viruses could spill over

into humans.

The ability to build coronavirus genomes without leaving traces of manipulation has existed for years. Dr. Ralph Baric of the University of North Carolina at Chapel Hill, a world-leading coronavirus expert and collaborator of Dr. Shi, told an Italian television documentary last June, "In sequence databases there were sequences for a large number of bat coronaviruses that were SARS-like, reported out of China." He added that "whether the virus existed beforehand, it would only be within the records of the Institute of Virology in Wuhan."

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For some scientists, the location of the first detected outbreak is enough to raise suspicions. In the words of Dr. Richard Ebright of Rutgers University, "the outbreak occurred on the doorstep of laboratories that conduct the world's largest research project on horseshoe-bat viruses, that have the world's largest collection of horseshoe-bat viruses, and that possessed and worked with the world's closest sequenced relative of the outbreak virus. The laboratories actively searched for new horseshoe-bat viruses in horseshoe-bat colonies in caves in remote rural areas in Yunnan province, brought those new horseshoe-bat viruses to Wuhan, and then mass-produced and studied those new horseshoe-bat viruses, year-round, inside Wuhan."

Such concerns have gained prominence over the past year and were recently explored in a much-discussed article in New York magazine, "The Lab-Leak Hypothesis" by Nicholson Baker.

In January 2020, a police officer stands guard outside the seafood market in Wuhan, China, where the coronavirus was first detected.
PHOTO: HECTOR RETAMAL/AFP/GETTY IMAGES

SARS viruses are known to have escaped previously from laboratories in Singapore, Taiwan and twice in Beijing. Dr. Maciej Boni of Pennsylvania State University told us that if the virus escaped from the Wuhan lab (though he thinks this is unlikely), he would expect that "some of the early December cases should be traceable to WIV employees, family members of WIV employees or frequent social contacts of WIV employees. If this evidence is presented, it will be the first 'positive evidence' that SARS-CoV-2 may have a lab origin."

What would it take to properly investigate possible lab origins? Dr. Relman said that "it will be critical to obtain independently verified, time-stamped records of sample

inventories, data, lab notebooks and records, internal and external communications, personnel health records and serum samples, and access to personnel so that they can be interviewed in private without fear of repercussions." Yet the path to such a credible investigation seems nearly impossible in the current geopolitical climate.

Several scientists also told us they were troubled by the presence on the WHO team of Dr. Peter Daszak of the New York-based EcoHealth Alliance. Dr. Daszak has been a longtime collaborator of Dr. Shi since they worked together to trace SARS viruses to bats after the 2003 epidemic. His organization has administered more than $100 million in U.S. federal grants to fund overseas fieldwork and laboratory experiments, including those performed by WIV, to find and characterize new viruses in order to predict the next pandemic, according to the EcoHealth Alliance.

Last February, Dr. Peter Daszak organized a statement in The Lancet, a prominent medical journal, to 'condemn conspiracy theories suggesting that Covid-19 doesn't have a natural origin.'

Last February, Dr. Daszak organized a statement in The Lancet, a prominent medical journal, to "condemn conspiracy theories suggesting that Covid-19 doesn't have a natural origin." The statement was drafted when little was yet known about the virus. Dr. Daszak declined to comment for this piece, but a spokesman for Dr. Daszak told us: "The Lancet letter was written during a time in which Chinese scientists were receiving death threats and the letter was intended as a showing of support for them as they were caught between important work trying to stop an outbreak and the crush of online harassment." Yet, in June, Dr. Daszak wrote an opinion piece for the Guardian headlined, "Ignore the conspiracy theories: scientists know Covid-19 wasn't created in a lab."

The spokesman for Dr. Daszak told us that any questions about his potential conflict of interest should be referred to WHO. Dr. Ben Embarek said that he sees no problem in having Dr. Daszak on his investigative team: "Of course the WHO team will have discussion with the scientists and researchers in Wuhan. And therefore it is good to have on the team someone who knows the area well."

Miles Pomper, a co-author of an expert guide to investigating outbreak origins published in October by the Middlebury Institute of International Studies at Monterey, said that "The independence of the WHO investigation may be seriously compromised by the process used to choose investigators.... In particular, the choice of Dr. Daszak, who has a personal stake in ensuring current Chinese practices continue and who is a longtime collaborator of a scientist at the center of the investigation, is likely to taint its results."

Another co-author of the guide, Dr. Filippa Lentzos, said, "We also need to take a hard look in the mirror. It is our own virologists, funders and publishers who are driving and endorsing the practice of actively hunting for viruses and the high-risk research of deliberately making viruses more dangerous to humans. We need to be more open about the heavily vested interests of some of the scientists given prominent platforms to make claims about the pandemic's origins."

As a scientist and a science writer, we believe that both natural and lab-based scenarios of Covid-19's origins must be rigorously investigated, not only to avert future pandemics but for the sake of science's reputation. The formal investigation launched by WHO is only

taking steps to look into natural origins. That needs to change.

—Dr. Chan is a researcher at the Broad Institute of MIT and Harvard. Mr. Ridley is a member of the House of Lords and the author, most recently, of "How Innovation Works: And Why It Flourishes in Freedom."

Appeared in the January 16, 2021, print edition.

To stop the next pandemic, we need to unravel the origins of COVID-19

David A. Relman[a,b,c,d,1]

We find ourselves ten months into one of the most catastrophic global health events of our lifetime and, disturbingly, we still do not know how it began. What's even more troubling is that despite the critical importance of this question, efforts to investigate the origins of the severe acute respiratory syndrome coronavirus 2 (SARS CoV 2) virus and of the associated disease, coronavirus disease 2019 (COVID 19), have become mired in politics, poorly supported assumptions and assertions, and incomplete information.

SARS CoV 2 is a betacoronavirus whose apparent closest relatives, RaTG13 and RmYN02, are reported to have been collected from bats in 2013 and 2019, respectively, in Yunnan Province, China (1). COVID 19 was first reported in December 2019 more than 1,000 miles away in Wuhan City, Hubei Province, China. Beyond these facts, the "origin story" is missing many key details, including a plausible and suitably detailed recent evolutionary history of the virus, the identity and provenance of its most recent ancestors, and surprisingly, the place, time, and mechanism of transmission of the first human infection. Even though a definitive answer may not be forthcoming, and even though an objective analysis requires addressing

To avoid or mitigate the dire consequences of this and future pandemics (here, people in PPE bury a victim in Delhi, India in June), unraveling the origins of SARS-CoV-2 and COVID-19 will be essential—even though a definitive answer may be elusive, and an objective analysis means broaching some uncomfortable possibilities. Image credit: Shutterstock/PradeepGaurs.

[a]Department of Medicine, Stanford University School of Medicine, Stanford, CA 94305; [b]Department of Microbiology & Immunology, Stanford University School of Medicine, Stanford, CA 94305; [c]Center for International Security and Cooperation, Stanford University, Stanford, CA 94305; and [d]Infectious Diseases Section, Veterans Affairs Palo Alto Health Care System, Palo Alto, CA 94304

The author declares no competing interest.

[1]Email: relman@stanford.edu.

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some uncomfortable possibilities, it is crucial that we pursue this question. Preventing the next pandemic depends on understanding the origins of this one.

There are several potential origin scenarios. First, SARS CoV 2 may have evolved in bats, which are known reservoirs of immense coronavirus diversity (2), and then spread directly, or indirectly via an inter mediate host, to humans through natural mechanisms. The degree of anticipated but undiscovered natural diversity clearly lends support to this scenario, as well as support to other scenarios. Second, SARS CoV 2 or a recent ancestor virus may have been collected by humans from a bat or other animal and then brought to a laboratory where it was stored knowingly or un knowingly, propagated and perhaps manipulated ge netically to understand its biological properties, and then released accidentally.

Some have argued that a deliberate engineering scenario is unlikely because one would not have had the insight *a priori* to design the current pandemic virus (3). This argument fails to acknowledge the pos sibility that two or more as yet undisclosed ancestors (i.e., more proximal ancestors than RaTG13 and RmYN02) had already been discovered and were be ing studied in a laboratory for example, one with the SARS CoV 2 backbone and spike protein receptor binding domain, and the other with the SARS CoV 2 polybasic furin cleavage site. It would have been a logical next step to wonder about the properties of a recombinant virus and then create it in the labora tory. Alternatively, the complete SARS CoV 2 sequence could have been recovered from a bat sample and vi able virus resurrected from a synthetic genome to study it, before that virus accidentally escaped from the lab oratory. The third scenario, seemingly much less l kely, involves laboratory manipulation or release, with the clear intention of causing harm.

Even though strong opinions abound, none of these scenarios can be confidently ruled in or ruled out with currently available facts. Just because there are no public reports of more immediate, proximal ancestors in natural hosts, doesn't mean that these ancestors don't exist in natural hosts or that COVID 19 didn't began as a spillover event. Nor does it mean that they have not been recovered and studied, or deliberately recombined in a laboratory.

Why do these distinctions matter? If we find more concrete evidence of a "spill over" event with SARS CoV 2 passing directly from bat to human, then efforts to understand and manage the bat human interface need to be significantly strengthened. But if SARS CoV 2 escaped from a lab to cause the pandemic, it will become critical to understand the chain of events and prevent this from happening again. Rather than resorting to hunches or finger pointing, each scenario must be systematically and objectively analyzed using the best available science based approaches. There is a path to greater clarity. It requires scientific rigor, fo rensic approaches, deliberate methods, transparency, and cooperation.

In an effort to reveal the origins of the pandemic, researchers so far have focused on the SARS CoV 2 genome sequence. However, the sequence of the pandemic virus tells us only so much. First, the closest known relatives, RaTG13 and RmYN02, are not that close (4). Second, there is probably more than one recent ancestral lineage that contributes to SARS CoV 2 because its genome shows evidence of recom bination between different parental viruses. In nature, recombination is common among coronaviruses. But it's also common in some research laboratories where recombinant engineering is used to study those viruses. The bottom line is simple: We need to iden tify the immediate parent(s) of SARS CoV 2, and they're missing.

To find its parents and understand its recent history, we need 1) additional genome sequences of coronaviruses from relevant bats and other suspect hosts some of these likely exist already in laborato ries, given the efforts so far undertaken to survey bats in particular (2, 5); 2) measurements of SARS CoV 2 evolution under a variety of defined conditions so that differences between viral genomes can be under stood better as differences in time on an evolutionary clock; and 3) data from antibody surveys of humans at high risk of coronavirus exposure and from past cases of similar disease, so that previously unrecognized en counters can be revealed. In addition, we need to ad dress whether there is information about host or environmental samples that contain recent ancestors of SARS CoV 2, data perhaps not yet publicly avail able. More generally, are there relevant scientific data, including from coronavirus engineering work in labo ratories, that have not been shared widely? Who knew what about relevant viruses and cases of disease be fore December 2019, and when? This information will go a long way toward clarifying the origins of this pan demic, even if certainty continues to elude us.

A deliberative process for investigating the origins of this pandemic must be representative of all relevant disciplines, expertise, and stakeholders; must achieve political neutrality, scientific balance, and access to all relevant information and samples; and must operate with transparency and independent oversight. Without these features, it will not be credible, trustworthy, or effective.

The means are just as important as the goals. An investigative process should be transparent, collabo rative, international, and, to the extent possible, de void of political interest. Recent, productive scientific collaborations between the United States and China, for example, provide hope that such a process can be achieved. But the kind of effort required will need to expand far beyond what's taken place so far, and na tions other than the United States and China will need to be involved. Conflicts of interest by researchers, administrators, and policymakers on all sides must be revealed and addressed, and all relevant global

constituencies must be included. Both the World Health Organization and *The Lancet* COVID 19 Commission (6) have hinted that they have taken some first steps, but their efforts so far have been cloaked in secrecy (7, 8). A deliberative process for investigating the origins of this pandemic must be representative of all relevant disciplines, expertise, and stakeholders; must achieve political neutrality, scientific balance, and access to all relevant information and samples; and must operate with transparency and independent oversight. Without these features, it will not be credible, trustworthy, or effective.

A more complete understanding of the origins of COVID 19 clearly serves the interests of every person in every country on this planet. It will limit further recriminations and diminish the likelihood of conflict; it will lead to more effective responses to this pandemic, as well as efforts to anticipate and prevent the next one. It will also advance our discussions about risky science. And it will do something else: Delineating COVID 19's origin story will help elucidate the nature of our very precarious coexistence within the biosphere.

1 Y.-Z. Zhang, E. C. Holmes, A genomic perspective on the origin and emergence of SARS-CoV-2. *Cell* **181**, 223–227 (2020).
2 A. Latinne *et al.*, Origin and cross-species transmission of bat coronaviruses in China. *Nat. Commun.* **11**, 4235 (2020).
3 K. G. Andersen, A. Rambaut, W. I. Lipkin, E. C. Holmes, R. F. Garry, The proximal origin of SARS-CoV-2. *Nat. Med.* **26**, 450–452 (2020).
4 M. F. Boni *et al.*, Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic. *Nat. Microbiol.* (2020).
5 Z. Wu *et al.*, Deciphering the bat virome catalog to better understand the ecological diversity of bat viruses and the bat origin of emerging infectious diseases. *ISME J.* **10**, 609–620 (2016).
6 J. D. Sachs *et al.*; The Lancet COVID-19 Commission. *Lancet* **396**, 454–455 (2020).
7 World Health Organization, WHO experts to travel to China. https://www.who.int/news-room/detail/07-07-2020-who-experts-to-travel-to-china/. Accessed 20 September 2020.
8 P. Nuki, S. Newey, Scientists to examine possibility Covid leaked from lab as part of investigation into virus origins. *The Telegraph*, 15 September 2020. https://www.telegraph.co.uk/global-health/science-and-disease/scientists-examine-possibility-covid-leaked-lab-part-investigation/. Accessed 27 September 2020.

From:	Kosub, David (NIH/OD) [E]
To:	Lauer, Michael (NIH/OD) [E]
Cc:	Columbus, Megan (NIH/OD) [E]; Rabin, Elise (NIH/OD) [E]
Subject:	FW: NIAID Response: E&C June 23 QFRs NIAID - OMB Passback - DUE TUE 12PM
Date:	Monday, December 7, 2020 1:24:32 PM
Attachments:	HWM206 - HHS QFRs COVID June 23 EC - Fauci- passback_NIAID.docx

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David

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Sent: Monday, December 7, 2020 12:12 PM
To: Kosub, David (NIH/OD) [E] (b) (6); Rabin, Elise (NIH/OD) [E] (b) (6)
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Let me know if you have any questions. Thank you,
Karen

From: "Hastings, Andrew (NIH/NIAID) [E]" (b) (6)
Date: Monday, December 7, 2020 at 11:56 AM
To: Karen LaMontagne (b) (6)
Cc: NIAID OCGR Leg (b) (6)
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We appreciate the opportunity to review. Please let us know if you have any questions.

Thanks,
Drew

Cell #: (b) (6)

Andrew K. Hastings, Ph.D.
Public Health Analyst
Legislative Affairs and Correspondence Management Branch
Office of Communications and Government Relations
NIAID/NIH/DHHS
Bldg. 31, Room 7A17, MSC 2520
Bethesda, MD 20892-2520
(b) (6)

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Sent: Monday, December 7, 2020 8:59 AM
To: NIAID OCGR Leg (b) (6)
Subject: E&C June 23 QFRs NIAID - OMB Passback - DUE TUE 12PM

Good Morning, Team NIAID,

Attached is the OMB passback to the 6/23 hearing QFRs. Please review and respond to each comment indicating whether NIAID accepts or rejects w/ explanation.

ASL has requested our **responses by noon tomorrow, Tuesday 12/8** because OMB is concerned that Congress might adjourn by end of the week. Please let me know if that quick turnaround isn't possible.

Thank you,
Karen

Committee on Energy and Commerce

Hearing on
"Oversight of the Trump Administration's Response to the COVID-19 Pandemic"

June 23, 2020

Anthony S. Fauci, M.D., Director, National Institute of Allergy and Infectious Diseases, National Institutes of Health

The Honorable Frank Pallone, Jr. (D-NJ)

1. It is perplexing that the Trump Administration decided to cancel a research grant that was specifically focused on coronavirus emergence while we are in the midst of a coronavirus pandemic.

   Over 70 Nobel-prize winning American scientists raised alarm about this move, saying it "sets a dangerous precedent by interfering in the conduct of science" and "deprives the nation and the world of highly regarded science that could help control one of the greatest health crises in modern history and those that may arise in the future." More than 30 different scientific societies expressed concern with this decision as well.

   The reported reason for this grant's cancellation was because the Administration "does not believe the current project outcome aligns with the program goals and agency priorities."

   a. What does the science around the coronavirus show regarding the virus's origins? Does the science show that the coronavirus was initially created in a lab or does it show that it was transmitted from an animal to a human?

NIH Response:

(b) (5)

   b. How would research such as the EcoHealth Alliance grant titled, "Understanding the Risk of Bat Coronavirus Emergence" (funded under grant R01 AI110964 and terminated on April 24, 2020), be relevant to the coronavirus pandemic we are experiencing today?

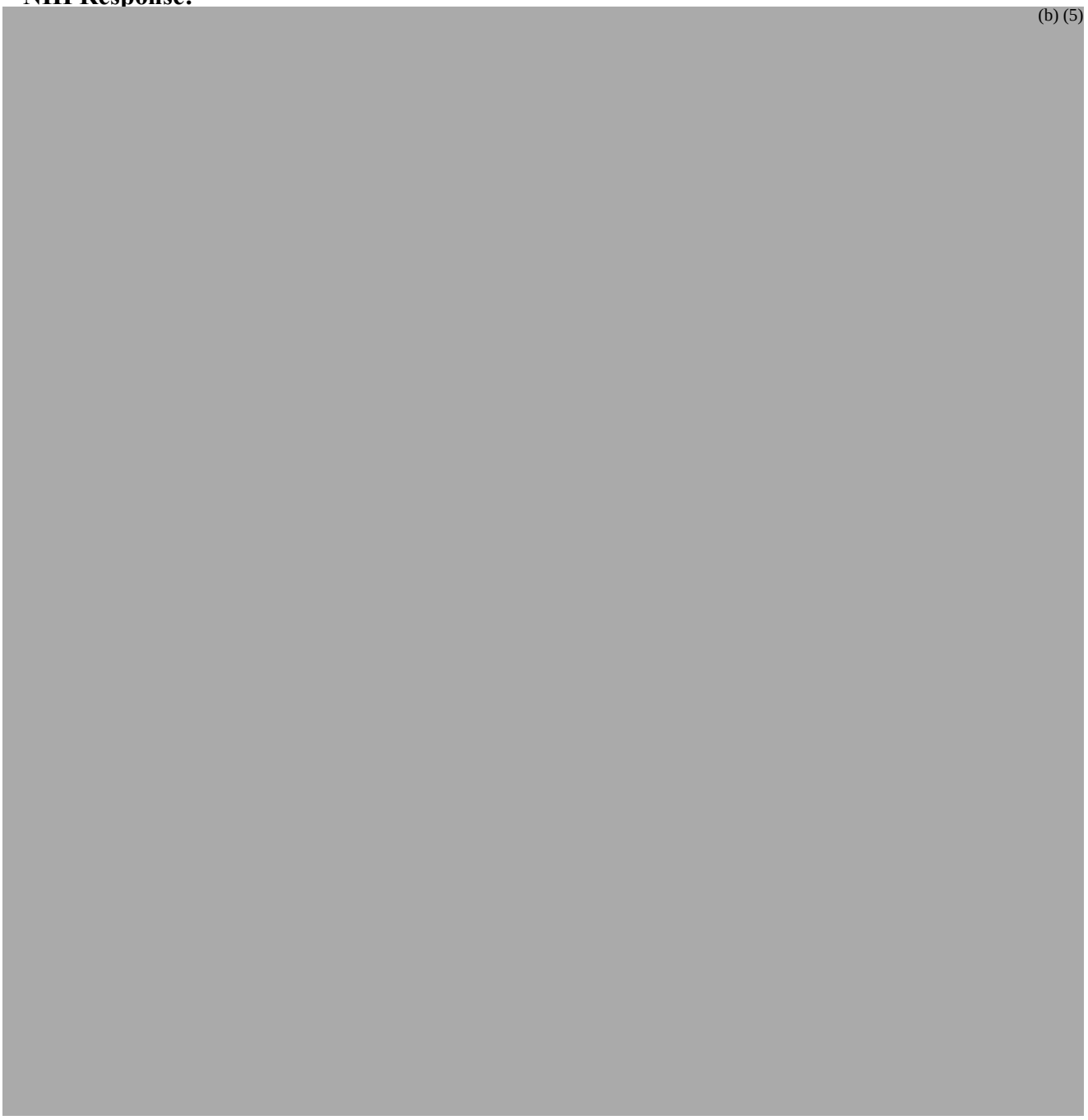
NIH Response:

(b) (5)

a. What actions is Operation Warp Speed or the ACTIV partnership taking to address inequities in our research and development of vaccines or treatments for COVID-19?

NIH Response:

(b) (5)



Question 2 from The Honorable Frank Pallone, Jr. (D-NJ) continued

Participation aside, we must also make sure approved treatments are effective for all communities. In the case of coronavirus treatment candidates, for example, while results from the Remdesivir clinical trial were positive, the recovery rate ratio reported for Black,

Hispanic/Latino, and Asian participants was less than that of White participants. No such reporting line for American Indians or Alaska Natives existed.

Additionally, while news has emerged about another possible breakthrough treatment from the University of Oxford, there is some evidence that some minority populations may respond differently to this type of drug compared to White patients

b. What have the studies shown regarding why Remdesivir may be less effective for Black, Hispanic/Latino, and Asian patient populations? How will the Department of Health and Human Services (HHS) ensure that clinical trials for medical treatments for COVID-19 move forward that benefits or risks for certain populations are adequately communicated?

NIH Response:

(b) (5)

[redacted]

[1] https://www.nejm.org/doi/full/10.1056/NEJMoa2007764

(b) (5)

[redacted]

The Honorable Anna G. Eshoo (D-CA)

1. When does the National Institutes of Health (NIH) anticipate beginning human clinical trials on candidates you are supporting?

NIH Response:

(b) (5)

[redacted]

(b) (5)

2. How many people will need to enroll in these clinical trials to get adequate data?

NIH Response:

(b) (5)

3. How quickly will you be able to assess a vaccine candidate's safety and effectiveness, the standards for the Food and Drug Administration (FDA) approval, after the trials begin?

NIH Response:

(b) (5)

(b) (5)

[redacted]

4. Would early clinical trial data showing that a patient develops high levels of antibodies without severe side effects be enough to demonstrate safety and effectiveness of a vaccine?

NIH Response:

(b) (5)

[redacted]

5. What additional data is necessary to prove that a vaccine is safe and effective?

NIH Response:

[2] https://www fda.gov/media/139638/download
[3] https://www.fda.gov/media/142749/download

(b) (5)

[redacted]

The Honorable Diana DeGette (D-CO)

1. We have seen the importance of medical research that relies on fetal tissue for developing vaccines including polio, rubella, measles, chickenpox, adenovirus, rabies, as well as treatments for debilitating diseases such as rheumatoid arthritis, cystic fibrosis, and hemophilia. Hundreds of millions of lives have been saved worldwide because of these advancements. What ways can research using fetal tissue be used to help scientists find a treatment, cure, or vaccine for COVID-19?

NIH Response:

(b) (5)

[redacted]

The Honorable Jerry McNerney (D-CA)

1. Do you think that the President's words, actions, or lack of actions, much of which either have ignored or acted against expert medical or epidemiological advice, has enabled the virus to spread beyond what it should have, causing unnecessary illness and death?

NIH Response:

(b) (5)

[redacted]

The Honorable Gus M. Bilirakis (R-FL)

1. What have you learned about the management of chronic care conditions (like diabetes, hypertension, asthma, etc.) with regard to complications and poor outcomes associated with COVID-19?

    a. Are there differences between patients who manage their condition well versus those who don't?

NIH Response:

(b) (5)

[redacted]

b. Can certain treatments make these patients even more susceptible to adverse COVID-19 outcomes – how is this data captured and communicated to patients and their providers expeditiously?

NIH Response:

(b) (5)

2. As policy makers consult the data to direct response efforts, where do you suggest the goal posts be erected – in other words, where should the bulk of our attention and resources be directed as states reopen?

    a. Is it about total confirmed cases, hospitalizations, or deaths?

NIH Response:

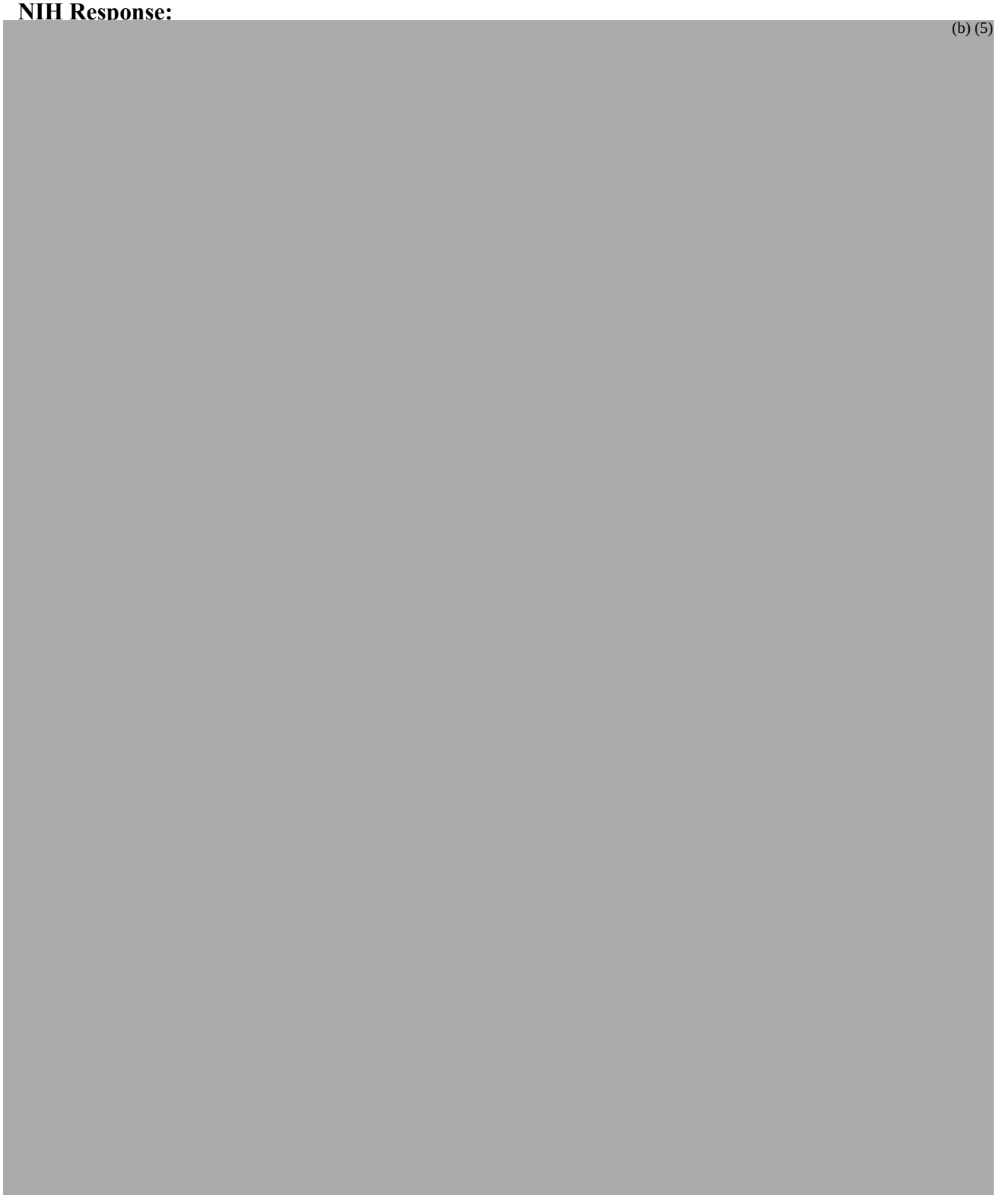
(b) (5)

[4] https://www.covid19treatmentguidelines nih.gov/
[5] https://www.whitehouse.gov/openingamerica/

b. Does a response addressing mortality have different considerations than one that prioritizes transmissibility?

NIH Response:

(b) (5)



(b) (5)

[redacted]

3. As we learn more about how COVID has unfolded in our country, we are seeing that it has had a disproportionate impact on certain populations, especially those in nursing homes, frontline healthcare workers, and Native Americans. The underlying challenges that caused these populations to be hard hit in the first place will still be around when we get to the resurgence of COVID in the fall. For example, nursing home patients will continue to have major underlying health conditions; healthcare workers will continue to have the highest exposure risks, even as the demands placed on them increase; and Native Americans will continue to have challenges receiving primary and secondary care services.

    a. Recognizing the challenges for each of these populations, can you describe what special considerations should be made for testing and treatment needs of these populations above and beyond what a response plan might be for the general population?

NIH Response:

(b) (5)

[redacted]

[6] https://www.covid19treatmentguidelines nih.gov/

(b) (5)

[redacted]

b. Can you describe the role of the Federal government to ensure that it is able to provide sufficient testing and treatment needs of these populations?

NIH Response:

(b) (5)

[redacted]

4. Are there any underreported successes in the Administration's COVID-19 response that you would like to discuss?

NIH Response:

(b) (5)

[redacted]

The Honorable Earl L. "Buddy" Carter (R-GA)

1. My understanding is that there are a number of drugs currently in shortage or at-risk of being in shortage. In some cases, the ingredients that go into making these drugs are manufactured exclusively overseas which presents national security concerns. I also read that some of the products in the national stockpile needed to be discarded because they had passed their expiration date.

    a. What do you think about using the existing commercial distribution network here in the U.S. to manage and replenish a supply of pharmaceutical products identified by the government as being at high risk of market disruption?

NIH Response:

(b) (5)

    b. Wouldn't a government-private sector arrangement to ensure we have a stockpile of needed medicines available enable us to address the ongoing shortage concerns and more urgently, ensure we are prepared for future unforeseen health care outbreaks?

NIH Response:

(b) (5)

    c. How can we develop a longer-term solution to this problem so we are ready for the evolution of the current crisis and for critical patient needs for these products in the future?

NIH Response:

(b) (5)

2. All of the vaccines being developed appear to be focused on the spike protein which can and does mutate. Should we be looking at the non-mutating part of the virus?

    a. In particular, what about consideration of other targets for immune-therapy?

NIH Response:

(b) (5)

[redacted]

3. I understand that the National Institute of Allergy and Infectious Diseases (NIAID) has worked in the past with an immunotherapy company that tested ligand epitope antigen presentation system (LEAPS) technology as a new immune-based treatment for influenza virus infection in a mouse model. The study demonstrated a reduction in virus replication in the lungs, enhance survival, and modulate the protective immune responses that eliminate the virus while preventing excessive cytokines that could injure the host. In other words, it reduced mortality and morbidity. And that further work in collaboration with the University of Georgia Vaccine Center is prepared to move forward with further research in this direction.

    a. Do you think this approach (based on previous studies at NIAID) holds some promise as an adjunct to antiviral treatment of COVID-19?

NIH Response:

(b) (5)

[redacted]

(b) (5)

From:	Lauer, Michael (NIH/OD) [E]
To:	Kosub, David (NIH/OD) [E]
Cc:	Columbus, Megan (NIH/OD) [E]; Rabin, Elise (NIH/OD) [E]; Lauer, Michael (NIH/OD) [E]
Subject:	Re: NIAID Response: E&C June 23 QFRs NIAID - OMB Passback - DUE TUE 12PM
Date:	Tuesday, December 8, 2020 11:23:11 PM

Thanks David – looks fine.

Mike

From: "Kosub, David (NIH/OD) [E]" (b) (6)
Date: Tuesday, December 8, 2020 at 12:40 PM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Cc: "Columbus, Megan (NIH/OD) [E]" (b) (6), "Rabin, Elise (NIH/OD) [E]" (b) (6)
Subject: RE: NIAID Response: E&C June 23 QFRs NIAID - OMB Passback - DUE TUE 12PM

Good day Mike, wanted to follow up on this proposed response. The two questions we were asked to review focused around (1) the origins of the outbreak and (2) how the EcoHealth grant relates to the current pandemic. I am wondering if the following answers may more directly answer the questions (which were pulled from vetted language), and also includes your statement at the end of the 2nd answer. Appreciate your look again.

1. It is perplexing that the Trump Administration decided to cancel a research grant that was specifically focused on coronavirus emergence while we are in the midst of a coronavirus pandemic. Over 70 Nobel-prize winning American scientists raised alarm about this move, saying it "sets a dangerous precedent by interfering in the conduct of science" and "deprives the nation and the world of highly regarded science that could help control one of the greatest health crises in modern history and those that may arise in the future." More than 30 different scientific societies expressed concern with this decision as well. The reported reason for this grant's cancellation was because the Administration "does not believe the current project outcome aligns with the program goals and agency priorities."
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Response: (b) (5)

(b) (5)

[redacted]

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To: Kosub, David (NIH/OD) [E] (b) (6)
Cc: Columbus, Megan (NIH/OD) [E] (b) (6); Rabin, Elise (NIH/OD) [E] (b) (6); Lauer, Michael (NIH/OD) [E] (b) (6)
Subject: Re: NIAID Response: E&C June 23 QFRs NIAID - OMB Passback - DUE TUE 12PM

Thanks David – let's use this language: (b) (5) [redacted]

Thanks, Mike

From: "Kosub, David (NIH/OD) [E]" (b) (6)
Date: Monday, December 7, 2020 at 1:24 PM
To: "Lauer, Michael (NIH/OD) [E]" (b) (6)
Cc: "Columbus, Megan (NIH/OD) [E]" (b) (6), "Rabin, Elise (NIH/OD) [E]" (b) (6)
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From:	Lauer, Michael (NIH/OD) [E]
To:	Aleksei Chmura; Peter Daszak
Cc:	Stemmy, Erik (NIH/NIAID) [E]; Erbelding, Emily (NIH/NIAID) [E]; Linde, Emily (NIH/NIAID) [E]; Bulls, Michelle G. (NIH/OD) [E]; Compliance Review; Ta, Kristin (NIH/OD) [E]
Subject:	Re: PLEASE READ -- Re: Please read and acknowledge receipt -- update regarding 2R01AI110964-06
Date:	Friday, October 23, 2020 2:57:16 PM
Attachments:	NIH Response to EcoHealth Response to Suspension_10_23_20.pdf

Dear Dr. Chmura and Dr. Daszak

Please see attached.

Sincerely,
Michael S Lauer, MD

Michael S Lauer, MD
NIH Deputy Director for Extramural Research
1 Center Drive, Building 1, Room 144
Bethesda, MD 20892
Phone: (b) (6)
Email: (b) (6)

DEPARTMENT OF HEALTH & HUMAN SERVICES

Public Health Service

National Institutes of Health
National Institute of Allergy
and Infectious Diseases
Bethesda, Maryland 20892

23 October 2020

Drs. Aleksei Chmura and Peter Daszak
EcoHealth Alliance, Inc.
460 W 34th St
Suite 1701
New York, NY 10001

Re: NIH Grant R01AI110964

Dear Drs. Chmura and Daszak:

I am following up on Mr. Krinsky's August 13, 2020, letter on behalf of EcoHealth Alliance, Inc. ("EcoHealth") responding to NIH's suspension of grant R01AI110964, which funds the project *Understanding the Risk of Bat Coronavirus Emergence* (the "Project"). Per my letter of July 8, 2020, NIH reinstated the grant but suspended all award activities because we have concerns that the Wuhan Institute of Virology (WIV), which previously served as a subrecipient of the Project, had not satisfied safety requirements that applied to its subawards with EcoHealth, and that EcoHealth had not satisfied its obligations to monitor the activities of its subrecipient to ensure compliance. EcoHealth objected to the suspension on the grounds that WIV has no *current* connection to the Project or EcoHealth's research, and EcoHealth had not issued any subawards in connection with the Grant *at the time of the suspension*.

The fact that EcoHealth does not currently have a subrecipient relationship with WIV and had not issued subawards to WIV at the time of suspension does not absolve EcoHealth of any past non-compliance with the terms and conditions of award for grant R01AI110964. While EcoHealth did not issue a subaward to WIV for year 6 of the grant, WIV served as a subrecipient for years 1 through 5. NIH awarded EcoHealth grant R01AI110964 in 2014, with a project period of June 1, 2014, through June 30, 2024, as renewed. In EcoHealth's grant application, EcoHealth listed Drs. Zheng Li Shi and Xing Yi Ge of WIV as co-investigators and senior/key personnel. It stated that "Drs. Shi, Zhang, and Daszak have collaborated together since 2002 and have been involved in running joint conferences, and shipping samples into and out of China." EcoHealth listed WIV as a Project/Performance Site Location. In describing WIV's facilities, EcoHealth described WIV as China's premier institute for virological research" and touted WIV's "fully equipped biosafety level 3 laboratory" and "a newly opened BLS-4 laboratory." In support of the application, Dr. Zheng Li Shi's personal statement indicated that "My lab will be responsible for diagnosis, genomics and isolation of coronavirus from wild and domestic animals in Southern China and for analyzing their receptor binding domains." The application stated that "Wuhan Institute of Virology and the Wuhan University Center for Animal Experiment BSL-3

lab have an Internal Biosafety Committee and are accredited BSL-2 and BSL 3 laboratories. All experimental work using infectious material will be conducted under appropriate biosafety standards. Disposal of hazardous materials will be conducted according to the institutional biosafety regulations."

EcoHealth requested funding specifically for activities to be carried out by WIV. NIH awarded EcoHealth a total of $749,976 for WIV's work in the following annual amounts for years 1 through 5:

	-Yr 1	-Yr 2	-Yr 3	-Yr 4	-Yr 5
Total Direct Costs	$123,699	$128,718	$147,335	$147,335	$147,335
F&A Costs @ 8%	$9,896	$10,297	$11,787	$11,787	$11,787
TOTAL COSTS	$133,595	$139,015	$159,122	$159,122	$159,122

As stated in the Notices of Award for each budget period of the grant, the awards were subject to terms and conditions, which include the NIH Grants Policy Statement (GPS) and applicable HHS grant regulations. As I indicated in my letter of July 8, 2020, as a term and condition of award EcoHealth was required to "monitor the activities of the subrecipient as necessary to ensure that the subaward is used for authorized purposes, in compliance with Federal statutes, regulations, and the terms and conditions of the subaward . . ." 45 C.F.R. § 75.352(d). See also, 45 C.F.R. § 75.342(a) ("The non-Federal entity is responsible for oversight of the operations of the Federal award supported activities."). Moreover, EcoHealth was required to "Establish and maintain effective internal control over the Federal award that provides reasonable assurance that the non-Federal entity is managing the Federal award in compliance with Federal statutes, regulations, and the terms and conditions of the Federal award[.]" 45 C.F.R. § 75.303(a). The Notice of Award stated that as a term and condition of award, "Research funded under this grant must adhere to the [CDC/NIH Biosafety in Microbiological and Biomedical Laboratories (BMBL)]." Moreover, the NIH GPS provides that NIH grant recipients are expected to provide safe working conditions for their employees and foster work environments conducive to high-quality research. NIH GPS, Section 4. The terms and conditions of the grant award flow down to subawards to subrecipients, so these terms applied to WIV. 45 C.F.R. § 75.101.

As I stated, NIH has concerns of non-compliance with terms and conditions of award—namely, that WIV had not satisfied safety requirements under the award and that EcoHealth Alliance had not satisfied its obligations to monitor the activities of its subrecipient to ensure compliance. Accordingly, NIH suspended all activities related to R01AI110964, pursuant to 45 C.F.R. § 75.371, Remedies for Noncompliance, which permits suspension of award activities in cases of non-compliance, and the NIH GPS, Section 8.5.2, which permits NIH to take immediate action to suspend a grant when necessary to protect the public health and welfare.

In my letter of July 8, 2020, I provided EcoHealth with the opportunity to object and to provide information and documentation challenging the suspension. Specifically, I sought information and materials that speak to WIV's lab safety and EcoHealth's oversight of its subrecipient, and an inspection of WIV's laboratory records and facilities. I indicated that as a specific condition of award, during the period of suspension, EcoHealth Alliance may not allow research under this

project to be conducted and that no funds from grant R01AI110964 may be provided to or expended by EcoHealth Alliance or any subrecipients.

EcoHealth objected to the requests on the grounds that "NIAID is not authorized under 45 CFR§§ 75.371, 75.205, and 75.207, entitled *Specific Award Conditions*, to impose, *inter alia*, conditions that consist of demands for information regarding entities that are neither subrecipients of grant funds nor project affiliates."

These provisions are irrelevant to NIH's requests. NIH is required to permit the opportunity for recipients to object and provide information and documentation challenging a suspension, 45 C.F.R. § 75.374, so we specifically gave EcoHealth the opportunity to provide information that speaks to NIH's concerns. Moreover, as a granting agency, NIH is required to "manage and administer the Federal award in a manner so as to ensure that Federal funding is expended and associated programs are implemented in full accordance with U.S. statutory and public policy requirements: Including, but not limited to, those protecting public welfare [and] the environment[.]" 45 C.F.R. § 75.300(a). In addition to seeking information that speaks to compliance with terms and conditions of award, NIH is entitled to "make site visits as warranted by program needs." 45 C.F.R. § 75.342. As a term and condition of award, NIH "must have the right of access to any documents, papers, or other records of the non-Federal entity which are pertinent to the Federal award, in order to make audits, examinations, excerpts, and transcripts" (45 C.F.R. § 75.364); and must have "timely and reasonable access to the non-Federal entity's personnel for the purpose of interview and discussion related to such documents" (id.). These requirements flow down to subawards to subrecipients. 45 C.F.R. § 75.101. "Non-Federal entities must comply with requirements in [45 C.F.R. Part 75] regardless of whether the non-Federal entity is a recipient or subrecipient of a Federal award." 45 C.F.R. 75.101. As the grantee, EcoHealth was required to have in place, "A requirement that the subrecipient permit the pass-through entity and auditors to have access to the subrecipient's records and financial statements as necessary for the pass-through entity to meet the requirements of this part." 45 C.F.R. § 75.352(a)(5). For each of these reasons, NIH is justified in seeking the materials, information, and a site visit specified in my letter of July 8, 2020.

In addition to objecting to NIH's authority to seek the materials, information, and a site visit, EcoHealth has responded that it lacks knowledge or information regarding the requests; that it is not in possession, custody, or control of the specified items; and that it has no authority to grant NIAID and the U.S. National Academy of Sciences access to WIV's facility to conduct an inspection. EcoHealth's responses have not satisfied NIH's concerns that EcoHealth had failed to adequately monitor the compliance of its subrecipient, and that the subrecipient, WIV, had failed to comply with safety requirements.

Notwithstanding this, NIH is providing an additional opportunity for EcoHealth to provide information and documentation challenging these concerns of non-compliance. Accordingly, in addition to reiterating our prior requests (1) through (6) per our letter of July 8, 2020, NIH requests the following information and materials, which must be complete and accurate:

1. Provide copies of all EcoHealth Alliance – WIV subrecipient agreements as well as any other documents and information describing how EcoHealth Alliance monitored WIV's compliance with the terms and conditions of award, including with respect to biosafety.
2. Describe EcoHealth's efforts to evaluate WIV's risk of noncompliance with Federal statutes, regulations, and the terms and conditions of the subaward.
3. Provide copies of all WIV biosafety reports from June 1, 2014 through May 31, 2019.

During the ongoing period of suspension, NIH will continue to review the activities under this award, taking into consideration information provided by EcoHealth Alliance, to further assess whether EcoHealth Alliance and WIV complied with the terms and conditions of award, including compliance with other terms and conditions of award that may be implicated. We remind you that during the period of suspension, EcoHealth Alliance may not allow research under this project to be conducted. Further, no funds from grant R01AI110964 may be provided to or expended by EcoHealth Alliance or any subrecipients; all such charges are unallowable. It is EcoHealth Alliance's responsibility as the recipient of this grant award to ensure that the terms of this suspension are communicated to and understood by all subrecipients. EcoHealth Alliance must provide adequate oversight to ensure compliance with the terms of the suspension. Any noncompliance of the terms of this suspension must be immediately reported to NIH. EcoHealth Alliance will receive a revised Notice of Award from NIAID indicating the continued suspension of these research activities and funding restrictions as a specific condition of award.

Please note that this action does not preclude NIH from taking additional corrective or enforcement actions pursuant to 45 C.F.R. Part 75, including, but not limited to, terminating the grant award or disallowing costs. NIH may also take other remedies that may be legally available if NIH discovers other violations of terms and conditions of award on the part of EcoHealth Alliance or WIV.

Sincerely,

Michael S Lauer, MD
NIH Deputy Director for Extramural Research
Email: (b) (6)

cc: Dr. Erik Stemmy (NIAID)
Ms. Emily Linde (NIAID)

Organizer: Lauer, Michael (NIH/OD) [E] (b) (6)

From: Showe, Melanie (NIH/OD) [E][/o=ExchangeLabs/ou=Exchange Administrative Group (FYDIBOHF23SPDLT)/cn=Recipients/cn=fbbbc74184e64f7e8a12d9faf8deb58f-showem]

Location: Zoom - see below

Importance: Normal

Subject: NIH Bipartisan Briefing with E&C Committee re EcoHealth

Start Time: Mon 6/28/2021 2:30:00 PM (UTC-05:00)

End Time: Mon 6/28/2021 3:30:00 PM (UTC-05:00)

Re: CONFIRMED | Drs. Tabak and Lauer Bipartisan Briefing with Authorizers re EcoHealth, Mon, 6/28, 3:30-4:30 pm ET

6.28 Briefing Packet

DATE:	Monday, June 28, 2021
TIME:	3:30-4:30 pm ET
COORDINATES:	**Join ZoomGov Meeting** https://nih.zoomgov.com/ (b) (6) Meeting ID: 161 864 0460 Passcode: nihec **One tap mobile** +16692545252,, (b) (6) # US (San Jose) +16468287666,, (b) (6) # US (New York)
PURPOSE:	NIH Bipartisan Briefing with E&C Committee re EcoHealth
ATTENDEES:	E&C Committee members Lawrence Tabak Michael Lauer Larry Lohmann Kelsey Mellette (HHS/ASL) Jenn Schmalz (HHS/ASL) Anne Tatem (HHS/ASL) Kimberly Espinosa (HHS/ASL, tentative)

To: Simon, Dina (NIH/OD) [C] (b) (6); Showe, Melanie (NIH/OD) [E] (b) (6)
Cc: Burrus-Shaw, Cyndi (NIH/OD) [E] (b) (6) Higgins, Lauren (NIH/OD) [E] (b) (6); Lohmann, Larry (NIH/OD) [E] (b) (6)
From: Casselle, Julia (NIH/OD) [E][/o=ExchangeLabs/ou=Exchange Administrative Group (FYDIBOHF23SPDLT)/cn=Recipients/cn=13031ef577de4ca791adddf09f2f6125-casselleje]
Sent: Thur 6/24/2021 3:37:43 PM (UTC-05:00)
Subject: Re: CONFIRMED | Drs. Tabak and Lauer Bipartisan Briefing with Authorizers re EcoHealth, Mon, 6/28, 3:30-4:30 pm ET

Good afternoon, Dina and Melanie.

The Energy & Commerce Committee would like to change the briefing to virtual, but it will still be 60 minutes. Please see details below.

DATE:	Monday, June 28, 2021
TIME:	3:30-4:30 pm ET
COORDINATES:	**Join ZoomGov Meeting** https://nih.zoomgov.com/j/ (b) (6) Meeting ID: 161 864 0460 Passcode: nihec **One tap mobile** +16692545252,, (b) (6) US (San Jose) +16468287666,, (b) (6) US (New York)
PURPOSE:	NIH Bipartisan Briefing with E&C Committee re EcoHealth
ATTENDEES:	E&C Committee members Lawrence Tabak Michael Lauer Larry Lohmann Kelsey Mellette (HHS/ASL) Jenn Schmalz (HHS/ASL) Anne Tatem (HHS/ASL) Kimberly Espinosa (HHS/ASL, tentative)

Thanks,
Julia

From: "Simon, Dina (NIH/OD) [C]" (b) (6)
Date: Wednesday, June 23, 2021 at 1:47 PM
To: "Casselle, Julia (NIH/OD) [E]" (b) (6), "Showe, Melanie (NIH/OD) [E]" (b) (6)
Cc: Cyndi Burrus-Shaw (b) (6), "Higgins, Lauren (NIH/OD) [E]" (b) (6), "Lohmann, Larry (NIH/OD) [E]" (b) (6)
Subject: Re: CONFIRMED | Drs. Tabak and Lauer Bipartisan Briefing with Authorizers re EcoHealth, Mon, 6/28, 3:30-4:30 pm ET

Thank you

From: "Casselle, Julia (NIH/OD) [E]" (b) (6)
Date: Wednesday, June 23, 2021 at 1:45 PM
To: "Simon, Dina (NIH/OD) [C]" (b) (6), "Showe, Melanie (NIH/OD) [E]" (b) (6)
Cc: "Burrus-Shaw, Cyndi (NIH/OD) [E]" (b) (6), "Higgins, Lauren (NIH/OD) [E]"

(b) (6), "Lohmann, Larry (NIH/OD) [E]" (b) (6)
Subject: Re: CONFIRMED | Drs. Tabak and Lauer Bipartisan Briefing with Authorizers re EcoHealth, Mon, 6/28, 3:30-4:30 pm ET

Hi, Dina.

Thanks for checking. It would be in-person on the Hill.

Julia

From: "Simon, Dina (NIH/OD) [C]" (b) (6)
Date: Wednesday, June 23, 2021 at 1:43 PM
To: "Casselle, Julia (NIH/OD) [E]" (b) (6), "Showe, Melanie (NIH/OD) [E]" (b) (6)
Cc: Cyndi Burrus-Shaw (b) (6), "Higgins, Lauren (NIH/OD) [E]" (b) (6), "Lohmann, Larry (NIH/OD) [E]" (b) (6)
Subject: Re: CONFIRMED | Drs. Tabak and Lauer Bipartisan Briefing with Authorizers re EcoHealth, Mon, 6/28, 3:30-4:30 pm ET

Hi, Julia –

Thanks. Just for clarity, will the meeting be in-person on the Hill or NIH?

From: "Casselle, Julia (NIH/OD) [E]" (b) (6)
Date: Wednesday, June 23, 2021 at 11:37 AM
To: "Simon, Dina (NIH/OD) [C]" (b) (6), "Showe, Melanie (NIH/OD) [E]" (b) (6)
Cc: "Burrus-Shaw, Cyndi (NIH/OD) [E]" (b) (6), "Higgins, Lauren (NIH/OD) [E]" (b) (6), "Lohmann, Larry (NIH/OD) [E]" (b) (6)
Subject: CONFIRMED | Drs. Tabak and Lauer Bipartisan Briefing with Authorizers re EcoHealth, Mon, 6/28, 3:30-4:30 pm ET

Good morning, Dina and Melanie.

This briefing will be in-person and is confirmed for Monday, 6/28 at 3:30-4:30 pm ET. As soon as I have more details about location and attendees, I will provide updates.

Thanks,
Julia

Julia Casselle
Assistant to the Director, Office of Legislative Policy and Analysis
National Institutes of Health
Building 1, Room 244
Bethesda, MD 20892-0160
Main: (301) 496-3471
Direct: (b) (6)
Mobile: (b) (6)
Fax: (301) 496-0840
Email: (b) (6)

From:	Hallett, Adrienne (NIH/OD) [E]
To:	Tabak, Lawrence (NIH/OD) [E]; Lauer, Michael (NIH/OD) [E]; Simon, Dina (NIH/OD) [C]; Burrus-Shaw, Cyndi (NIH/OD) [E]; Showe, Melanie (NIH/OD) [E]
Cc:	Casselle, Julia (NIH/OD) [E]; Lohmann, Larry (NIH/OD) [E]; Everett, Chris (NIH/OD) [E]
Subject:	6.28 Briefing Packet
Date:	Friday, June 25, 2021 9:29:18 AM
Attachments:	E&C WIV Response Briefing 6.28.pdf

One fact to note: Diane Cutler is on detail to the Committee from the HHS OIG office. She is planning to attend the briefing.

House Committee on Energy and Commerce Briefing Materials

Logistics:

DATE:	Monday, June 28, 2021
TIME:	3:30 – 4:30 pm
COORDINATES:	BY Video Format TBD
PURPOSE:	NIH Bipartisan Briefing with E&C Committee re EcoHealth
ATTENDEES:	Lawrence Tabak Michael Lauer House E&C Committee Staff Alan Slobodin (Minority) Bijuan "BJ" Koohmaraie (Minority) Diane Cutler (Minority) Kevin McAloon (Majority, tentative) Chris Knauer (Majority, tentative) Larry Lohmann (NIH OLPA) Kelsey Mellette (HHS/ASL) Jenn Schmalz (HHS/ASL) Anne Tatem (HHS/ASL, tentative) Kimberly Espinosa (HHS/ASL, tentative)

Background:

- On March 18, 2021, E&C's Ranking Member Cathy McMorris Rodgers (R-WA), along with two subcommittee Ranking Members (Reps. Guthrie and Griffiths), sent Dr. Collins a letter to investigate the origins of COVID-19.
    - The letter is 11 pages long with 49 questions and sub-questions.
    - NIH sent a narrative response to this letter on May 21, 2021 and offered a briefing.
- On June 10, 2021, E&C's Ranking Member, along with 25 Republican Members, sent Dr. Collins a follow-up letter with 10 additional questions regarding the origins of COVID-19.
- Note: Diane Cutler is on detail to the Committee from the HHS OIG office.

(b) (5)

(b) (5)

Run of Show:

- HHS ASL staff will open the call and make introductions.
- They will then reiterate the parameters for the call.
    - The briefing is in response to the first letter.
    - The response to the letter from June 10, 2021 is in process.
    - The Call has a hard stop at 1 hour.
- HHS will then hand it over to Dr. Tabak and Dr. Lauer.
- Dr Tabak will open and proceed through the grant timeline (attached).
- Dr. Tabak and Dr. Lauer proceed through the questions from the letter with committee staff.
- Open for Q&A.

Background/Briefing Materials:

- Timeline
- March 18, 2021 letter from E&C
- May 21, 2021 response
- June 10, 2021 letter from E&C
- Staff profiles

Timeline:

At the April 17, 2020 White House coronavirus task force briefing, President Trump announced that the administration would "end that grant very quickly" referring to the 2R01AI110964-06 NIH grant (or "the grant") of which your letter requests information.

On April 19, 2020, NIH sent a letter to the EcoHealth Alliance, the institutional awardee of the grant, ordering the suspension of funds to the Wuhan Institute of Virology ("WIV"), one of the grants sub-recipients.

On April 24, 2020 NIH sent a second letter to EcoHealth Alliance, terminating the grant.

On May 20, 2020, NIH sent a letter to the University of California, Irvine, suspending all activities related to RF1 MH120020-01, Genetically engineered anterograde monosynaptic viral tracers for multi-species neural circuit analysis, Dr. Xiangmin Xu (Contact PI), for which the Wuhan Institute of Virology is a subaward participant, awarded by the National Institute of Mental Health (NIMH).

In June 2020, NIAID awarded grants to new centers for research in emerging infectious diseases; one of the 11 grants was awarded to EcoHealth Alliance.

On July 8, 2020, NIH sent a letter to EcoHealth Alliance (attached), indicating the grant was going to be reinstated. However, funding and activities were suspended pending complete, accurate, and satisfactory return of answers, material, and information regarding a number of specific concerns about biosafety practices at its sub-recipient WIV. Furthermore, EcoHealth Alliance was instructed to correct its repeated noncompliance due to its failure to report all sub-awards in the Federal Subaward Report System. EcoHealth Alliance had been directed in NIH Notices of Award to generate these reports as required by the Transparency Act sub-award and executive compensation reporting requirement of 2 C.F.R. Part 170.

The July 8 letter to EcoHealth Alliance indicated that the suspension of the grant was taken in accordance with 45 C.F.R. § 75.371, which permits suspension of award activities in cases of non-compliance, and the NIH Grants Policy Statement, Section 8.5.2, which permits NIH to take immediate action to suspend a grant when necessary to protect the public health and welfare. This action is not appealable under 42 C.F.R. §50.404 and the NIH GPS Section 8.7.

On August 14, 2020, EcoHealth Alliance responded by letter declining to address any of the seven specific concerns NIH requested in the July 8 letter. The grant has been reinstated with all funding and activities suspended pending EcoHealth Alliance's answers to the government's safety and compliance concerns. As this matter is still pending, no further documentation can be provided at this time.

On October 23, 2020, NIH sent a letter to EcoHealth Alliance in response to their response to suspension. The letter noted that EcoHealth not currently having a subrecipient relationship with WIV and not issuing subawards to WIV at the time of suspension did not absolve EcoHealth of any past non-compliance with the terms and conditions of award for grant R01AI110964.

In April of 2021, EcoHealth Alliance submitted documents in response to the October letter.

On June 11, 2021, the HHS OIG initiated an audit into the EcoHealth Alliance grant and all actions related to it.

FRANK PALLONE, JR., NEW JERSEY
CHAIRMAN

CATHY McMORRIS RODGERS, WASHINGTON
RANKING MEMBER

ONE HUNDRED SEVENTEENTH CONGRESS

Congress of the United States
House of Representatives
COMMITTEE ON ENERGY AND COMMERCE
2125 RAYBURN HOUSE OFFICE BUILDING
WASHINGTON, DC 20515-6115
Majority (202) 225-2927
Minority (202) 225-3641

March 18, 2021

The Honorable Francis Collins, M.D., Ph.D.
Director
National Institutes of Health
9000 Rockville Pike
Bethesda, MD 20892

Dear Dr. Collins,

We write to request information, assistance, and needed-leadership from the National Institutes of Health (NIH) to advance an independent, scientific investigation into the origins of the COVID-19 pandemic.

The COVID-19 pandemic has been the worst public health crisis in the U.S. in about a hundred years. Over a year has passed since the deadly virus reached our shores and yet, the origin of the virus has yet to be determined. An independent, expert investigation of the origin of COVID-19 is of paramount importance to public health and biosecurity. As noted by Stanford Medical School Professor David Relman:

> A more complete understanding of the origins of COVID-19 clearly serves the interests of every person in every country on this planet. It will limit further recriminations and diminish the likelihood of conflict; it will lead to more effective responses to this pandemic, as well as efforts to anticipate and prevent the next one. It will also advance our discussions about risky science. And it will do something else: Delineating COVID-19's origin story will help elucidate the nature of our very precarious coexistence within the biosphere.[1]

Recently, the World Health Organization (WHO) attempted to investigate the origin of COVID-19. The WHO said that this investigative mission would be guided by the science, be

[1] David A. Relman, *Opinion: To stop the next pandemic, we need to unravel the origins of COVID-19*, PNAS (Nov. 2020), *available at* https://www.pnas.org/content/117/47/29246.

"open-minded," and "not exclude[e] any hypothesis."[2] Unfortunately, China did not provide complete access or independence for the critical WHO mission. On February 13, 2021, National Security Advisor Jake Sullivan issued the following statement:

> We have deep concerns about the way in which the early findings of the COVID-19 investigation were communicated and questions about the process used to reach them. It is imperative that this report be independent, with expert findings free from intervention or alteration by the Chinese government. To better understand this pandemic and prepare for the next one, China must make available its data from the earliest days of the outbreak.[3]

Because of rising tensions between the U.S. and China, the WHO scrapped plans for an interim report.[4] An international group of science experts, including specialists in virology, microbiology, and zoology, asked for a new review.[5]

The NIH, as a premier scientific institution, must lead in order to foster a transparent, independent, and science-based investigation into the origin of the COVID-19 pandemic. Such an effort must meet the WHO's stated goals of an open-minded investigation that does not exclude any plausible hypothesis.[6] In addition, the NIH is well-positioned to gather and provide information through oversight of its grants and other federal awards. Thus, the NIH is in a unique position to investigate the possibility that the pandemic stemmed from a laboratory accident or leak, especially regarding the Wuhan Institute of Virology (WIV).

NIH raised concerns over a possible link between WIV and the COVID-19 outbreak during its review of federal awards to EcoHealth Alliance, a global environmental health nonprofit organization dedicated to protecting wildlife and public health from the emergence of disease. Of the $13.7 million in federal awards that NIH authorized for EcoHealth Alliance, 17

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[2] Smriti Mallapaty, *Where did COVID come from? WHO investigation begins but faces challenges*, NATURE (Nov. 11, 2020), *available at* https://www nature.com/articles/d41586-020-03165-9.

[3] The White House, Statement of National Security Advisor Jake Sullivan (Feb. 13, 2021), *available at* https://www.whitehouse.gov/briefing-room/statements-releases/2021/02/13/statement-by-national-security-advisor-jake-sullivan/.

[4] Betsy McKay, Drew Hinshaw and Jeremy Page, *WHO Investigators to Scrap Plans for Interim Report on Probe of Covid-19 Origins*, THE WALL STREET JOURNAL (Mar. 4, 2021), *available at* https://www.wsj.com/articles/who-investigators-to-scrap-interim-report-on-probe-of-covid-19-origins-11614865067?mod=latest_headlines

[5] Jaime Metzl, et al, *Call for a Full and Unrestricted International Forensic Investigation into the Origins of COVID-19* (March 4, 2021), *available at* https://s.wsj net/public/resources/documents/COVID%20OPEN%20LETTER%20FINAL%20030421%20(1).pdf. The co-organizer of the letter and a WHO advisor on human genome editing, Jaime Metzl, PhD, said there is an eighty-five percent chance the pandemic started with an accidental leak from the WIV or Wuhan CDC laboratory, *available at* https://jamiemetzl.com/origins-of-sars-cov-2/. ("I have no definitive way of proving this thesis but the evidence is, in my view, extremely convincing. If forced to place odds on the confidence of my hypothesis, I would say there's an 85% chance the pandemic started with an accidental leak from the Wuhan Institute of Virology or Wuhan CDC and a 15% chance it began in some other way (in fairness, here is an article making the case for a zoonotic jump "in the wild"). If China keeps preventing a full and unrestricted international forensic investigation into the origins of the pandemic, I believe it is fair to deny Beijing the benefit of the doubt.")

[6] Washington Post Editorial Board, *We're still missing the origin story of this pandemic. China is sitting on the answers*, THE WASHINGTON POST (Feb. 5, 2021), *available at* https://www.washingtonpost.com/opinions/2021/02/05/coronavirus-origins-mystery-china/?arc404=true.

projects sponsored by the National Institute of Allergy and Infectious Disease (NIAID) have provided over $7.9 million in federal awards for research of viral emergence from bats in Southeast Asia.[7] EcoHealth Alliance passed some of its funding to the WIV, and in 2020, NIH made efforts to obtain information from EcoHealth Alliance about WIV related to concerns about the origins of COVID-19. In April 2020, NIH wrote to EcoHealth Alliance and Columbia University about an NIH-funded project entitled, "Understanding the Risk of Bat Coronavirus Emergency:"

> It is our understanding that one of the sub-recipients of the grant funds is the Wuhan Institute of Virology ('WIV'). It is our understanding that WIV studies the interaction between corona viruses and bats. The scientific community believes that the coronavirus causing COVID-19 jumped from bats to humans likely in Wuhan where the COVID-19 pandemic began. There are now allegations that the current crisis was precipitated by the release from WIV of the coronavirus responsible for COVID-19. Given these concerns, we are pursuing suspension of WIV from participation in Federal programs. It is in the public interest that NIH ensure that a sub-recipient has taken all appropriate precautions to prevent the release of pathogens that it is studying. This suspension of the sub-recipient does not affect the remainder of your grant assuming that no grant funds are provided to WIV following receipt of this email during the period of suspension.[8]

In January 2021, the U.S. Department of State issued a fact sheet about the activity at the WIV.[9] Among other revelations, it reported the following:

- The U.S. government has reason to believe that several researchers inside the WIV became sick in autumn 2019, before the first identified case of the outbreak, with symptoms consistent with both COVID-19 and common seasonal illnesses. This raises questions about the credibility of WIV senior researcher Shi Zhengli's public claim that there was "zero infection" among the WIV's staff and students of SARS-CoV-2 or SARS-related viruses.[10]

- Starting in at least 2016, WIV researchers conducted experiments involving RaTG13, the bat coronavirus identified by the WIV in January 2020 as the closest sample to SARS-CoV-2 (96.2 percent similar).[11] There was no indication that this research was suspended at any time prior to the COVID-19 outbreak.

- The WIV has a published record of conducting "gain-of-function" research to engineer chimeric viruses.[12] But the WIV has not been transparent or consistent about its record of

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[7] NIH RePORTER, *Research Portfolio Online Reporting Tools* (queried Mar. 4, 2021), *available at* https://reporter.nih.gov/search/qlYUeI9DIk2JfWUdCcWxcA/projects/charts.
[8] Mark Moore, *NIH investigating Wuhan lab at center of coronavirus pandemic*, NEW YORK POST (Apr. 28, 2020), *available at* https://nypost.com/2020/04/28/nih-investigating-wuhan-lab-at-center-of-coronavirus-pandemic/.
[9] U.S. Department of State, *Fact Sheet: Activity at the Wuhan Institute of Virology*, Office of the Spokesperson (Jan. 15, 2021), *available at* https://2017-2021.state.gov/fact-sheet-activity-at-the-wuhan-institute-of-virology//index html.
[10] *Id.*
[11] *Id.*
[12] *Id.*

studying viruses similar to the COVID-19 virus, including "RaTG13," which was sampled from a cave in Yunnan Province in 2013 after several miners died of SARS-like illness.[13]

- WHO investigators must have access to the records of the WIV's work on bat and other coronaviruses before the COVID-19 outbreak. As part of a thorough inquiry, they must have a full accounting of why the WIV altered and then removed online records of its work with RaTG13 and other viruses.[14]

- Despite the WIV presenting itself as a civilian institution, the U.S. has determined that the WIV has collaborated on projects with China's military.[15] The WIV has engaged in classified research, including laboratory animal experiments, on behalf of the Chinese military since at least 2017.[16]

- The U.S. and other donors who funded or collaborated on civilian research at the WIV have a right and obligation to determine whether any of our research funding was diverted to secret Chinese military projects at the WIV.[17]

Notably, the State Department's former lead investigator who oversaw the Task Force into the COVID-19 virus origin stated recently that he not only believes the virus escaped from the WIV, but that it may have been the result of research that the Chinese military, or People's Liberation Army, was doing on a bioweapon.[18]

Accordingly, it is imperative to determine not only where SARS-CoV-2 originated, but also how and if NIH's funding and research to projects at the WIV could have contributed to SARS CoV-2. To assist our requests and inquiry, please provide the following by April 19, 2021:

1. An assessment from a classified U.S. Defense Intelligence Agency (DIA) report included the possibility that the origins of SARS CoV-2 could have emerged accidentally from a laboratory in Wuhan, China due to unsafe laboratory practices.[19] The DIA report cited U.S. government and Chinese researchers who found "about 33 percent of the original 41 identified cases did not have direct exposure" to the market.[20] That, along with what is known of the WIV's work in past few years, raised reasonable suspicion that the

[13] *Id.*
[14] *Id.*
[15] *Id.*
[16] *Id.*
[17] *Id.*

[18] Jennifer Griffin, Former top State Dept. investigator says COVID-19 outbreak may have resulted from bioweapons research accident, Fox News (March 13, 2021), *available at* https://www.foxnews.com/world/top-state-official-coronavirus-bioweapon-accident

[19] Fred Guterl, Naveed Jamali and Tom O'Connor, *The Controversial Experiments ad Wuhan Lab Suspected of Starting the Coronavirus Pandemic*, NEWSWEEK (Apr. 27, 2020), *available at* https://www.newsweek.com/controversial-wuhan-lab-experiments-that-may-have-started-coronavirus-pandemic-1500503.
[20] *Id.*

pandemic may have been caused by a lab error, not a wet market.[21] Further, a WHO inspector on the recent mission noted that "we know not all of those first 174 early COVID-19 cases visited the market, including the man diagnosed in December 2019 with the earliest onset date."[22] What information does the NIH have on the earliest COVID-19 cases?

2. According to an editorial on February 23, 2021, in *The Wall Street Journal* by former Secretary of State Mike Pompeo and Miles Yu, "[China's] army of scientists claim to have discovered almost 2,000 new viruses in a little over a decade."[23] How many of these discovered viruses does the NIH have information on and were any of these viruses discovered at the WIV?

3. According to *The Wall Street Journal* editorial mentioned in the previous question, some have alleged that the WIV's virus-carrying animals were sold as pets and may even show up at local wet markets.[24] Is the NIH aware of these allegations? If so, please provide any information the NIH has related to these allegations.

4. Please provide all information that NIH has about laboratory accidents and/or biosafety practices at the WIV since January 1, 2015.

5. Please provide all information that NIH has from NIH staff, grantees, sub-grantees, contractors, or subcontractors about communications and events at the WIV from August 2019 to the present.

6. Please provide all information that NIH has from NIH staff, grantees, sub-grantees, contractors, or subcontractors about their communications with China-based NIH, Chinese National Science Foundation, CDC, and China CDC about events at the WIV from August 2019 to the present.

<u>State Department Cables</u>

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[21] *Id.*

[22] Dominic Dwyer, I was the Australian doctor on the WHO's COVID-19 mission to China. Here's what we found about the origins of the coronavirus, THE CONVERSATION (Feb. 21, 2021), *available at*https://www.theguardian.com/commentisfree/2021/feb/22/i-was-on-the-whos-covid-mission-to-china-heres-what-we-found. *See also* Jeremy Page and Drew Hinshaw, *China Refuses to Give WHO Raw Data on Early Covid-19 Cases*, THE WALL STREET JOURNAL (Feb. 12, 2021), *available at* https://www.wsj.com/articles/china-refuses-to-give-who-raw-data-on-early-covid-19-cases-11613150580#:~:text=BEIJING%E2%80%94Chinese%20authorities%20refused%20to,over%20the%20lack%20of%20detail. ("Chinese authorities refused to provide World Health Organization investigators with raw, personalized data on early Covid-19 cases that could help them determine how and when the coronavirus first began to spread in China, according to WHO investigators who described heated exchanges over the lack of detail. The Chinese authorities turned down requests to provide such data on 174 cases of Covid-19 that they have identified from the early phase of the outbreak in the Chinese city of Wuhan in December 2019. Investigators are part of a WHO team that this week completed a monthlong mission in China aimed at determining the origins of the pandemic.")

[23] *Id.*

[24] Mike Pompeo and Miles Yu, *NIH Presses U.S. Nonprofit for Information on Wuhan Virology Lab*, THE WALL STREET JOURNAL (Feb. 23, 2021), available at https://www.wsj.com/articles/chinas-reckless-labs-put-the-world-at-risk-11614102828.

7. What information does NIH have about the WIV's responses to the 2018 U.S. Department of State cables (attached to this letter) regarding safety concerns?

8. The April 2018 cable from the U.S. Department of State stated that the WIV planned to invite University of Texas Medical Branch Galveston (UTMBG) researchers to do research in Wuhan's labs. Please provide any information NIH received that indicates whether the WIV invited UTMBG researchers, and whether UTMBG researchers conducted any research in Wuhan's labs.

    a. If there was such research, please provide information and any documents related to this research.

9. Why was it pertinent to the NIH investigation that the "nonprofit [EcoHealth Alliance] must provide the "WIV's responses to the 2018 Department of State cables regarding safety concerns"?[25]

    a. Did EcoHealth Alliance provide this information? If so, how did NIH use the information to further its investigation?

<u>EcoHealth Alliance, Columbia University Health Sciences</u>

10. Was the 2019 NIH federal award to EcoHealth Alliance reviewed and approved by the HHS Potential Pandemic Pathogen Care and Oversight (P3CO) committee?[26]

    a. If so, please provide the documentation with the committee's decision.

    b. Please also provide the names of the individuals who were members of the committee at the time.

11. Please provide all correspondence and communications between NIH and EcoHealth Alliance, since January 1, 2020, related to federal funding involving the WIV. The documentation should include, but not be limited to, correspondence between NIH and EcoHealth Alliance dated sometime in April 2020, on July 8, 2020, and sometime in August 2020.

12. In April 2020, NIH suspended a 2019 federal award to EcoHealth Alliance, in part, because NIH did not believe the work aligned with "program goals and agency priorities."[27] Please specify the work that was done by the EcoHealth Alliance that did

[25] Meredith Wadman, *NIH imposes 'outrageous' conditions on resuming coronavirus grant targeted by Trump*, SCIENCEMAG (Aug. 19, 2020), *available at* https://www.sciencemag.org/news/2020/08/nih-imposes-outrageous-conditions-resuming-coronavirus-grant-targeted-trump.
[26] National Institutes of Health, *Notice Announcing the Removal of the Funding Pause for Gain-of-Function Research Project* (Dec. 19, 2017), *available at* https://grants nih.gov/grants/guide/notice-files/NOT-OD-17-071.html.
[27] *Id.*

not align with the agency's program goals and priorities, and when that work was conducted.

a. Was an evaluation of EcoHealth Alliance's work and whether it aligned with the agency's program goals and priorities conducted by the NIH before the award was issued? If yes, please provide any related documentation. If not, why not?

13. In April 2020 correspondence with EcoHealth Alliance, NIH wrote that it "received reports that the Wuhan Institute of Virology…has been conducting research at its facilities in China that pose serious bio-safety concerns."[28] What are the sources for those reports to NIH and what were the specific allegations reported?

14. Why did the NIH request that EcoHealth Alliance provide a sample of the pandemic coronavirus that the WIV used to determine its genetic sequence for SARS CoV-2?[29]

    a. Why is this information important to NIH's investigation?

    b. Has NIH obtained the sample and if so, what evaluations have been done, and for what purpose?

    c. If NIH has not yet obtained the sample, what are the planned studies and evaluations NIH will conduct with the sample when it is obtained?

15. What is the nature of NIH's concerns about purported restrictions at the WIV including "diminished cell-phone traffic in October 2019, and the evidence that there may have been roadblocks surrounding the facility from October 14-19, 2019[,]" about the WIV lab or virus origin?[30]

    a. What is the basis of information to NIH about the purported restrictions at the WIV?

    b. What are the other purported restrictions at the WIV in October 2019?

16. After terminating EcoHealth Alliance's 2019 project entitled "Understanding the Risk of Bat Coronavirus Emergence," the NIH later offered to reinstate the EcoHealth Alliance funding in July 2020 if EcoHealth Alliance agreed to meet certain conditions.[31]

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[28] Betsy McKay, *NIH Presses U.S. Nonprofit for Information on Wuhan Virology Lab*, THE WALL STREET JOURNAL (Aug. 19. 2020), *available at* https://www.wsj.com/articles/nih-presses-u-s-nonprofit-for-information-on-wuhan-virology-lab-11597829400.
[29] Meredith Wadman, *NIH imposes 'outrageous' conditions on resuming coronavirus grant targeted by Trump*, SCIENCEMAG (Aug. 19, 2020), *available at* https://www.sciencemag.org/news/2020/08/nih-imposes-outrageous-conditions-resuming-coronavirus-grant-targeted-trump.
[30] *Id.*
[31] Betsy McKay, *NIH Presses U.S. Nonprofit for Information on Wuhan Virology Lab*, THE WALL STREET JOURNAL (Aug. 19. 2020), *available at* https://www.wsj.com/articles/nih-presses-u-s-nonprofit-for-information-on-wuhan-virology-lab-11597829400.

a. Please provide all of the information presented to NIH from EcoHealth Alliance in response to NIH's conditions for reinstatement.

b. What actions did NIH take based upon the information received? How has the information been used in NIH's investigation?

c. One condition for the federal award reinstatement was for EcoHealth Alliance to arrange for an outside inspection of the WIV and its records, "with specific attention to addressing the question of whether WIV staff had SARS-CoV-2their possession prior to December 2019."[32] Why is it pertinent to the NIH's investigation if staff at WIV had SARS-CoV-2 in their possession prior to December 2019? What is the potential significance if the staff did have the virus in their possession prior to December 2019?

d. What information does NIH have that was used for the basis of requesting that the EcoHealth Alliance "must 'explain the apparent disappearance' of a scientist who worked in the Wuhan lab," and on social media was rumored to be "patient zero" of the pandemic?[33]

i. What is the potential significance about the whereabouts of this scientist and the photo being removed from the website?

17. Please provide all correspondence and communications between NIH and Columbia University related to federal funding involving the WIV, including email correspondence in April 2020 between Dr. Michael Lauer, Deputy Director of extramural research, and Naomi Schrag of Columbia University.

a. In an April 2020 email, Dr. Lauer advised Naomi Schrag of Columbia University that it would be helpful for NIH "to know about all China-based participants in this work since the Type 1 grant started in 2014 - who they were and how much money they received."[34] Why did NIH request that Columbia University provide information about all of the China-based participants?

i. What is the pertinence of the timeframe starting in 2014 for the requested information?

ii. Did Columbia University provide the NIH with the requested information about all of the China-based participants from all grantees since 2014? If so, please provide the information1. If not, why not?

<u>Federal Funding Records</u>

[32] *Id.*
[33] *Id.*
[34] Meredith Wadman and Jon Cohen, *NIH's axing of bat coronavirus grant a 'horrible precedent' and might break rules, critics say*, SCIENCEMAG (Apr. 30, 2020), *available at* https://www.sciencemag.org/news/2020/04/nih-s-axing-bat-coronavirus-grant-horrible-precedent-and-might-break-rules-critics-say.

18. Please provide ledgers or any accounting for dispersion of all NIH federal funding awards that EcoHealth Alliance has sent to the WIV, including through contracts, grants, donations, cooperative agreements, staffing, or any other support or means. In addition, please provide the results and outcomes from the funding and support.[35]

19. What is the total amount of NIH federal funding per year from 2017 through 2021 that has directly or indirectly supported the WIV scientists or research through grant recipients, including to EcoHealth Alliance; Wildlife Trust, Inc.; Columbia University Health Sciences; Trustees of Columbia University; University of North Carolina Chapel Hill; Vanderbilt University; University of Virginia; and Oregon Health and Science University?[36]

20. According to a report in *The Washington Post* on April 14, 2020, the WIV issued a news release in English about the final visit from U.S. Embassy scientist diplomats in Beijing, which occurred on March 27, 2018.[37] Does the NIH have a copy of this news release? If so, please provide a copy.

21. For NIH award recipients that have provided support to the WIV since January 1, 2012, please provide annual reports, trip reports related to the WIV, documentation of any survey or field trips by the WIV, and interim data summaries from the WIV.

22. Please provide copies of all grantee annual reports, progress reports, projects, studies, and observations since 2014 where foreign sites for all Type 1 and Type 2 awards have been documented as involving the WIV.

23. Please provide copies of all grantee annual reports, progress reports, projects, studies, and observations since 2014 for NIH domestic grantee awards with a foreign component involving the WIV.

24. Please provide the name(s) of the NIH program manager(s) or officer(s) responsible for overseeing the grants to EcoHealth Alliance and time period(s) of responsibility.

25. Please provide the name(s) of the NIH Scientific Review Officers responsible for reviewing and approving any NIH financial awards to EcoHealth Alliance and any other funding recipients that supported the WIV.

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[35] Betsy McKay, *NIH Presses U.S. Nonprofit for Information on Wuhan Virology Lab*, THE WALL STREET JOURNAL (Aug. 19. 2020), *available at* https://www.wsj.com/articles/nih-presses-u-s-nonprofit-for-information-on-wuhan-virology-lab-11597829400.

[36] National Institutes of Health, Research Portfolio online Reporting Tools, NIH RePorter *available at* https://report nih.gov/ (last accessed March 6, 2020).

[37] Josh Rogin, *Opinion: State Department cables warned of safety issues at Wuhan lab studying bat coronaviruses*, THE WASHINGTON POST (Apr. 14, 2020), *available at* https://www.washingtonpost.com/opinions/2020/04/14/state-department-cables-warned-safety-issues-wuhan-lab-studying-bat-coronaviruses/.

26. According to an editorial in *The Wall Street Journal*, the WIV housed tens of thousands of bat samples and laboratory animals in 2019.[38] Please provide any information the NIH has on the number of bat samples and animals at the WIV.

    a. Did any NIH scientists who are fluent in Mandarin review the Chinese scientific literature on the WIV research related to coronaviruses that is dated before February 1, 2020?

27. Does the NIH have the unpublished sequences of bat coronaviruses that were maintained in the WIV database before December 30, 2019, or before the database was removed from the internet?[39] Does NIH have the full sequences of the eight viruses sampled in the Yunnan province on an EcoHealth Alliance bat-virus sampling trip in 2015?

    a. Please provide NIH's analysis if the sequences have been analyzed.

    b. If NIH does not have the sequences, can NIH get this information from the EcoHealth Alliance or from other NIH-funded sources?

28. Please provide the original version of "Origin and cross-species transmission of bat coronaviruses in China" that was submitted to *Nature* by EcoHealth Alliance on October 6, 2019, published August 25, 2020, and funded in part by NIAID (award number R01AI110964).[40] If NIH does not have the October 6, 2019 report, can NIH obtain it from EcoHealth Alliance for this response? If so, please provide the report.

29. Have NIH, EcoHealth Alliance, or other NIH award recipient(s) been denied permission or access to results of any WIV research, which indirectly received financial support from NIH awards? If so, please provide the date(s), individuals involved, and circumstances of each denial.

We request that the NIH provide the requested documents and information in a coordinated response from all stakeholders and the appropriate divisions within NIH, including but not limited to subject matter experts from NIH's Division of Security and Emergency Response, the Office of Management Assessment, the Center for Scientific Review, the National Institute of Allergy and Infectious Diseases, and the Office of Extramural Research. After the requested information has been provided, we ask that the NIH provide a briefing to the Minority Committee staff to discuss the information that the NIH has related to the origins of SARS-CoV-2, including any potential links to the WIV. Finally, we request that you appoint an NIH working group representing an appropriate diversity of scientific disciplines to collect data and

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[38] Mike Pompeo and Miles Yu, *NIH Presses U.S. Nonprofit for Information on Wuhan Virology Lab*, THE WALL STREET JOURNAL (Feb. 23, 2021), *available at* https://www.wsj.com/articles/chinas-reckless-labs-put-the-world-at-risk-11614102828.

[39] Washington Post Editorial Board, *We're still missing the origin story of this pandemic. China is sitting on the answers*, THE WASHINGTON POST (Feb. 5, 2021), *available at* https://www.washingtonpost.com/opinions/2021/02/05/coronavirus-origins-mystery-china/?arc404=true.

[40] Latinne, A., Hu, B., Olival, K.J. et al,. *Origin and cross-species transmission of bat coronaviruses in China*, Nature (Aug. 25, 2020), *available at* https://www.nature.com/articles/s41467-020-17687-3#Ack1.

information related to COVID-19 origins (including the WIV), and that the NIH working group coordinate and consult with foreign scientific agencies involved in similar work.

Your assistance with this request is greatly appreciated. If you have any questions, please contact Alan Slobodin or Diane Cutler of the Minority Committee staff.

Sincerely,

Cathy McMorris Rodgers
Republican Leader
Committee on Energy and Commerce

Brett Guthrie
Republican Leader
Subcommittee on Health

H. Morgan Griffith
Republican Leader
Subcommittee on Oversight and Investigations

Attachment

Cc: The Honorable Frank Pallone, Chairman
The Honorable Diana DeGette, Chair, Subcommittee on Oversight and Investigations
The Honorable Anna Eshoo, Chair, Subcommittee on Health

DEPARTMENT OF HEALTH & HUMAN SERVICES

Public Health Service

National Institutes of Health
Bethesda, Maryland 20892

May 21, 2021

The Honorable Cathy McMorris Rodgers
U.S. House of Representatives
Washington, DC 20515

Dear Representative McMorris Rodgers:

Thank you for your letter regarding the National Institutes of Health's (NIH) support for biomedical research related to SARS-CoV-2, "gain of function" (GOF) research, and the NIH grant to the EcoHealth Alliance. As Principal Deputy Director of NIH, I am pleased to respond to your inquiry.

Neither NIH nor the National Institute of Allergy and Infectious Diseases has ever approved any grant that would have supported GOF research on coronaviruses that would have increased their transmissibility or lethality for humans.

Some scientists use the term GOF research broadly to refer to *any* modification of a biological agent that confers new or enhanced activity to that agent. In some cases, this research is performed to give new properties to agents to allow them to grow and be studied in the lab; for example, the agent may be modified so that it can be studied in research animals. However, not all research that some label as GOF research entails the same level of risk. The subset of GOF research that is anticipated to enhance the *transmissibility* and/or *virulence* of potential pandemic pathogens, which could make them more dangerous to humans, has been the subject of substantial scrutiny and deliberation.

In 2017, the U.S. Department of Health and Human Services (HHS) issued its Framework for Guiding Funding Decisions about Proposed Research Involving Enhanced Potential Pandemic Pathogens (HHS P3CO Framework). The HHS P3CO Framework is intended to guide HHS funding decisions on proposed research that is reasonably anticipated to create, transfer, or use Potential Pandemic Pathogens (PPPs) resulting from the enhancement of a pathogen's transmissibility or virulence in humans (enhanced PPP) and seeks to preserve the benefits of life sciences research involving enhanced PPPs while minimizing potential biosafety and biosecurity risks.

As your letter notes and has been publicly stated, NIH awarded a grant to EcoHealth Alliance Inc., a research organization based in New York City, in June 2014. The application was subjected to rigorous peer review and did not propose research to enhance any coronavirus to be more transmissible or virulent.

The research proposed in the grant application sought to understand how bat coronaviruses evolve naturally in the environment to become transmissible to the human population. This

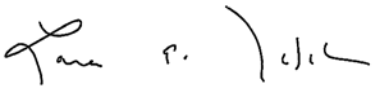
included studying viral diversity in bat reservoirs, surveying people who work in live animal markets or other jobs with high exposure to wildlife for evidence of bat-coronavirus infection, and analyzing data to predict which newly discovered viruses pose the greatest threat to human health. To support its work, EcoHealth made sub-awards to the Wuhan Institute of Virology and other institutions based in East Asia where coronaviruses tend to emerge and are prevalent. NIH is not currently funding the Wuhan Institute of Virology.

I would be happy to further discuss this grant, and this issue, at your convenience. NIH is committed to upholding the highest standards within the conduct of science and the oversight of federal funding.

In conclusion, NIH strongly supports the need for further investigation by the World Health Organization (WHO) into the origins of the SARS-CoV-2 coronavirus. Working with a cross-regional coalition of 13 countries, we urge the WHO to begin the second phase of their study without delay.

Thank you again for the opportunity to address these questions. An identical response has been sent to the co-signers of your letter.

Sincerely,



Lawrence A. Tabak, D.D.S., Ph.D.
Principal Deputy Director

cc: The Honorable Frank Pallone
Chairman, House Committee on Energy and Commerce

FRANK PALLONE, JR., NEW JERSEY
CHAIRMAN

CATHY McMORRIS RODGERS, WASHINGTON
RANKING MEMBER

ONE HUNDRED SEVENTEENTH CONGRESS

Congress of the United States

House of Representatives

COMMITTEE ON ENERGY AND COMMERCE
2125 RAYBURN HOUSE OFFICE BUILDING
WASHINGTON, DC 20515–6115
Majority (202) 225–2927
Minority (202) 225–3641

June 10, 2021

The Honorable Francis Collins, M.D., Ph.D.
Director
National Institutes of Health
9000 Rockville Pike
Bethesda, MD 20892

Dear Dr. Collins:

As the committee of jurisdiction over public health, the Energy and Commerce Committee has authorizing responsibilities over the U.S. National Institutes of Health (NIH). We strongly support a comprehensive investigation into the origins of the COVID-19 pandemic, including the possibility of an accidental laboratory leak.

The Chinese Communist government has not yet allowed Chinese scientists to cooperate with an investigation into COVID-19 origins, and has admitted to destroying samples and records pertinent to such an investigation.[1] Thus, it is imperative we assemble all data and information in U.S. possession about bat coronavirus research experiments and lab safety protocols from all sources outside of China, particularly from EcoHealth Alliance (EHA). EHA is an NIH grantee who has been involved in bat coronavirus research in China and has issued grant subawards to the Wuhan Institute of Virology (WIV). It is also essential to collect information about the WIV, the laboratory that was conducting bat coronavirus experiments located in Wuhan, China, the epicenter of the COVID-19 outbreak. As a federal cognizant grant-making agency that funded bat coronavirus research at the WIV through EHA awards, NIH is in a unique position to publicly share detailed research reports in its possession. Importantly, NIH has full access to EHA records and EHA has refused to cooperate with our inquiry. Therefore, it is critical for NIH to cooperate with our objective fact-finding investigation as we continue to collect data about U.S. funded bat coronavirus research.

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[1] Josh Chin, *China Told Labs to Destroy Coronavirus Samples to Reduce Safety Risks*, The Wall Street Journal (May 16, 2020) *available at* https://www.wsj.com/articles/china-told-labs-to-destroy-coronavirus-samples-to-reduce-biosafety-risks-11589684291/.

Since the Republican committee leaders March 18, 2021 letter to NIH, our investigation has found a number of additional issues that raise very serious concerns about the adequacy of NIH's oversight of grantees. The following newly found issues appear troubling and given the significance of these concerns, we expect the NIH to respond fully and substantively. Minority committee staff is continuing to work with your staff to schedule an NIH briefing. The NIH should be prepared to address these issues at the briefing, in addition to all of the questions from the March 18, 2021 letter that presently remain unanswered.

1. NIH's Award of $2 million to EHA Despite Grant Suspension

On May 25, 2021, a spokesperson for EHA told Fox Business that its NIH funding is frozen and NIH did not give them guidance on when funds will be unfrozen.[2] EHA's representation about their NIH funding was not forthcoming. NIH terminated grant R01AI110964 to EHA entitled, "Understanding the Risk of Bat Coronavirus Emergence" in April 2020.[3] NIH eventually converted the grant termination to a suspension on July 8, 2020, pending EHA's responses to seven requests from NIH related to WIV's actions. NIH could unfreeze the funding if EHA cooperates with NIH's requests, but apparently EHA has not yet done so. Despite EHA's obstruction of NIH requests, NIH gave new financial awards to EHA in June 2020 and August 2020, totaling $2,127,602.[4] By NIH authorizing new funding to EHA, an NIH-suspended grantee, the NIH undercut its July 8, 2020 suspension and has incentivized its grantees to defy NIH oversight with impunity.

2. NIH's Inadequate Oversight of EHA's Other Support

You testified during a May 25, 2021 Congressional hearing that NIH was, "...of course not aware of other sources of funds or other activities they might have undertaken outside of what our approved grant allowed," when asked about NIH grant recipient EHA, and the WIV, an EHA subaward recipient.[5] Pursuant to the NIH Grants Policy, EHA was required to report all "other support," in-kind contributions such as laboratory space, equipment and supplies, and facilities and other resources for all individuals designated as the Principal Investigator (PI) personnel.[6] Per the NIH grants policy, the grant Principal Investigator Dr. Peter Daszak and EHA were required to report its other research funding sources and activities to NIH.[7] Without

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[2] Fox News, *Biden State Department quietly ended team's work probing COVID origin*, State Department (May 25, 2021) *available at* https://www.foxnews.com/politics/biden-state-department-shut-down-team-covid-origin-investigation.

[3] National Institutes of Health, *Understanding the Risk of Bat Coronavirus Emergence*, REPORTER (last accessed June 2, 2021) *available at* https://reporter.nih.gov/search/p1odLH_U1kyZgyOhClrN2w/project-details/9320765#similar-Projects/.

[4] USASpending.gov, *Cooperative agreement numbers U01AI151797 and U01AI153420*, EcoHealth Alliance available at

[5] House Committee on Appropriations, *FY 2022 Budget Request for the National Institutes of Health*, Hearings (May 25, 2021) *available at* https://appropriations.house.gov/events/hearings/fy-2022-budget-request-for-the-national-institutes-of-health.

[6] National Institutes of Health, Other Support, Grants & Funding (last accessed June 1, 2021) available at https://grants.nih.gov/grants/forms/othersupport.htm.

[7] *Id.*

further details or documentation, your testimony bolsters the notion that NIH oversight is largely ignorant of other awards to the grantee.

3. NIH's Inadequate Oversight of EHA's Delinquent Financial Reports

As the prime recipient of NIH grant R01AI110964, EHA gave a total $598,500 in five subaward transactions to the WIV from 2015 to 2019 for the WIV to, "conduct high-quality testing, sequencing, and analyses of field samples; maintenance of cold-chains from field to lab; ensuring quality control of sample storage and testing; collaborating on scientific publications and programmatic reporting."[8] EHA also gave a total of $201,217.10 in two subaward transactions to the Wuhan University School of Public Health (WUSPH) to "conduct targeted site-analyses, human behavioral surveillance including qualitative and quantitative surveys; analyses of data; collaborating on scientific publications and programmatic reporting," from 2016 through 2017.[9]

EHA is required to report its subawards to GSA's FFATA Subaward Reporting System (FSRS) by the end of the month following the month when the subaward was made.[10] For example, when EHA issued a $133,000 subaward to the WIV on May 29, 2015, EHA was required to report that subaward to FSRS by June 30, 2015.[11] USASpending is the U.S. government's open federal spending data source and when the grant number R01AI110964 data is downloaded, details reveal that EHA did not report subawards for that grant until 2020, even though EHA made subawards starting in 2015.[12] EHA reported all seven subaward transactions for R01AI110964 on July 13, 2020, five days following NIH's July 8, 2020 letter to EHA instructing EHA to ensure EHA reported all subaward data to FSRS.[13] Before the year 2020, only one other EHA subaward grant is reported in USASpending.gov, in which three subaward transactions for NIH grant number R56TW009502 are recorded in 2014.[14] EHA's apparent non-compliance of required financial reporting raises concerns about the adequacy of NIH oversight of NIH grants.

4. NIH's Possible Funding of EHA for Duplicative Research in China

EHA received federal funding as both a prime and sub-recipient not only from NIH, but also from the U.S. Agency for International Development (USAID) for its bat coronavirus research. The project descriptions and research articles are so similar that a distinction between the NIH bat coronavirus research objectives and achievements for the awards to EHA are almost interchangeable with EHA's USAID-funded bat coronavirus research objectives and

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[8] *Id.*
[9] *Id.*
[10] USAspending.gov, *Data Sources,* About (last accessed June 1, 2021), *available at* https://www.usaspending.gov/about.
[11] *Id.*
[12] USASpending.gov, *Advanced Search: Recipient – EcoHealth Alliance* (June 1, 2021) *available at* USASpending.gov/.
[13] *Id.*
[14] *Id.* See NIH grant number R56TW009502.

achievements.[15] The NIH grant progress reports will reveal details about the bat coronavirus research that can be compared to the reports from USAID-funded research. In its research funded by the USAID, EHA partnered with the WIV and with East China Normal University.[16] We are very concerned that the NIH and USAID may have funded duplicate projects and that EHA partnered with additional unreported entities in China for NIH-funded research.

5. NIH's Inadequate Reconciliation of EHA's Grant Subawards

As far back as 2005, Peter Daszak of EHA has authored over 20 bat coronavirus and other zoonic pathogen research articles with Dr. Zhengli Shi of the WIV, plus other researchers, about experiments funded by NIH.[17] Their collaborative research has resulted in a 2005 publication entitled "Bats Are Natural Reservoirs of SARS-Like Coronaviruses," funded by NIH.[18] In 2013, they published "Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor," funded by NIH and USAID. [19] Their numerous publications acknowledge NIH as a research sponsor yet the only EHA support to the WIV in USASpending.gov was reported by EHA on July 13, 2020 (see concern number three above).[20] Vanity Fair reported that Dr. Shi "herself listed U.S. government grant support of more than $1.2 million on her curriculum vitae: $665,000 from the NIH between 2014 and 2019; and $559,500 over the same period from USAID."[21] EHA's late and potentially incomplete reporting of the WIV as its sub-award recipient raises questions about EHA's compliance with required financial reporting and also raises concerns about NIH's oversight of grant awards to EHA.

6. NIH's Inadequate Oversight of EHA's Place of Performance Reporting

The Federal Funding Accountability and Transparency Act of 2006 (FFATA) requires that federal award reporting must include the primary location of where the work will be performed, (including the city, state, congressional district, and country).[22] For EHA's NIH awards, China is not listed as the place of performance in USASpending.gov and instead, EHA's

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[15] USASpending.gov, *Advanced Search: Recipient – EcoHealth Alliance* (June 1, 2021) *available at* USASpending.gov/.
[16] USAID PREDICT-1 CONSORTIUM, *Reducing Pandemic Risk, Promoting Global Health*, Final Report (Dec. 2014) *available at* https://ohi.sf.ucdavis.edu/sites/g/files/dgvnsk5251/files/files/page/predict-final-report-lo.pdf.
[17] NIH Reporter, *Anthropogenic change & emerging zoonic paramyxoviruses*, Project Number 5R01TW005869-04 (Budget Start Date June 1, 2005) *available at* https://reporter.nih.gov/search/WMYBIQPE20aG4fAZLFj0lw/project-details/6923645#details, NIH National Library of Medicine, *Advanced Search for 'Shi, Daszak,'* National Center for Biotechnology Information (June 2, 2021) *available at* https://pubmed.ncbi.nlm.nih.gov/?term=Daszak%2C+Shi&sort=date&sort_order=asc&size=200.
[18] NIH National Library of Medicine, *Bats Are Natural Reservoirs of SARS-Like Coronaviruses*, PubMed (Sept.5, 2005) *available at* https://pubmed.ncbi.nlm.nih.gov/16195424/.
[19] Ge, XY., *et al., Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor*, Nature 503, 535–538 (May 16, 2013) *available at* https://doi.org/10.1038/nature12711.
[20] *Id.*
[21] Katherine Eban, The Lab-Leak Theory – Inside the Fight to Uncover COVID-19 Origins, Vanity Fair (June 3, 2021) *available at* https://www.vanityfair.com/news/2021/06/the-lab-leak-theory-inside-the-fight-to-uncover-covid-19s-origins.
[22] PL 109-282, Sept. 26, 2006 *available at* https://www.govinfo.gov/content/pkg/PLAW-109publ282/pdf/PLAW-109publ282.pdf.

primary place of performance is identified as New York.[23] The NIH grant documents, and the financial and progress reports we have requested will contain travel budgets and research details that will confirm the location(s) where EHA actually performed its research. Published research articles about NIH-funded experiments describe EHA's bat coronavirus research and surveillance activities often partnered with the WIV in China. We are very concerned about the discrepancy in EHA's primary place of performance as being New York in USASpending.gov when research articles, publications, and media interviews suggest EHA's primary place of performance is not domestic.[24]

7. NIH's Lack of Visibility into EHA's Grant Subawards

USASpending.gov limits visible data to prime and subaward recipients, and does not disclose funds that are further disbursed subaward recipients.[25] EHA is a subaward recipient of NIH grant funds from the Arizona State University and the Trustees of Columbia University in New York City.[26] As a subaward recipient, EHA does not publicly report when it further distributes subaward funds to other organizations such as the WIV or other recipients in China.[27] NIH questions to EHA in the July 8, 2020 grant suspension letter suggest that NIH lacks information and visibility on sub-grant awards that are either issued or received by EHA.[28]

8. NIH's Inadequate Oversight of EHA's Grant Fund Accounting

In our April 18, 2021 letter to EHA, we raised the issue that EHA reported a $319,570 cash award grant and a $126,792 cash award grant disbursed by wire to China for the purpose of "[u]understanding the risk of bat coronavirus emergence" on its IRS Form 990, calendar year 2016.[29] EHA reported giving $321,700 for coronavirus and emerging diseases to China on its IRS Form 990, calendar year 2015.[30] EHA IRS Form 990's for other years do not include that purpose or identify the WIV as an organization to which funds were paid. With EHA organized as a 501 (c)(3) non-profit organization, its IRS Form 990's are public documents able to be reviewed by NIH. As a non-federal entity that expends more $750,000 or more in federal funds in one year, EHA is required to submit a Single Audit report, previously known as the OMB Circular A-133 audit. The purpose of a Single Audit report is to provide assurance to the Federal Government that a non-federal entity has adequate internal controls in place, and is generally in

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[23] *Id.*
[24] Nidhi Subbaraman, *'Heinous!': Coronavirus researcher shut down for Wuhan-lab link slams new funding restrictions*, Nature (Aug. 21, 2020), *available at* https://www.nature.com/articles/d41586-020-02473-4.
[25] USASpending.gov, *Advanced Search: Recipient - EcoHealth Alliance* (June 1, 2021) *available at* USASpending.gov/.
[26] *Id.*
[27] *Id.*
[28] Internal Revenue Service, EHA 990 final, Schedule F, Parts I and II (May 3, 2017) *available at* https://apps.irs.gov/pub/epostcard/cor/311726494_201606_990_2017090514700974.pdf.
[29] U.S. Energy and Commerce Republicans, *Letter to EcoHealth Alliance*, The COVID-19 Origins Investigation (Apr. 16, 2021) *available at* https://republicans-energycommerce.house.gov/the-covid-19-origins-investigation/.
[30] Internal Revenue Service, *EHA 990 final 2015, Schedule F, Parts I and II* (May 3, 2017) *available at* https://apps.irs.gov/pub/epostcard/cor/311726494_201606_990_2017090514700974.pdf.

compliance with program requirements.[31] In EHA's Single Audit reports for years 2016 to 2020, no payments are evident for EHA funds paid to the WIV.[32]

9. NIH's Inadequate Oversight of Its Funded Researchers in China

The WIV named NIH and EHA on its website as WIV international partner as of and prior to the date of our March 18, 2021 letter to NIH.[33] By March 22, 2021, the WIV had removed NIH as a partner from its website.[34] The NIH has characterized its relationship Chinese scientists as respectable scientific partners.[35] However, within three days following our letter to NIH which inquired about NIH grants to the WIV, the WIV quickly concealed its long-standing relationship with NIH by deleting evidence of its NIH partnership from its website. This action does not seem consistent with NIH's claim that the WIV and its scientists were a respectable scientific partner. It has been reported that some Chinese scientists working with EHA are current or former members of the People's Liberation Army of China.[36] It has also been reported that the Chinese military were conducting research at the WIV.[37] We are concerned that NIH-funded coronavirus research in China may not have undergone proper biodefense risk analysis.

10. NIH's Lack of Cooperation with Congressional Oversight Inquiry

NIH is supposed to be a transparent institution and the grant documents we requested should be a matter of public record.[38] Contrary to your public statement implying that we asked for "pretty sensitive materials, not quite classified, but getting close to that," the grant documents we requested are releasable to the public per NIH's own policy and should have already been provided to us.[39]

As you are aware, the NIH grant documents and progress reports we requested will include details pertinent to our COVID-19 origins investigation, including information about: all research participants and collaborating organizations; location(s) of work performed; instruments, equipment and monies provided to grant sub-recipients; financial accounting

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[31] U.S. Department of Health and Human Services, *Single Audit* (Apr. 25, 2016) *available at* (https://www.hhs.gov/about/agencies/asfr/data-act-program-management-office/single-audit/index.html.
[32] Federal Audit Clearinghouse, *EcoHealth Alliance, Inc and Wildlife Preservation Trust Int. Single Audit Reports 2017-2021* (June7, 2021) *available at* https://facdissem.census.gov/SearchResults.aspx.
[33] Internet Archive Wayback Machine, *Wuhan Institute of Virology, CAS*, Partnerships (Mar. 18, 2021) *available at* https://web.archive.org/web/20210318052528/http://english.whiov.cas.cn/International_Cooperation2016/Partnerships/.
[34] Internet Archive Wayback Machine, *Wuhan Institute of Virology, CAS*, Partnerships (Mar. 22, 2021) *available at* https://web.archive.org/web/20210322053537/http://english.whiov.cas.cn/International_Cooperation2016/Partnerships/
[35] House Committee on Appropriations, *FY 2022 Budget Request for the National Institutes of Health*, Hearings (May 25, 2021) *available at* https://appropriations.house.gov/events/hearings/fy-2022-budget-request-for-the-national-institutes-of-health.
[36] Alexis, Shi Zhengli: Weaponizing Coronaviruses, with Pentagon Funding, at a Chinese Military Lab, https://enviroshop.com/shi-zhengli-weaponizing-coronaviruses-with-pentagon-funding-at-a-chinese-military-lab/
[37] *Id.*
[38] National Institutes of Health, *NIH Grants Policy Statement*, Policy and Compliance (June 1, 2021) *available at* https://grants.nih.gov/policy/nihgps/index.htm.
[39] *Id.*

reports; research techniques and accomplishments; research products such as: technologies, patent applications, data or databases, physical collections, and models; significant changes in use or care of human subjects, vertebrate animals, biohazards, and/or select agents; and budgetary information and project outcomes.[40]

As the federal grant awarding agency, NIH must have the right of access to any of EHA's documents or other records which are pertinent to NIH federal awards.[41] The NIH grants policy states that the Freedom of Information Act (FOIA) and U.S. Department of Health and Human Services regulations require NIH to release certain grant documents and records requested by members of the public, regardless of the intended use of the information.[42] Per NIH policy, NIH will generally release funded applications and progress reports pursuant to a FOIA request.[43] NIH considers most grant-related information in the application or post-award phases as being public information (emphasis added).[44]

In support of this inquiry and the public interest in the origins of the COVID-19 pandemic, please provide written responses to the following by June 24, 2021:

1. We again renew our request for NIH's immediate compliance with our oversight inquiry for production of the grant documents and progress reports forthwith that we first requested on March 18, 2021.

2. What is NIH's policy for awarding funds to organizations when the organization has NIH grant funds in suspended status and are not cooperating NIH requests? If the NIH permits new award funding under these circumstances, please provide the policy, and explain how such funding does not undercut NIH's ability to oversee grantees and does not incentivize grantees to defy NIH's requests for information.

3. Please explain all oversight steps NIH has taken to ensure EHA's full compliance with federal financial subaward reporting requirements for all NIH grants. Please explain if EHA reported to NIH any subaward recipients other than the WIV or the WUSPH for NIH grant R01AI110964. Please provide all financial records of all NIH funds given to Dr. Zhengli Shi of the WIV.

4. For all NIH awards in which EHA was a subrecipient, please provide a financial accounting of EHA's subawards to the WIV or other organizations in China.

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[40] Hugh Hewitt, *Dr. Francis Collis On The U.S. Funding of the Wuhan Lab and Congressional Oversight,* The Hugh Hewitt Show (June 2, 2021) *available at* https://hughhewitt.com/dr-francis-collins-on-the-u-s-funding-of-the-wuhan-lab-and-congressional-oversight/, National Institutes of Health, *Research Performance Progress Report,* Grants & Funding (May 4, 2021) *available at* https://grants.nih.gov/grants/rppr/index.htm.
[41] *Id.*
[42] National Institutes of Health, *NIH Grants Policy Statement*, Policy and Compliance (June 1, 2021) *available at* https://grants.nih.gov/policy/nihgps/index.htm.
[43] *Id.*
[44] *Id.*

5. How does NIH ensure it does not award unapproved duplicate grants for same or similar research already funded by other agencies, to EHA or other NIH grant recipients? For all NIH awards to EHA, please provide accounting information for EHA subawards to recipients in China.

6. Please explain how NIH has reviewed EHA annual Single Audit reports to ensure how EHA has met program and reporting requirements.

7. How does NIH audit the financial reports submitted to the IRS by its 501(c)(3) non-profit organization grant award recipients to ensure NIH awards are accurately reported? How does NIH ensure its grantees do not act as a pass-through or money laundering provider to send U.S. research funding to China?

8. Please explain NIH's policy for ensuring its awardees accurately report the actual place of research performance. For all NIH-funded research, please provide all China site locations where EHA's work was performed.

9. Please explain if EHA reported its other funding or in-kind support, including awards from federal agency, to NIH. Please explain if EHA reported any support from organizations in China.

10. Did NIH perform a biodefense risk analysis for coronavirus research conducted at the WIV as research with potential for dual use of research concern, pandemic pathogen or bioweapon development, as outlined in the HHS *Framework for Guiding Funding Decisions about Proposed Research Involving Enhanced Potential Pandemic Pathogens*?[45] Please describe NIH's coordination procedures with the U.S. Intelligence Community that are completed before NIH funds research projects in foreign countries with existing biodefense programs.

Please make arrangements to schedule the briefing for Committee staff by June 24, 2021. If you have any questions, please contact Alan Slobodin or Diane Cutler of the Minority Committee staff. Thank you for your attention to this request.

Sincerely,

Cathy McMorris Rodgers
Republican Leader
Committee on Energy and Commerce

Fred Upton
Republican Leader
Subcommittee on Energy

[45] U.S. Department of Health and Human Services, *Framework for Guiding Funding Decisions about Proposed Research Involving Enhanced Potential Pandemic Pathogens*, Science Safety Security (Dec. 2017) *available at* https://www.phe.gov/s3/dualuse/Pages/p3co.aspx.

Bob Latta
Republican Leader
Subcommittee on Communications and Technology

Brett Guthrie
Republican Leader
Subcommittee on Health

David McKinley
Republican Leader
Subcommittee on Environment and Climate Change

H. Morgan Griffith
Republican Leader
Subcommittee on Oversight and Investigations

Gus Bilirakis
Republican Leader
Subcommittee on Consumer Protection and Commerce

Michael C. Burgess, M.D.
Member of Congress

Steve Scalise
Member of Congress

Adam Kinzinger
Member of Congress

Bill Johnson
Member of Congress

Billy Long
Member of Congress

Larry Bucshon, M.D.
Member of Congress

Markwayne Mullin
Member of Congress

Richard Hudson
Member of Congress

Tim Walberg
Member of Congress

Earl L. "Buddy" Carter
Member of Congress

Jeff Duncan
Member of Congress

Gary Palmer
Member of Congress

Neal P. Dunn, M.D.
Member of Congress

John Curtis
Member of Congress

Debbie Lesko
Member of Congress

Greg Pence
Member of Congress

Dan Crenshaw
Member of Congress

John Joyce, M.D.
Member of Congress

Kelly Armstrong
Member of Congress

Alan Slobodin
Job Title
Chief Investigative Counsel, Republican/Staff Director, Republican

Education

- **George Washington University Law School**
  - JD
  - 1984
- **Temple University-of The Commonwealth System of Higher Education**
  - BBA, business management, magna cum laude
  - 1979

Career History

- **Chief Investigative Counsel, Republican/Staff Director, Republican** House Subcommittee on Oversight and Investigations

January 2021 - Present

- **Chief Investigative Counsel** House Subcommittee on Oversight and Investigations

January 2019 - January 2021

- **Chief Investigative Counsel** House Subcommittee on Oversight and Investigations

December 2017 - January 2019

- **Chief Investigative Counsel** House Subcommittee on Oversight and Investigations

October 2017 - December 2017

- **Chief Investigative Counsel** House Subcommittee on Oversight and Investigations

2014 - October 2017

- **Deputy Chief Counsel** House Subcommittee on Oversight and Investigations

May 2004 - 2013

- **Senior Counsel, Oversight** House Subcommittee on Oversight and Investigations

1995 - April 2004

- **President and General Counsel, Legal Studies Division** Washington Legal Foundation

1989 - 1995

- **Counsel, Republican** House Subcommittee on Constitution, Civil Rights, and Civil Liberties

1986 - 1989

- **Assistant General Counsel** Washington Legal Foundation

1985 - 1986

- **Attorney** Ross, Dixon and Bell LLP

1984 - 1985

B.J. Koohmaraie
Job Title
Chief Counsel, Republican

Education

- **University of Nebraska College of Law**
  - JD
  - 2014
- **Nebraska Wesleyan University**
  - BS, political science
  - 2011

Career History

- **Chief Counsel, Republican**House Committee on Energy and Commerce

January 2021 - Present

- **Chief Counsel, Republican**House Subcommittee on Oversight and Investigations

February 2021 - Present

- **Coalitions Director/Deputy Chief Counsel**House Committee on Energy and Commerce

June 2020 - January 2021

- **Deputy Chief Counsel**House Subcommittee on Consumer Protection and Commerce

August 2019 - June 2020

- **Counsel**House Subcommittee on Consumer Protection and Commerce

January 2019 - August 2019

- **Counsel**House Subcommittee on Consumer Protection and Commerce

March 2017 - January 2019

- **Assistant Attorney General**Nebraska Office of the Attorney General

September 2014 - February 2017

- **Senior Certified Law Clerk**Nebraska Office of the Attorney General

March 2013 - September 2014

- **Research Assistant**University of Nebraska College of Law

August 2012 - May 2013

- **Regulatory Policy Intern**American Action Forum

May 2012 - August 2012

- **Staff Assistant**Rep. Adrian Smith (R-NE-3)

May 2010 - July 2011

- **Intern** Rep. Adrian Smith (R-NE-3)

April 2010 - May 2010

Diane Cutler
Job Title
U.S. Department of Health and Human Services Office of Inspector General Detailee

Career History

- **U.S. Department of Health and Human Services Office of Inspector General Detailee** House Committee on Energy and Commerce

January 2021 - Present

- **U.S. Department of Health and Human Services Office of Inspector General Detailee** House Committee on Energy and Commerce

August 2019 - January 2021

Chris Knauer
Job Title
Oversight Staff Director, Democratic

Education

- **McCourt School of Public Policy**
  - MPP
  - 1990
- **University of California Berkeley**
  - BA
  - 1987

Career History

- **Oversight Staff Director, Democratic** House Subcommittee on Oversight and Investigations

March 2015 - Present

- **Senior Investigator** House Committee on Oversight and Reform

January 2012 - February 2015

- **Investigator** House Committee on Oversight and Reform

January 2011 - January 2012

- **Senior Investigator** House Committee on Oversight and Reform

September 2009 - January 2011

- **Education Coordinator** House Committee on Oversight and Reform

August 2009 - August 2009

- **Senior Investigative Counsel** House Committee on Oversight and Reform

March 2009 - August 2009

- **Senior Investigator/Professional Staff Member** House Committee on Energy and Commerce

March 2007 - February 2009

- **Senior Investigator** House Committee on Energy and Commerce

January 2007 - February 2007

- **Investigator** House Committee on Energy and Commerce

1993 - January 2007

- **Evaluator** U.S. Government Accountability Office

1991 - 1993

Kevin McAloon
Job Title
Oversight Investigator, Democratic

Education

- **Villanova University**
    - MA, political science
    - 2009
- **Villanova University**
    - BA, political science
    - 2008

Career History

- **Oversight Investigator** House Subcommittee on Oversight and Investigations

January 2019 - Present

- **Professional Staff Member** House Committee on Energy and Commerce

March 2017 - January 2019

- **Senior Communications Analyst** U.S. Government Accountability Office

June 2015 - March 2017

- **Program Analyst Team Leader** U.S. Department of Health and Human Services Office of the Inspector General

February 2008 - May 2015

From: Lauer, Michael (NIH/OD) [E]
To: Brown, Tiffany (NIH/OD/OMA) [E]
Subject: TImeline
Date: Tuesday, June 22, 2021 10:01:37 AM
Attachments: EcoHealth Alliance grant R01AI110964 timeline 6 13 21.docx

EcoHealth Alliance grant R01AI110964 timeline
Mike Lauer (OER)
June 13, 2021

- June 5, 2013: Type 1 proposal submitted
- December 18, 2013: Reviewed, (b) (5)
- May 27, 2014: Type 1 awarded
    - Proposals and RPPRs in separate folder
    - NOAs in separate folder
- July 7, 2016: Letter from NIAID with determination that this is not "Gain-of-Function" research
- January 19, 2018: State Department Cables re WIV
- November 5, 2018: Type 2 submitted
- February 14, 2019: Type 2 reviewed, (b) (5)
- July 24, 2019: Type 2 awarded
- April 14, 2020: Larry Tabak ("LT") loops in Mike Lauer ("ML") on email string regarding Animal Rights and Congressional complaints
- April 19, 2020: ML sends letter to EcoHealth suspending WIV subaward
- April 20, 2020: Joshua Rogin Op-Ed in Washington Post about State Department cables
- April 22, 2020: ML send LT detailed information about EcoHealth and WIV
- April 24, 2020: ML sends letter to EcoHealth terminating entire grant (appealable under 42 CFR 50, subpart D)
- May 6, 2020: ML sends detailed information about EcoHealth and WIV to OIG OI / ONS
- May 21, 2020: Protest letter from 77 Nobel laureates
- May 22, 2020: Letter from Krinsky (attorney) to ML appealing termination
- July 8, 2020: Letter from ML to EcoHealth – grant reinstated but suspended (not appealable under 42 CFR 50, subpart D); request information and answers to questions; note failure to submit required reports to Federal Subaward Reporting System
- August 13, 2020: Letter from Krinsky (attorney) to ML objecting to suspension
- October 23, 2020: Letter from ML to EcoHealth rebutting Krinsky and requesting additional documents
- February 16, 2021: News story about WIV receiving OLAW assurance
- March 4, 2021: Daszak send email to ML requesting phone call; ML speaks with NIAID DEA; ML re-sends two prior letters (July 8, 2020 and October 23, 2020) to Daszak on March 10, 2021
- March 18, 2021: CMR letter (one of many Congressional queries)
- April 11, 2021: Daszak response to ML; no documents
- April 13, 2021: ML again asks Daszak for documents
- April 23, 2021: Daszak submits some documents to ML, being reviewed by OPERA and OGC
- May 16, 2021: OPERA analyses complete, (b) (5)
- May 26, 2021: DDER, OPERA, and OGC meeting: (b) (5)
- June 11, 2021: OIG notifies NIH of planned audit of NIH and EcoHealth