DEPARTMENT OF HEALTH & HUMAN SERVICES

Public Health Service

National Institutes of Health
Freedom of Information Office
Building 31, Room 5B-35
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Bethesda, Maryland 20892-2107
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Via Email: rcotca@judicialwatch.org

June 1, 2021

Ramona R. Cotca
Judicial Watch, Inc.
425 Third Street SW, Suite 800
Washington, DC 20024

Re: NIH FOIA Case No.: 54052; Judicial Watch v. HHS, Case No. 21-cv-00696

Dear Ms. Cotca:

This is a partial response to the Freedom of Information Act (FOIA) request that is the subject of the complaint filed in *Judicial Watch v. HHS*, 21-cv-00696, now pending in the U.S. District Court for the District of Columbia. Your FOIA request, dated April 22, 2020, was received by the National Institutes of Allergy and Infectious Diseases (NIAID) on the same day.

You requested the following:

1. All internal NIAID communications regarding the Wuhan Institute of Virology in Wuhan, China.
2. All agreements, contracts and related documents between NIAID and the Wuhan Institute of Virology.
3. All records, including agreements, funds disbursement records and related NIAID communications regarding a reported $3.7 million in grants provided by NIH to the Wuhan Institute of Virology.

The date range for the records request is January 1, 2013 to April 22, 2020.

In accordance with the Court's order dated March 16, 2021, we have processed 300 pages of responsive records this month. Of these pages, NIH has sent 20 pages for consultation to: The State Department and the Department of Defense for further review and return to us. NIH will provide a further response regarding the consulted material once the consultations are complete. Attached to this letter are 280 pages from the current May production.

The information being withheld is protected from release pursuant to Exemptions 4, 5, and 6 of the FOIA, 5 U.S.C. § 552 (b)(4), (b)(5) and (b)(6); and sections 5.31(d), (e) and (f) of the HHS FOIA Regulations, 45 CFR Part 5. Exemption 4 protects from disclosure trade secrets and commercial or financial information that is privileged and confidential. Exemption 5 permits the withholding of internal government records which are predecisional and contain staff advice, opinion, and recommendations. This exemption is intended to preserve free and candid internal dialogue leading to decision-making. Exemption 6 exempts from disclosure records the release of which would cause a clearly unwarranted invasion of personal privacy.

Please direct any questions regarding this response to Derek Hammond of the Department of Justice, who can be reached at derek.hammond@usdoj.gov, or (202) 252-2511.

Sincerely,

for Gorka Garcia-Malene
Freedom of Information Act Officer, NIH

From: Auchincloss, Hugh (NIH/NIAID) [E]
Sent: Wed, 15 Apr 2020 21:44:58 +0000
To: Fenton, Matthew (NIH/NIAID) [E]
Subject: Re: HEADS UP: Wuhan lab research

[redacted] (b) (5). Stay tuned.

Sent from my iPad

On Apr 15, 2020, at 5:41 PM, Fenton, Matthew (NIH/NIAID) [E] [redacted] (b) (6) wrote:

Hugh – just an FYI about this grant . I spoke with Larry about this twice today. He [redacted] (b) (5)

Matthew

From: Tabak, Lawrence (NIH/OD) [E] [redacted] (b) (6)
Sent: Wednesday, April 15, 2020 10:59 AM
To: Collins, Francis (NIH/OD) [E] [redacted] (b) (6); Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Erbelding, Emily (NIH/NIAID) [E] [redacted] (b) (6); Fenton, Matthew (NIH/NIAID) [E] [redacted] (b) (6); Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6); Lauer, Michael (NIH/OD) [E] [redacted] (b) (6); Schwetz, Tara (NIH/OD) [E] [redacted] (b) (6); Wolinetz, Carrie (NIH/OD) [E] [redacted] (b) (6)
Subject: HEADS UP: Wuhan lab research
Importance: High

Francis, Tony -

The **WH has strongly embraced concerns** raised by Congressman Gaetz who 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."

This is a large multi- country study with Wuhan being one site. The principal investigator, Peter Daszak, is based in NY at Ecohealth Alliance, Inc

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

Obtained via FOIA by Judicial Watch, Inc.

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

The 3.7M dollar figure is the total over 6 years to all sites which include (several in) China, Thailand, Cambodia, Laos, Vietnam, Malaysia, Indonesia, and Myanmar. We estimate that approximately 826,300 has been spent at this site since the inception of the grant. Yearly costs appear to be about 80K/year. It is in year 6 of a total of 10 year.

More by phone.
Larry

From: Auchincloss, Hugh (NIH/NIAID) [E]
Sent: Thu, 16 Apr 2020 19:58:19 +0000
To: Crawford, Chase (NIH/NIAID) [E];Harper, Jill (NIH/NIAID) [E];Gilles, Sharon (NIH/NIAID) [E];Marston, Hilary (NIH/NIAID) [E];Johnson, Martin S. (NIH/NIAID) [E];Billet, Courtney (NIH/NIAID) [E]
Cc: Sullivan, Fantasia (NIH/NIAID) [C];NIAID OCGR Leg
Subject: RE: ACTION Requested ASAP (4/16): Review draft NIAID response to Senate Qs - Wuhan Institute of Virology

Ok with me.

From: Crawford, Chase (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Thursday, April 16, 2020 3:52 PM
To: Auchincloss, Hugh (NIH/NIAID) [E] [redacted] (b) (6); Harper, Jill (NIH/NIAID) [E] [redacted] (b) (6); Gilles, Sharon (NIH/NIAID) [E] [redacted] (b) (6); Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6); Johnson, Martin S. (NIH/NIAID) [E] [redacted] (b) (6); Billet, Courtney (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Sullivan, Fantasia (NIH/NIAID) [C] [redacted] (b) (6); NIAID OCGR Leg <NIAIDOCGRLeg@mail.nih.gov>
Subject: ACTION Requested ASAP (4/16): Review draft NIAID response to Senate Qs - Wuhan Institute of Virology
Importance: High

Good Afternoon,

OCGR-Leg has drafted the **attached proposed response** to recent Congressional requests for information on NIAID support for research activities at the **Wuhan Institute of Virology** (additional background on Congressional interest can be found in the email chain below the signature line). As you may recall the Wuhan Institute of Virology has been supported through subawards from an NIAID-supported EcoHealth Alliance project (R01AI110964).

NIAID also has been asked [redacted] (b) (5) (b) (5)

ACTION
As soon as possible, please review the attached draft NIAID response and provide any edits in track changes.

Please let us know if you have any questions.

Thanks,
Chase

Chase Crawford, D.V.M., M.S.
Public Health Analyst

Obtained via FOIA by Judicial Watch, Inc.

Legislative Affairs and Correspondence Management Branch
Office of Communications and Government Relations
NIAID/NIH/DHHS

From: Crawford, Chase (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Monday, April 13, 2020 5:41 PM
To: NIAID BUGS [redacted] (b) (6)
Cc: Auchincloss, Hugh (NIH/NIAID) [E] [redacted] (b) (6); Harper, Jill (NIH/NIAID) [E] [redacted] (b) (6); NIAID OCGR Leg [redacted] (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
[redacted] (b) (6)

From: LaMontagne, Karen (NIH/OD) [E] [redacted] (b) (6)
Sent: Monday, April 13, 2020 4:23 PM
To: NIAID OCGR Leg [redacted] (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 [redacted] (b) (6)
Date: Monday, April 13, 2020 at 3:42 PM

Obtained via FOIA by Judicial Watch, Inc.

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.*

Obtained via FOIA by Judicial Watch, Inc.

PO Box 26029
Washington, DC 20001
Phone: 860.882.2492
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From: Handley, Gray (NIH/NIAID) [E]
Sent: Mon, 13 Apr 2020 16:37:28 +0000
To: Auchincloss, Hugh (NIH/NIAID) [E]
Subject: FW: Daily Mail: REVEALED: U.S. government gave $3.7million grant to Wuhan lab at center of coronavirus leak scrutiny that was performing experiments on bats from the caves where the disease is believed to have originated
Attachments: Daszak Wuhan Exceprts.docx

From: Post, Diane (NIH/NIAID) [E] (b) (6)
Sent: Monday, April 13, 2020 9:54 AM
To: Handley, Gray (NIH/NIAID) [E] (b) (6); Mulach, Barbara (NIH/NIAID) [E] (b) (6)
Cc: Bernabe, Gayle (NIH/NIAID) [E] (b) (6); Dominique, Joyelle (NIH/NIAID) [E] (b) (6); Marston, Hilary (NIH/NIAID) [E] (b) (6)
Subject: RE: Daily Mail: REVEALED: U.S. government gave $3.7million grant to Wuhan lab at center of coronavirus leak scrutiny that was performing experiments on bats from the caves where the disease is believed to have originated

Hi Gray,

This funding is not tied to CEIRS or CIVICs, it is part of a R01 grant that is led by EcoHealth Alliance, New York (Daszak, PI - R01-AI-110964). The abstract that describes the grant work is below. Attached is a summary of the work that was being done in Wuhan.

Let us know if you need additional information about the grant.

Thank you,
Diane

Project Summary: Understanding the Risk of Bat Coronavirus Emergence Novel zoonotic, bat-origin CoVs are a significant threat to global health and food security, as the cause of SARS in China in 2002, the ongoing outbreak of MERS, and of a newly emerged Swine Acute Diarrhea Syndrome in China. In a previous R01 we found that bats in southern China harbor an extraordinary diversity of SARSr-CoVs, some of which can use human ACE2 to enter cells, infect humanized mouse models causing SARS-like illness, and evade available therapies or vaccines. We found that people living close to bat habitats are the primary risk groups for spillover, that at one site diverse SARSr-CoVs exist that contain every genetic element of the SARS-CoV genome, and identified serological evidence of human exposure among people living nearby. These findings have led to 18 published peer-reviewed papers, including two papers in Nature, and a review in Cell. Yet salient questions remain on the origin, diversity, capacity to cause illness, and risk of spillover of these viruses. In this R01 renewal we will address these issues through 3 specific aims: Aim 1. Characterize the diversity and distribution of high spillover-risk SARSr-CoVs in bats in southern China. We will use phylogeographic and viral discovery curve analyses to target additional bat sample collection and molecular CoV screening to fill in gaps in our previous sampling and fully characterize natural SARSr-CoV diversity in southern China. We will sequence receptor binding domains (spike proteins) to identify viruses with the highest potential for spillover which we will include in our experimental investigations (Aim 3). Aim 2. Community, and clinic-based syndromic, surveillance to capture SARSr-CoV spillover, routes of exposure and potential public health consequences. We will conduct biological-behavioral surveillance in high-risk populations, with known bat contact, in community and clinical settings to 1) identify risk factors for serological and PCR evidence of bat SARSr-CoVs; & 2) assess possible health effects of SARSr-CoVs infection in people. We will analyze bat-CoV serology against human-wildlife contact and exposure data to quantify risk factors and health impacts of SARSr-CoV spillover. Aim 3. In vitro and in vivo characterization of SARSr-CoV spillover risk, coupled with spatial and phylogenetic analyses to identify the regions and viruses of public health concern. We will use S protein sequence data, infectious clone technology, in vitro and in vivo infection experiments and analysis of receptor binding to test the hypothesis that % divergence thresholds in S protein sequences predict spillover potential. We will combine these data with bat host distribution, viral diversity and phylogeny, human survey of risk behaviors and illness, and serology to identify SARSr-CoV spillover risk hotspots across southern China. Together these data and analyses will be critical for the future development of public health interventions and enhanced surveillance to prevent the re-emergence of SARS or the emergence of a novel SARSr-CoV. PUBLIC HEALTH RELEVANCE: Program Director/Principal Investigator: Daszak, Peter Renewal: Understanding the Risk of Bat Coronavirus Emergence Most emerging human viruses come from wildlife, and these represent a significant threat to public health and biosecurity in the US and globally, as was demonstrated by the SARS coronavirus pandemic of 2002-03. This project seeks to understand what factors allow coronaviruses, including close relatives to SARS, to evolve and jump into the human population by studying viral diversity in their animal reservoirs (bats), surveying people that live in high-risk communities in China for evidence of bat-coronavirus infection, and conducting laboratory experiments to analyze and predict which newly-discovered viruses pose the greatest threat to human health.

From: Handley, Gray (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Monday, April 13, 2020 9:04 AM
To: Post, Diane (NIH/NIAID) [E] [redacted] (b) (6); Mulach, Barbara (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Bernabe, Gayle (NIH/NIAID) [E] [redacted] (b) (6); Dominique, Joyelle (NIH/NIAID) [E] [redacted] (b) (6); Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6)
Subject: FW: Daily Mail: REVEALED: U.S. government gave $3.7million grant to Wuhan lab at center of coronavirus leak scrutiny that was performing experiments on bats from the caves where the disease is believed to have originated

Diane or Barbara,

Can you clarify the accuracy of this? [redacted] (b) (5) Can you clarify the situation because I am very likely to be asked about this.

Sorry if you have already answered this question ten times.

Thanks. Gray

From: Folkers, Greg (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Sunday, April 12, 2020 10:59 AM
Subject: Daily Mail: REVEALED: U.S. government gave $3.7million grant to Wuhan lab at center of coronavirus leak scrutiny that was performing experiments on bats from the caves where the disease is believed to have originated

Sunday, Apr 12th 2020

REVEALED: U.S. government gave $3.7million grant to Wuhan lab at center of coronavirus leak scrutiny that was performing

Obtained via FOIA by Judicial Watch, Inc.

experiments on bats from the caves where the disease is believed to have originated

- **The US National Institutes of Health, a government agency, awarded a $3.7million research grant to the Wuhan Institute of Virology**
- **The lab is the center of several conspiracy theories that suggest it is the original source of the coronavirus outbreak**
- **The institute experimented on bats from the source of the coronavirus**
- **They were captured more than 1,000 miles away in Yunnan**
- **Sequencing of the Covid-19 genome has traced it to bats to Yunnan's caves**
- **The U.S. government funded research on coronavirus transmission in the lab over the past decade**
- **Learn more about how to help people impacted by COVID**

By Frances Mulraney and Glenn Owen For The Mail On Sunday

Published: 20:49 EDT, 11 April 2020 | Updated: 00:21 EDT, 12 April 2020

The Chinese laboratory at the center of scrutiny over a potential coronavirus leak has been using U.S. government money to carry out research on bats from the caves which scientists believe are the original source of the deadly outbreak.

The Wuhan Institute of Virology undertook coronavirus experiments on mammals captured more than 1,000 miles away in Yunnan which were funded by a $3.7 million grant from the US government.

Sequencing of the COVID-19 genome has traced it back to bats found in Yunnan caves but it was first thought to have transferred to humans at an animal market in Wuhan.

The revelation that the Wuhan Institute was experimenting on bats from the area already known to be the source of COVID-19 - and doing so with American money - has sparked further fears that the lab, and not the market, is the original outbreak source.

Lawmakers and pressure groups were quick to hit out at U.S. funding being provided for the 'dangerous and cruel animal experiments at the Wuhan Institute'.

A laboratory at the center of scrutiny over the coronavirus pandemic has been carrying out research on bats from the cave which scientists believe is the original source of the outbreak

Obtained via FOIA by Judicial Watch, Inc.

Workers are seen next to a cage with mice inside the P4 laboratory in Wuhan. It has been revealed that the lab also carried out research on bats from the source location of COVID-19

The institute is located only 20 miles from the food market where it was originally believed that the outbreak began. Experts continue to say the virus was transmitted from animal to human and was not lab engineered in China as some conspiracy theories have claimed

US Congressman Matt Gaetz said: '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.'

On Saturday, Anthony Bellotti, president of the US pressure group White Coat Waste, condemned his government for spending tax dollars in China, adding: 'Animals infected with viruses or otherwise sickened and abused in Chinese labs reportedly may be sold to wet markets for consumption once experiments are done.'

The $37million Wuhan Institute of Virology, the most advanced laboratory of its type on the Chinese mainland, is based twenty miles from the now infamous wildlife market that was thought to be the location of the original transfer of the virus from animals to humans.

According to documents obtained by The Mail on Sunday, scientists there experimented on bats as part of a project funded by the US National Institutes of Health, which continues to licence the Wuhan laboratory to receive American money for experiments.

© Twitter / Matt Gaetz

Obtained via FOIA by Judicial Watch, Inc.

Rep. Matt Gaetz (R-Fla.), pictured, has criticized U.S. funding of research in the Wuhan Institute of Virology after it emerged that experiments were being conducted on bats from Yunnan, the location experts believe to be the original source of deadly COVID-19

Anthony Bellotti, the founder and National Campaign Manager of the White Coat Waste Project, slammed the use of US funding to perform experiments on bats in Wuhan

Obtained via FOIA by Judicial Watch, Inc.

China clamps down on research into the origins of coronavirus as officials demand the right to vet scientific papers

China is clamping down on research into the origins of the coronavirus after officials have demanded the right to inspect its scientific papers before they are made pubic.

Two websites for leading Chinese universities have allegedly recently published and then removed pages that discuss a new policy which requires academic papers about Covid-19 to undergo extra checks before they are published, according to The Guardian.

Both Fudan University and the China University of Geosciences (Wuhan) allegedly posted notices saying that research on the origins of the coronavirus will be subject to government checks.

The director of the SOAS China Institute in London, Professor Steve Tsang, said that the Chinese government is more concerned with 'controlling the narrative' surrounding coronavirus than public health or economic fallout.

The source who found the cached versions of the websites said they were concerned at what appeared to be a governmental coverup.

The NIH is the primary agency of the United States government responsible for biomedical and public health research.

The Wuhan Institute lists them on their website as a partner as well as several other American academic institutions.

Other U.S. partners include the University of Alabama, the University of North Texas, Harvard University, and the National Wildlife Federation.

As part of the NIH research at the institute, scientists grew a coronavirus in a lab and injected it into three-day-old piglets.

The news that COVID-19 bats were under research there means that a leak from the Wuhan laboratory can no longer be completely ruled out.

According to one unverified claim, scientists at the institute could have become infected after being sprayed with blood containing the virus, and then passed it on to the local community.

A second institute in the city, the Wuhan Centre for Disease Control – which is barely three miles from the market – is also believed to have carried out experiments on animals such as bats to examine the transmission of coronaviruses.

The Wuhan Institute, which keeps more than 1,500 strains of deadly viruses, specializes in the research of 'the most dangerous pathogens', in particular the viruses carried by bats.

Chinese officials decided to build the institute after the country was ravaged by an outbreak of SARS in 2002 and 2003.

SARS, another kind of coronavirus, killed 775 people and infected more than 8,000 globally in an epidemic.

Obtained via FOIA by Judicial Watch, Inc.

Bats have been linked with seven major epidemics over the past three decades

Since an outbreak of the novel coronavirus emerged in the city in December, it has been at the center of conspiracy theories which suggest that the bug originated there.

While scientists believe that the virus jumped to humans from wild animals sold as food in a market in Wuhan, conspiracy theorists promote different assumptions.

Some of them claim that the virus, formally known as SARS-CoV-2, could be a biological warfare weapon engineered there. Others suspect that it escaped from the lab.

China has repeatedly denied the allegations.

Obtained via FOIA by Judicial Watch, Inc.

Biosafety Level 4 Laboratory, Wuhan Institute of Virology. The institute is at the center of several controversial conspiracy theories that claim it is to blame for the coronavirus outbreak

A worker is seen ninside the P4 laboratory in Wuhan, capital of China's Hubei province in February 2020. It is feared COVID-19 may have leaked from a lab sparking the outbreak

Obtained via FOIA by Judicial Watch, Inc.

Shi Zhengli, a deputy director of the institute, told the press in February that she 'guaranteed with her own life' that the outbreak was not related to the lab.

She admits that when summoned back from a conference to investigate the new disease, she wondered at first if a coronavirus could have escaped from her unit.

She has warned about the danger of epidemics from bat-borne viruses.

But she says she did not expect such an outbreak in Wuhan, in the center of China, since her studies suggested subtropical areas in the south had the highest risk of such 'zoonotic' transmission to humans.

Shi told the respected science journal Scientific American last month of her relief when, having checked back through disposal records, none of the genome sequences matched their virus samples.

'That really took a load off my mind. I had not slept a wink for days,' she said.

Many international experts have also dismissed such theories.

Dr Keusch, Professor of Medicine and International Health at Boston University's Schools of Medicine and Public Health, stressed that no release of viruses from a high-level lab, such as the one in Wuhan, 'has ever happened'.

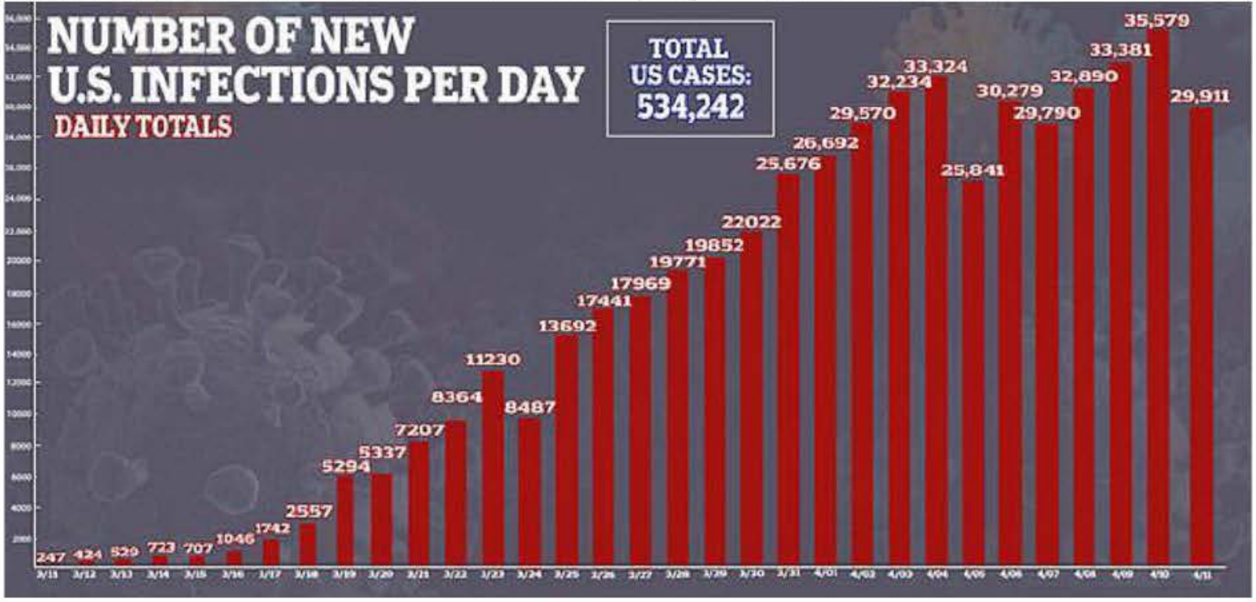
He defended his peers in the Chinese city as he said: 'The Wuhan lab is designed to the highest standards with redundant safety systems and the highest level of training.

'Many of its research faculty trained at a similar laboratory in Galveston, Texas. So we know the Wuhan team is as qualified as the Texas group...

'This means the assertion of a leak, rather than being highly likely, instead is highly unlikely.'

Last week, further doubt was cast on the animal market theory, however, after Cao Bin, a doctor at the Wuhan Jinyintan Hospital, highlighted research showing that 13 of the first 41 patients diagnosed with the infection had not had any contact with the market.

'It seems clear that the seafood market is not the only origin of the virus,' he said.



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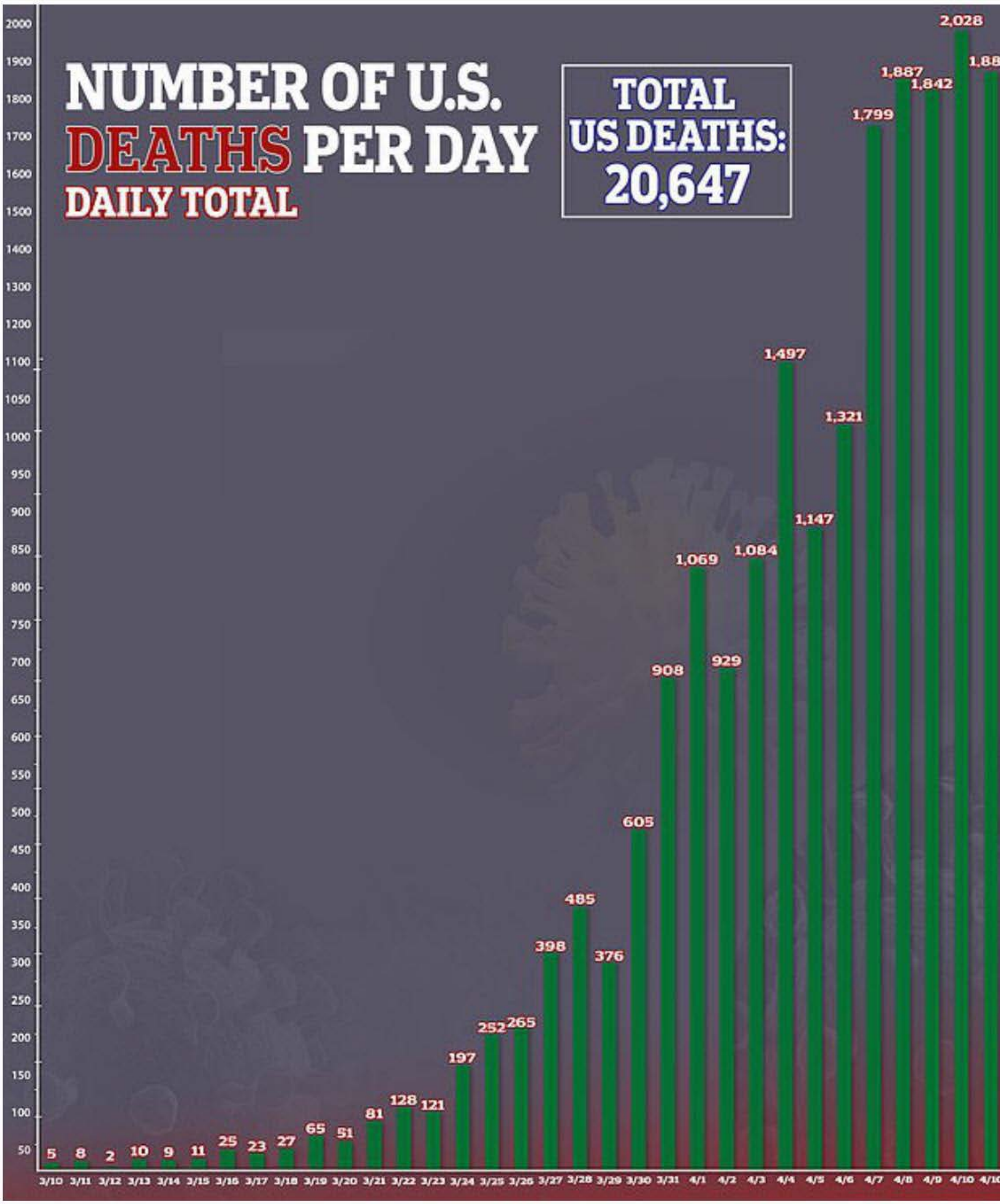

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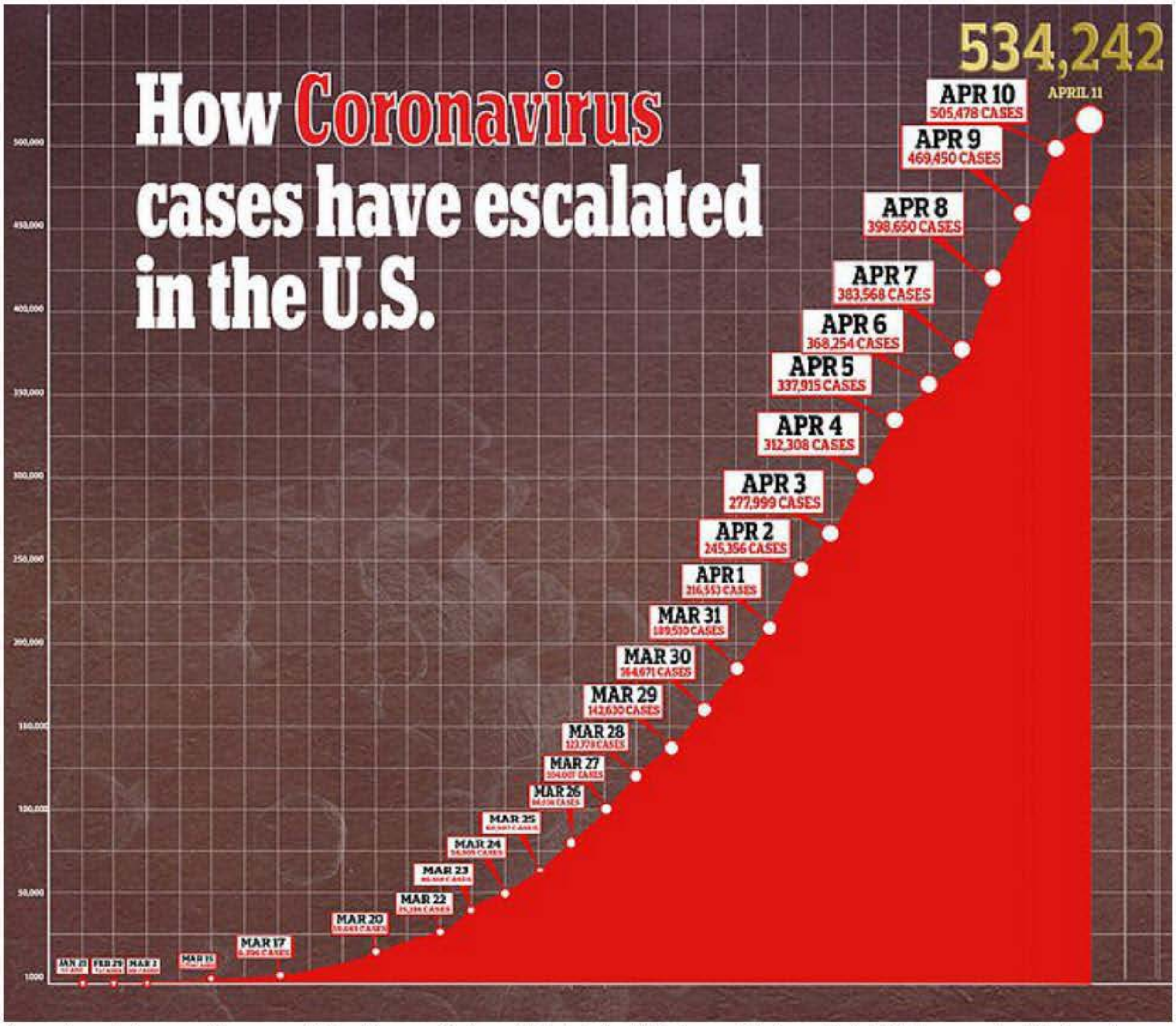

American biosecurity expert Professor Richard Ebright, of Rutgers University's Waksman Institute of Microbiology, New Jersey, said that while the evidence suggests COVID-19 was not created in one of the Wuhan laboratories, it could easily have escaped from there while it was being analyzed.

Prof Ebright said he has seen evidence that scientists at the Centre for Disease Control and the Institute of Virology studied the viruses with only 'level 2' security – rather than the recommended level 4 – which 'provides only minimal protections against infection of lab workers'.

He added: 'Virus collection, culture, isolation, or animal infection would pose a substantial risk of infection of a lab worker, and from the lab worker then the public.'

He concluded that the evidence left 'a basis to rule out [that coronavirus is] a lab construct, but no basis to rule out a lab accident'.

Results of the U.S-funded research at the Wuhan Institute were published in November 2017 under the heading: 'Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus.'

The exercise was summarized as: 'Bats in a cave in Yunnan, China were captured and sampled for coronaviruses used for lab experiments.

'All sampling procedures were performed by veterinarians with approval from the Animal Ethics Committee of the Wuhan Institute of Virology.

Obtained via FOIA by Judicial Watch, Inc.

'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. Bats were trapped and faecal swab samples were collected.'

Another study, published in April 2018, was titled 'fatal swine acute diarrhoea syndrome caused by an HKU2-related coronavirus of bat origin' and described the research as such: 'Following a 2016 bat-related coronavirus outbreak on Chinese pig farms, bats were captured in a cave and samples were taken.

Experimenters grew the virus in a lab and injected it into three-day-old piglets.

Intestinal samples from sick piglets were ground up and fed to other piglets as well.

The coronavirus pandemic has killed more than 108,000 people and infected over 1.7 million worldwide.'

On Saturday, the American outbreak became the deadliest in the world over 2,000 deaths in a day.

The national deaths toll is 20,087 and there are 522,643 confirmed cases as of Saturday evening.

China muzzled its Bat Woman: Beijing authorities hushed up the findings of a scientist who unlocked the genetic make-up of the coronavirus within days of the outbreak – which is vital for tests and vaccines

A Chinese scientist who is the one of the world's leading experts on coronaviruses was 'muzzled' after unraveling the genetic composition of the new disease, which is crucial for developing diagnostic tests and vaccines.

The revelation will fuel fresh concerns over **China**'s cover-up of the pandemic after it erupted in the city of Wuhan. Critics argue that Communist Party chiefs frustrated efforts to contain the outbreak before it exploded around the world.

At the centre of the new claims is Shi Zhengli, known as China's 'Bat Woman' after years spent on difficult virus-hunting expeditions in dank caves that have led to a series of important scientific discoveries.

The virologist was called back to her highsecurity laboratory in Wuhan at the end of last year after a mysterious new respiratory condition in the city was identified as a novel **coronavirus** – and within three days she completed its gene sequencing.

Obtained via FOIA by Judicial Watch, Inc.

A virology lab like the one Shi Zhengli completed the gene sequencing of the coronavirus

Her team's work, and several other breakthroughs in subsequent days, indicated the virus was linked to horseshoe bats found more than 1,000 miles away in Yunnan, a region of southern China.

Their findings showed it was similar to SARS, a respiratory disease that sparked an epidemic in 33 countries after emerging from China in 2002.

Gao Yu, a Chinese journalist freed last week after 76 days of lockdown in Wuhan, said he spoke to Shi during his incarceration and revealed: 'We learned later her institute finished gene-sequencing and related tests as early as January 2 but was muzzled.'

The Mail on Sunday has learned that on that same day, Yanyi Wang, director of the Wuhan Institute of Virology, sent an email to staff and key officials ordering them not to disclose information on the disease.

She warned, according to a leak on social media confirmed by activists and Hong Kong media, that 'inappropriate and inaccurate information'was causing 'general panic' – thought to refer to eight whistle-blowing doctors whose warnings to local citizens had led to their arrest.

Wang said the National Health Commission 'unequivocally requires that any tests, clinical data, test results, conclusions related to the epidemic shall not be posted on social media platforms, nor shall [it] be disclosed to any media outlets including government official media, nor shall [it] be disclosed to partner institutions.'

Eight days later, a team led by a professor in Shanghai who received samples from an infected patient, published a genome sequence on an open access platform.

His laboratory was closed for 'rectification' two days later.

Obtained via FOIA by Judicial Watch, Inc.

Obtained via FOIA by Judicial Watch, Inc.

Shi Zhengli is known as China's 'Bat Woman' after years spent on difficult virus-hunting expeditions in dank caves that have led to a series of important scientific discoveries

At the time, the public was being told that no new cases had been reported in Wuhan for more than a week and there was no clear evidence of human transmission, although dozens of health workers were starting to fall ill with the disease.

In an online lecture last month, Shi Zhengli said her team found on January 14 that the new virus could infect people – six days before this fact was revealed by China.

On the same day, the World Health Organisation issued a tweet backing China's denials of human transmissions.

Shi's team released its data identifying the disease on January 23 on a scientific portal before publication the next month by the journal Nature.

It said the genomic sequence was 96 per cent identical to another virus they found in horseshoe bats in Yunnan.

Shi is a specialist in emerging diseases and has earned global acclaim for work investigating links between bats and coronaviruses, aided by expeditions to collect samples and swabs in the fetid cave networks of southern China.

She was a key part of the team that traced SARS to horseshoe bats through civets, a cat-like creature often eaten in China.

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Obtained via FOIA by Judicial Watch, Inc.

(b) (4), (b) (5)

[redacted]

Obtained via FOIA by Judicial Watch, Inc.

(b) (4), (b) (5), (b) (6)

[redacted]

Obtained via FOIA by Judicial Watch, Inc.

(b) (5)

[redacted]

Obtained via FOIA by Judicial Watch, Inc.

(b) (4), (b) (5)

[redacted]

Obtained via FOIA by Judicial Watch, Inc.

(b) (4), (b) (5)

[redacted]

Obtained via FOIA by Judicial Watch, Inc.

(b) (4), (b) (5)

[redacted]

Obtained via FOIA by Judicial Watch, Inc.

From: Handley, Gray (NIH/NIAID) [E]
Sent: Mon, 13 Apr 2020 16:37:06 +0000
To: Auchincloss, Hugh (NIH/NIAID) [E]
Subject: FW: Daily Mail: REVEALED: U.S. government gave $3.7million grant to Wuhan lab at center of coronavirus leak scrutiny that was performing experiments on bats from the caves where the disease is believed to have originated
Attachments: FW: Urgent for Dr. Fauci: China's lab for studying SARS and Ebola is in Wuhan, the outbreak's center, Daszak Wuhan Exceprts.docx

---

From: Mulach, Barbara (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Monday, April 13, 2020 9:42 AM
To: Handley, Gray (NIH/NIAID) [E] [redacted] (b) (6); Post, Diane (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Bernabe, Gayle (NIH/NIAID) [E] [redacted] (b) (6); Dominique, Joyelle (NIH/NIAID) [E] [redacted] (b) (6); Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6)
Subject: RE: Daily Mail: REVEALED: U.S. government gave $3.7million grant to Wuhan lab at center of coronavirus leak scrutiny that was performing experiments on bats from the caves where the disease is believed to have originated

HI Gray,
It looks like they are just re-visiting an issue that came up in January. See attached for information that was sent to Melinda Haskins back in January as background for Dr. Fauci.

If you need anything else, just let us know.
Barbara

From: Handley, Gray (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Monday, April 13, 2020 9:04 AM
To: Post, Diane (NIH/NIAID) [E] [redacted] (b) (6); Mulach, Barbara (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Bernabe, Gayle (NIH/NIAID) [E] [redacted] (b) (6); Dominique, Joyelle (NIH/NIAID) [E] [redacted] (b) (6); Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6)
Subject: FW: Daily Mail: REVEALED: U.S. government gave $3.7million grant to Wuhan lab at center of coronavirus leak scrutiny that was performing experiments on bats from the caves where the disease is believed to have originated

Diane or Barbara,

Can you clarify the accuracy of this? [redacted] (b) (5) Can you clarify the situation because I am very likely to be asked about this.

Sorry if you have already answered this question ten times.

Thanks. Gray

From: Folkers, Greg (NIH/NIAID) [E] (b) (6)
Sent: Sunday, April 12, 2020 10:59 AM
Subject: Daily Mail: REVEALED: U.S. government gave $3.7million grant to Wuhan lab at center of coronavirus leak scrutiny that was performing experiments on bats from the caves where the disease is believed to have originated

Sunday, Apr 12th 2020

REVEALED: U.S. government gave $3.7million grant to Wuhan lab at center of coronavirus leak scrutiny that was performing experiments on bats from the caves where the disease is believed to have originated

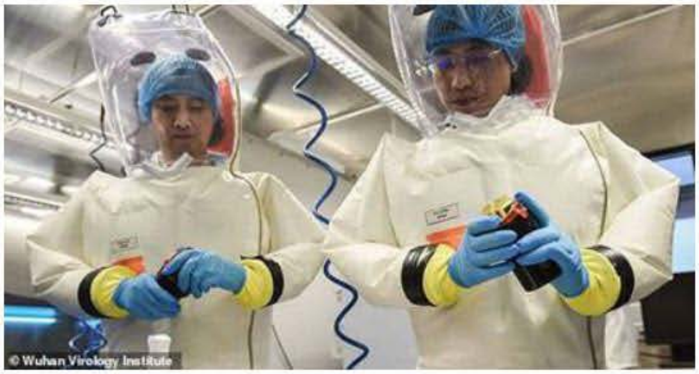
- **The US National Institutes of Health, a government agency, awarded a $3.7million research grant to the Wuhan Institute of Virology**
- **The lab is the center of several conspiracy theories that suggest it is the original source of the coronavirus outbreak**
- **The institute experimented on bats from the source of the coronavirus**
- **They were captured more than 1,000 miles away in Yunnan**
- **Sequencing of the Covid-19 genome has traced it to bats to Yunnan's caves**
- **The U.S. government funded research on coronavirus transmission in the lab over the past decade**
- **Learn more about how to help people impacted by COVID**

By Frances Mulraney and Glenn Owen For The Mail On Sunday
Published: 20:49 EDT, 11 April 2020 | Updated: 00:21 EDT, 12 April 2020

The Chinese laboratory at the center of scrutiny over a potential coronavirus leak has been using U.S. government money to carry out research on bats from the caves which scientists believe are the original source of the deadly outbreak.
The Wuhan Institute of Virology undertook coronavirus experiments on mammals captured more than 1,000 miles away in Yunnan which were funded by a $3.7 million grant from the US government.
Sequencing of the COVID-19 genome has traced it back to bats found in Yunnan caves but it was first thought to have transferred to humans at an animal market in Wuhan.
The revelation that the Wuhan Institute was experimenting on bats from the area already known to be the source of COVID-19 - and doing so with American money - has sparked further fears that the lab, and not the market, is the original outbreak source.

Lawmakers and pressure groups were quick to hit out at U.S. funding being provided for the 'dangerous and cruel animal experiments at the Wuhan Institute'.

Obtained via FOIA by Judicial Watch, Inc.



A laboratory at the center of scrutiny over the coronavirus pandemic has been carrying out research on bats from the cave which scientists believe is the original source of the outbreak

Workers are seen next to a cage with mice inside the P4 laboratory in Wuhan. It has been revealed that the lab also carried out research on bats from the source location of COVID-19

Obtained via FOIA by Judicial Watch, Inc.

The institute is located only 20 miles from the food market where it was originally believed that the outbreak began. Experts continue to say the virus was transmitted from animal to human and was not lab engineered in China as some conspiracy theories have claimed

US Congressman Matt Gaetz said: '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.'

On Saturday, Anthony Bellotti, president of the US pressure group White Coat Waste, condemned his government for spending tax dollars in China, adding: 'Animals infected with viruses or otherwise sickened and abused in Chinese labs reportedly may be sold to wet markets for consumption once experiments are done.'

The $37million Wuhan Institute of Virology, the most advanced laboratory of its type on the Chinese mainland, is based twenty miles from the now infamous wildlife market that was thought to be the location of the original transfer of the virus from animals to humans.

According to documents obtained by The Mail on Sunday, scientists there experimented on bats as part of a project funded by the US National Institutes of Health, which continues to licence the Wuhan laboratory to receive American money for experiments.

Rep. Matt Gaetz (R-Fla.), pictured, has criticized U.S. funding of research in the Wuhan Institute of Virology after it emerged that experiments were being conducted on bats from Yunnan, the location experts believe to be the original source of deadly COVID-19

Obtained via FOIA by Judicial Watch, Inc.

Anthony Bellotti, the founder and National Campaign Manager of the White Coat Waste Project, slammed the use of US funding to perform experiments on bats in Wuhan

China clamps down on research into the origins of coronavirus as officials demand the right to vet scientific papers

China is clamping down on research into the origins of the coronavirus after officials have demanded the right to inspect its scientific papers before they are made pubic.

Two websites for leading Chinese universities have allegedly recently published and then removed pages that discuss a new policy which requires academic papers about Covid-19 to undergo extra checks before they are published, according to The Guardian.

Both Fudan University and the China University of Geosciences (Wuhan) allegedly posted notices saying that research on the origins of the coronavirus will be subject to government checks.

The director of the SOAS China Institute in London, Professor Steve Tsang, said that the Chinese government is more concerned with 'controlling the narrative' surrounding coronavirus than public health or economic fallout.

The source who found the cached versions of the websites said they were concerned at what appeared to be a governmental coverup.

The NIH is the primary agency of the United States government responsible for biomedical and public health research.

The Wuhan Institute lists them on their website as a partner as well as several other American academic institutions.

Other U.S. partners include the University of Alabama, the University of North Texas, Harvard University, and the National Wildlife Federation.

As part of the NIH research at the institute, scientists grew a coronavirus in a lab and injected it into three-day-old piglets.

Obtained via FOIA by Judicial Watch, Inc.

The news that COVID-19 bats were under research there means that a leak from the Wuhan laboratory can no longer be completely ruled out.

According to one unverified claim, scientists at the institute could have become infected after being sprayed with blood containing the virus, and then passed it on to the local community.

A second institute in the city, the Wuhan Centre for Disease Control – which is barely three miles from the market – is also believed to have carried out experiments on animals such as bats to examine the transmission of coronaviruses.

The Wuhan Institute, which keeps more than 1,500 strains of deadly viruses, specializes in the research of 'the most dangerous pathogens', in particular the viruses carried by bats.

Chinese officials decided to build the institute after the country was ravaged by an outbreak of SARS in 2002 and 2003.

SARS, another kind of coronavirus, killed 775 people and infected more than 8,000 globally in an epidemic.

Bats have been linked with seven major epidemics over the past three decades

Obtained via FOIA by Judicial Watch, Inc.

Since an outbreak of the novel coronavirus emerged in the city in December, it has been at the center of conspiracy theories which suggest that the bug originated there.

While scientists believe that the virus jumped to humans from wild animals sold as food in a market in Wuhan, conspiracy theorists promote different assumptions.

Some of them claim that the virus, formally known as SARS-CoV-2, could be a biological warfare weapon engineered there. Others suspect that it escaped from the lab.

China has repeatedly denied the allegations.

© General Office of Hubei Provincial People's Government

Biosafety Level 4 Laboratory, Wuhan Institute of Virology. The institute is at the center of several controversial conspiracy theories that claim it is to blame for the coronavirus outbreak

Obtained via FOIA by Judicial Watch, Inc.

A worker is seen ninside the P4 laboratory in Wuhan, capital of China's Hubei province in February 2020. It is feared COVID-19 may have leaked from a lab sparking the outbreak

Shi Zhengli, a deputy director of the institute, told the press in February that she 'guaranteed with her own life' that the outbreak was not related to the lab.

She admits that when summoned back from a conference to investigate the new disease, she wondered at first if a coronavirus could have escaped from her unit.

She has warned about the danger of epidemics from bat-borne viruses.

But she says she did not expect such an outbreak in Wuhan, in the center of China, since her studies suggested subtropical areas in the south had the highest risk of such 'zoonotic' transmission to humans.

Shi told the respected science journal Scientific American last month of her relief when, having checked back through disposal records, none of the genome sequences matched their virus samples.

'That really took a load off my mind. I had not slept a wink for days,' she said.

Many international experts have also dismissed such theories.

Dr Keusch, Professor of Medicine and International Health at Boston University's Schools of Medicine and Public Health, stressed that no release of viruses from a high-level lab, such as the one in Wuhan, 'has ever happened'.

He defended his peers in the Chinese city as he said: 'The Wuhan lab is designed to the highest standards with redundant safety systems and the highest level of training.

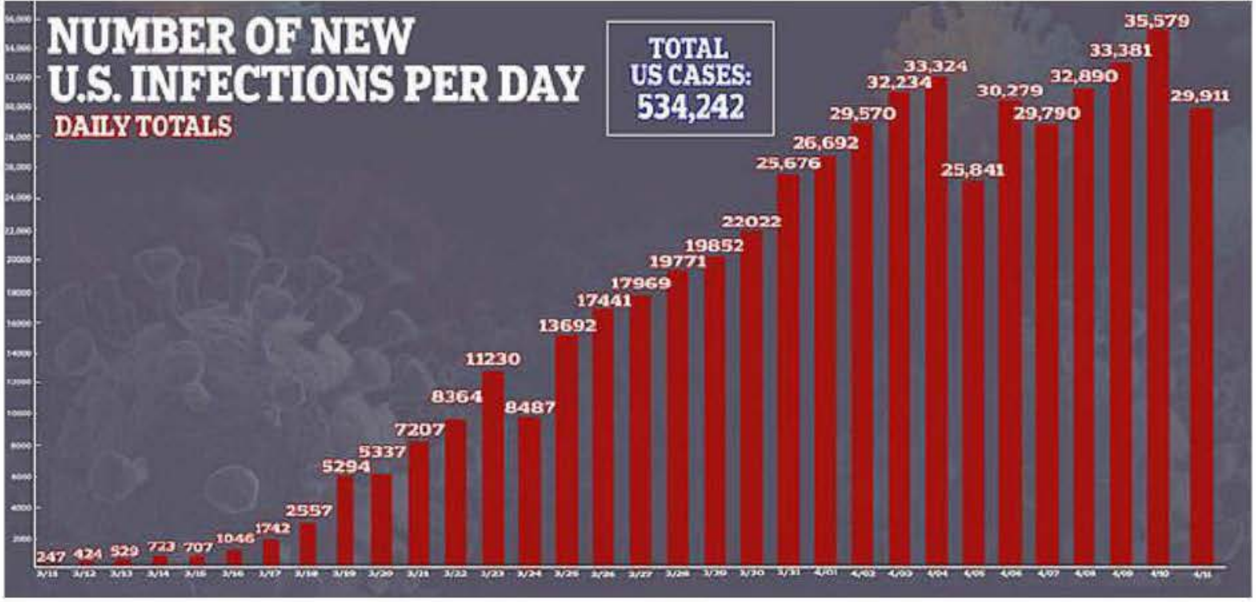
'Many of its research faculty trained at a similar laboratory in Galveston, Texas. So we know the Wuhan team is as qualified as the Texas group...

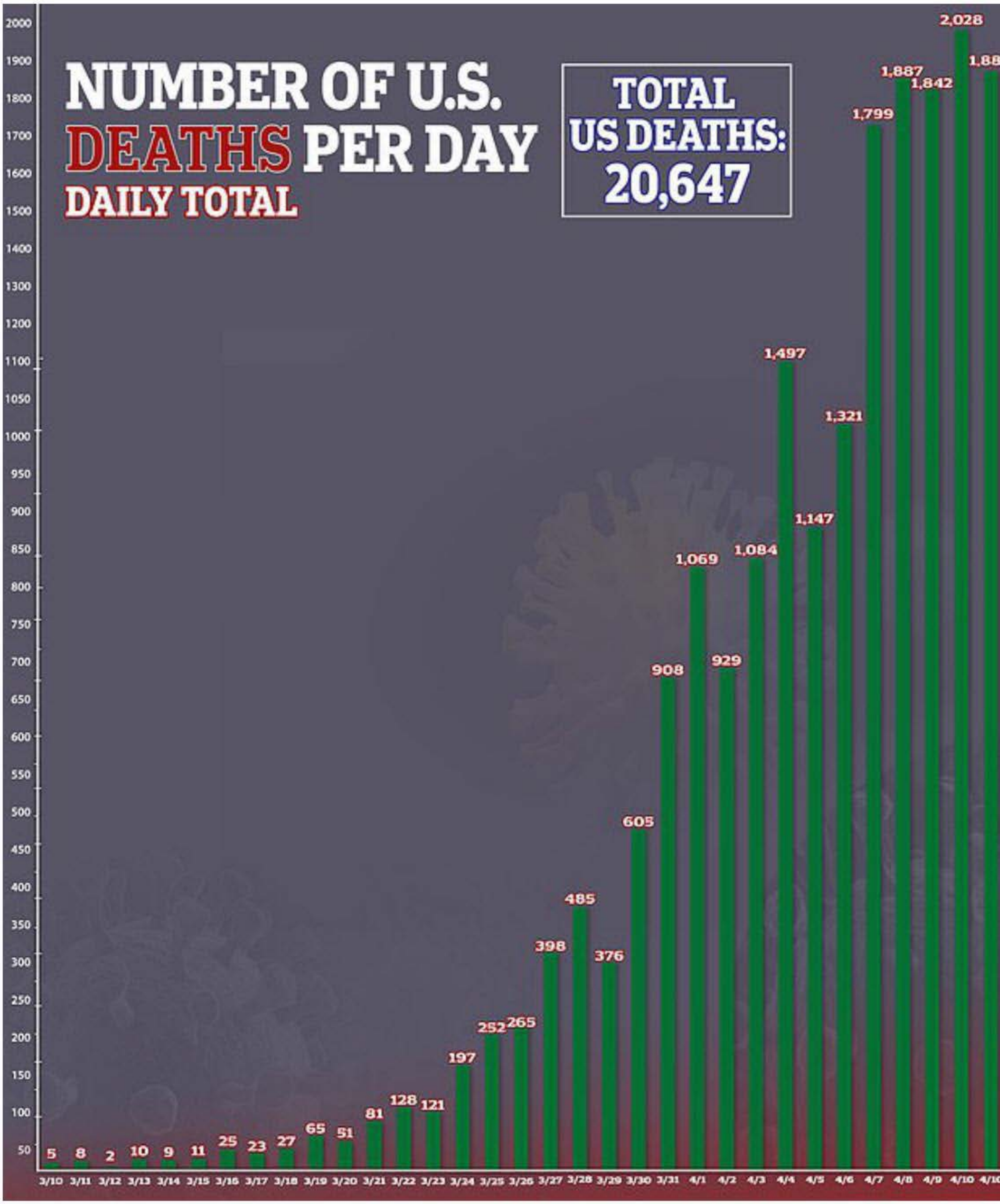
'This means the assertion of a leak, rather than being highly likely, instead is highly unlikely.'

Last week, further doubt was cast on the animal market theory, however, after Cao Bin, a doctor at the Wuhan Jinyintan Hospital, highlighted research showing that 13 of the first 41 patients diagnosed with the infection had not had any contact with the market.

Obtained via FOIA by Judicial Watch, Inc.

'It seems clear that the seafood market is not the only origin of the virus,' he said.




NUMBER OF U.S.
DEATHS PER DAY
DAILY TOTAL
TOTAL
US DEATHS:
20,647
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1200
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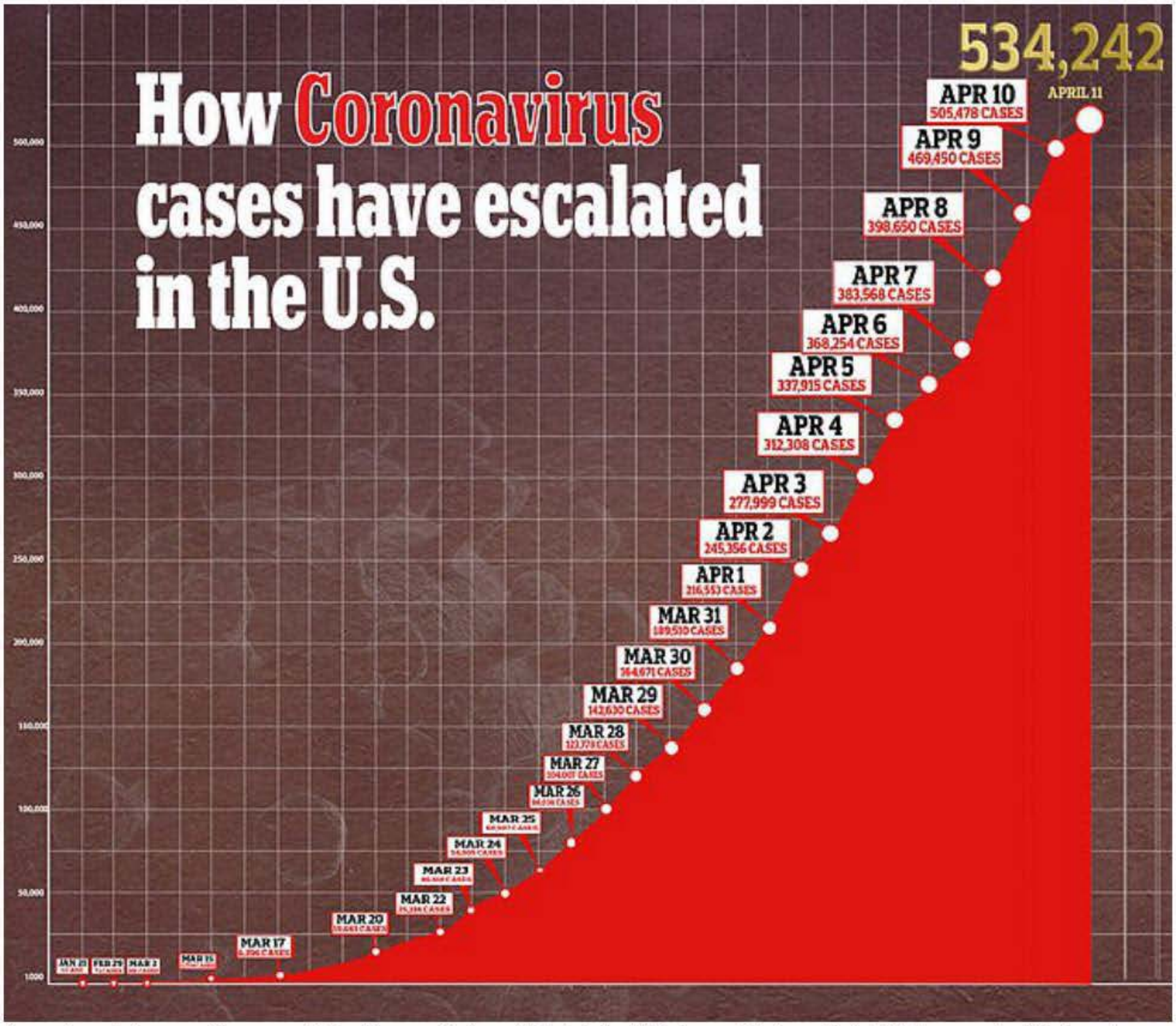
Obtained via FOIA by Judicial Watch, Inc.



American biosecurity expert Professor Richard Ebright, of Rutgers University's Waksman Institute of Microbiology, New Jersey, said that while the evidence suggests COVID-19 was not created in one of the Wuhan laboratories, it could easily have escaped from there while it was being analyzed.

Prof Ebright said he has seen evidence that scientists at the Centre for Disease Control and the Institute of Virology studied the viruses with only 'level 2' security – rather than the recommended level 4 – which 'provides only minimal protections against infection of lab workers'.

He added: 'Virus collection, culture, isolation, or animal infection would pose a substantial risk of infection of a lab worker, and from the lab worker then the public.'

He concluded that the evidence left 'a basis to rule out [that coronavirus is] a lab construct, but no basis to rule out a lab accident'.

Results of the U.S-funded research at the Wuhan Institute were published in November 2017 under the heading: 'Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus.'

The exercise was summarized as: 'Bats in a cave in Yunnan, China were captured and sampled for coronaviruses used for lab experiments.

'All sampling procedures were performed by veterinarians with approval from the Animal Ethics Committee of the Wuhan Institute of Virology.

Obtained via FOIA by Judicial Watch, Inc.

'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. Bats were trapped and faecal swab samples were collected.'

Another study, published in April 2018, was titled 'fatal swine acute diarrhoea syndrome caused by an HKU2-related coronavirus of bat origin' and described the research as such: 'Following a 2016 bat-related coronavirus outbreak on Chinese pig farms, bats were captured in a cave and samples were taken.

Experimenters grew the virus in a lab and injected it into three-day-old piglets.

Intestinal samples from sick piglets were ground up and fed to other piglets as well.

The coronavirus pandemic has killed more than 108,000 people and infected over 1.7 million worldwide.'

On Saturday, the American outbreak became the deadliest in the world over 2,000 deaths in a day.

The national deaths toll is 20,087 and there are 522,643 confirmed cases as of Saturday evening.

China muzzled its Bat Woman: Beijing authorities hushed up the findings of a scientist who unlocked the genetic make-up of the coronavirus within days of the outbreak – which is vital for tests and vaccines

A Chinese scientist who is the one of the world's leading experts on coronaviruses was 'muzzled' after unraveling the genetic composition of the new disease, which is crucial for developing diagnostic tests and vaccines.

The revelation will fuel fresh concerns over **China**'s cover-up of the pandemic after it erupted in the city of Wuhan. Critics argue that Communist Party chiefs frustrated efforts to contain the outbreak before it exploded around the world.

At the centre of the new claims is Shi Zhengli, known as China's 'Bat Woman' after years spent on difficult virus-hunting expeditions in dank caves that have led to a series of important scientific discoveries.

The virologist was called back to her highsecurity laboratory in Wuhan at the end of last year after a mysterious new respiratory condition in the city was identified as a novel **coronavirus** – and within three days she completed its gene sequencing.

Obtained via FOIA by Judicial Watch, Inc.

A virology lab like the one Shi Zhengli completed the gene sequencing of the coronavirus

Her team's work, and several other breakthroughs in subsequent days, indicated the virus was linked to horseshoe bats found more than 1,000 miles away in Yunnan, a region of southern China.

Their findings showed it was similar to SARS, a respiratory disease that sparked an epidemic in 33 countries after emerging from China in 2002.

Gao Yu, a Chinese journalist freed last week after 76 days of lockdown in Wuhan, said he spoke to Shi during his incarceration and revealed: 'We learned later her institute finished gene-sequencing and related tests as early as January 2 but was muzzled.'

The Mail on Sunday has learned that on that same day, Yanyi Wang, director of the Wuhan Institute of Virology, sent an email to staff and key officials ordering them not to disclose information on the disease.

She warned, according to a leak on social media confirmed by activists and Hong Kong media, that 'inappropriate and inaccurate information'was causing 'general panic' – thought to refer to eight whistle-blowing doctors whose warnings to local citizens had led to their arrest.

Wang said the National Health Commission 'unequivocally requires that any tests, clinical data, test results, conclusions related to the epidemic shall not be posted on social media platforms, nor shall [it] be disclosed to any media outlets including government official media, nor shall [it] be disclosed to partner institutions.'

Eight days later, a team led by a professor in Shanghai who received samples from an infected patient, published a genome sequence on an open access platform.

His laboratory was closed for 'rectification' two days later.

Obtained via FOIA by Judicial Watch, Inc.

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Shi Zhengli is known as China's 'Bat Woman' after years spent on difficult virus-hunting expeditions in dank caves that have led to a series of important scientific discoveries

At the time, the public was being told that no new cases had been reported in Wuhan for more than a week and there was no clear evidence of human transmission, although dozens of health workers were starting to fall ill with the disease.

In an online lecture last month, Shi Zhengli said her team found on January 14 that the new virus could infect people – six days before this fact was revealed by China.

On the same day, the World Health Organisation issued a tweet backing China's denials of human transmissions.

Shi's team released its data identifying the disease on January 23 on a scientific portal before publication the next month by the journal Nature.

It said the genomic sequence was 96 per cent identical to another virus they found in horseshoe bats in Yunnan.

Shi is a specialist in emerging diseases and has earned global acclaim for work investigating links between bats and coronaviruses, aided by expeditions to collect samples and swabs in the fetid cave networks of southern China.

She was a key part of the team that traced SARS to horseshoe bats through civets, a cat-like creature often eaten in China.

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Obtained via FOIA by Judicial Watch, Inc.

From: Mulach, Barbara (NIH/NIAID) [E]
Sent: Mon, 13 Apr 2020 13:39:11 +0000
To: Mulach, Barbara (NIH/NIAID) [E]
Subject: FW: Urgent for Dr. Fauci: China's lab for studying SARS and Ebola is in Wuhan, the outbreak's center
Attachments: R01AI110964 Renewal FACTS clearance.docx, Daszak Wuhan Exceprts.docx

---

From: Mulach, Barbara (NIH/NIAID) [E] (b) (6)
Sent: Thursday, January 23, 2020 9:27 PM
To: Haskins, Melinda (NIH/NIAID) [E] (b) (6)
Cc: NIAID OCGR Leg (b) (6); NIAID BUGS (b) (6); Handley, Gray (NIH/NIAID) [E] (b) (6); Erbelding, Emily (NIH/NIAID) [E] (b) (6); Cassetti, Cristina (NIH/NIAID) [E] (b) (6); Embry, Alan (NIH/NIAID) [E] (b) (6); Stemmy, Erik (NIH/NIAID) [E] (b) (6)
Subject: RE: Urgent for Dr. Fauci: China's lab for studying SARS and Ebola is in Wuhan, the outbreak's center

HI Melinda,

We've identified one grant with a sub-contract to Wuhan Institute of Virology (thanks for the lead) and one primary award to Wuhan University. We are trying to get clarification regarding whether or not the two organizations are related so we know if the second application is relevant to the request or not.

Grant: R01 AI119064-06
PI: Peter Daszak
Title: Understanding the Risk of Bat Coronavirus Emergence
Institution: ECOHEALTH ALLIANCE, INC.
Sub-award to Wuhan Institute of Virology
In the interest of time, I'm sending you two documents providing additional details regarding the role of Wuhan Institute of Virology. If you would like a shorter summary or a different format, just let us know.

Grant: R01 AI116442-05
PI: LAN, KE
Title: Versatile functions of LANA in KSHV pathogenesis
Institution: WUHAN UNIVERSITY
There is no reference in the application to BSL facilities or biocontainment, so this is probably not relevant for the current exercise. Let us know if you would like additional information on this.

I hope this is helpful. Let us know what else we can do to help.

Barbara

Obtained via FOIA by Judicial Watch, Inc.

-----Original Message-----
From: Haskins, Melinda (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Thursday, January 23, 2020 8:18 PM
To: NIAID BUGS [redacted] (b) (6); Handley, Gray (NIH/NIAID) [E] [redacted] (b) (6);
Erbelding, Emily (NIH/NIAID) [E] [redacted] (b) (6)
Cc: NIAID OCGR Leg [redacted] (b) (6)
Subject: Urgent for Dr. Fauci: China's lab for studying SARS and Ebola is in Wuhan, the outbreak's center

https://www.dailymail.co.uk/health/article-7922379/Chinas-lab-studying-SARS-Ebola-Wuhan-outbreaks-center.html

Colleagues,

Dr. Fauci will be brief multiple Senators tomorrow morning on our novel coronavirus response at the request of Senator Lamar Alexander, who has an interest in public health matters and China. Would you please confirm the exact nature or our support to the Wuhan Institute of Virology/Biosafety Lab. You'll want to read the Daily Mail article above.

Thanks for the quick response!

Melinda

Sent from my iPhone

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Obtained via FOIA by Judicial Watch, Inc.

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Obtained via FOIA by Judicial Watch, Inc.

Obtained via FOIA by Judicial Watch, Inc.

(b) (4), (b) (5)

[redacted]

Obtained via FOIA by Judicial Watch, Inc.

(b) (4), (b) (5), (b) (6)

[redacted]

Obtained via FOIA by Judicial Watch, Inc.

(b) (5)

[redacted]

Obtained via FOIA by Judicial Watch, Inc.

(b) (4), (b) (5)

[redacted]

Obtained via FOIA by Judicial Watch, Inc.

(b) (4), (b) (5)

[redacted]

Obtained via FOIA by Judicial Watch, Inc.

(b) (4), (b) (5)

[redacted]

Obtained via FOIA by Judicial Watch, Inc.

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Tue, 14 Apr 2020 12:52:48 +0000
To: Auchincloss, Hugh (NIH/NIAID) [E]
Subject: RE: Daszak and Wuhan lab

Thanks.

From: Auchincloss, Hugh (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Monday, April 13, 2020 5:45 PM
To: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6); Conrad, Patricia (NIH/NIAID) [E] [redacted] (b) (6)
Subject: Fwd: Daszak and Wuhan lab

This is higher but not extraordinarily higher than I originally indicated which was for some earlier work.

Sent from my iPad

Begin forwarded message:

From: "Erbelding, Emily (NIH/NIAID) [E]" [redacted] (b) (6)
Date: April 13, 2020 at 4:30:21 PM EDT
To: "Auchincloss, Hugh (NIH/NIAID) [E]" [redacted] (b) (6)
Cc: "Cassetti, Cristina (NIH/NIAID) [E]" [redacted] (b) (6)
Subject: Daszak and Wuhan lab

The entire amount of the new Daszak grant (year 6 funded in FY19) is about 3,64 M. The total amount that will go to Wuhan Institute of Virology under this grant will be about $750K ($76,301 have already been sent to Wuhan in year 1 according to the NOA).

The bat sampling work mentioned in the article (during years 2011-2015) was probably supported by years 1-5 of the Daszak grant but could also have been supported by USAID Predict program (which was also funding the Wuhan lab)

Emily Erbelding, M.D., M.P.H.
Director, Division of Microbiology and Infectious Diseases
NIAID/NIH
5601 Fishers Lane
Rockville, MD 20852
Tel: [redacted] (b) (6)

Obtained via FOIA by Judicial Watch, Inc.

From: Harper, Jill (NIH/NIAID) [E]
Sent: Tue, 14 Apr 2020 13:29:33 +0000
To: Crawford, Chase (NIH/NIAID) [E];Auchincloss, Hugh (NIH/NIAID) [E]
Cc: Robinson, Whitney (NIH/NIAID) [C];Sullivan, Fantasia (NIH/NIAID) [C];NIAID OCGR Leg;Harper, Jill (NIH/NIAID) [E]
Subject: RE: Request for availability -- 11:30a.m. call with DMID Re: Wuhan Institute of Virology

I can make that work.

From: Crawford, Chase (NIH/NIAID) [E] (b) (6)
Sent: Tuesday, April 14, 2020 9:29 AM
To: Auchincloss, Hugh (NIH/NIAID) [E] (b) (6); Harper, Jill (NIH/NIAID) [E] (b) (6)
Cc: Robinson, Whitney (NIH/NIAID) [C] (b) (6); Sullivan, Fantasia (NIH/NIAID) [C] (b) (6); NIAID OCGR Leg (b) (6)
Subject: RE: Request for availability -- 11:30a.m. call with DMID Re: Wuhan Institute of Virology

Does 10a.m. work for you, Jill?

From: Auchincloss, Hugh (NIH/NIAID) [E] (b) (6)
Sent: Tuesday, April 14, 2020 9:27 AM
To: Crawford, Chase (NIH/NIAID) [E] (b) (6); Harper, Jill (NIH/NIAID) [E] (b) (6)
Cc: Robinson, Whitney (NIH/NIAID) [C] (b) (6); Sullivan, Fantasia (NIH/NIAID) [C] (b) (6); NIAID OCGR Leg (b) (6)
Subject: RE: Request for availability -- 11:30a.m. call with DMID Re: Wuhan Institute of Virology

12:30-1 is only time I absolutely can't

From: Crawford, Chase (NIH/NIAID) [E] (b) (6)
Sent: Tuesday, April 14, 2020 9:24 AM
To: Harper, Jill (NIH/NIAID) [E] (b) (6); Auchincloss, Hugh (NIH/NIAID) [E] (b) (6)
Cc: Robinson, Whitney (NIH/NIAID) [C] (b) (6); Sullivan, Fantasia (NIH/NIAID) [C] (b) (6); NIAID OCGR Leg (b) (6)
Subject: RE: Request for availability -- 11:30a.m. call with DMID Re: Wuhan Institute of Virology

DMID has now offered the additional time slots of 10-11 or 12-1 and suggested that Cristina Cassetti join.

From: Harper, Jill (NIH/NIAID) [E] (b) (6)
Sent: Tuesday, April 14, 2020 9:23 AM
To: Crawford, Chase (NIH/NIAID) [E] (b) (6); Auchincloss, Hugh (NIH/NIAID) [E] (b) (6)

Obtained via FOIA by Judicial Watch, Inc.

Cc: Robinson, Whitney (NIH/NIAID) [C] [redacted] (b) (6); Sullivan, Fantasia (NIH/NIAID) [C] [redacted] (b) (6); NIAID OCGR Leg [redacted] (b) (6); Harper, Jill (NIH/NIAID) [E] [redacted] (b) (6)
Subject: RE: Request for availability -- 11:30a.m. call with DMID Re: Wuhan Institute of Virology

I have another call from 11:00-12:00.

From: Crawford, Chase (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Tuesday, April 14, 2020 9:18 AM
To: Auchincloss, Hugh (NIH/NIAID) [E] [redacted] (b) (6); Harper, Jill (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Robinson, Whitney (NIH/NIAID) [C] [redacted] (b) (6); Sullivan, Fantasia (NIH/NIAID) [C] [redacted] (b) (6); NIAID OCGR Leg [redacted] (b) (6)
Subject: Request for availability -- 11:30a.m. call with DMID Re: Wuhan Institute of Virology

Hi Hugh and Jill,

Are the two of you available at **11:30a.m. today** to join a call with DMID and OCGR-Leg to discuss recent congressional inquiries on NIH support for studies involving the Wuhan Institute of Virology (additional information below)?

Thanks,
Chase

From: Abbey, Lillian (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Monday, April 13, 2020 7:41 PM
To: Crawford, Chase (NIH/NIAID) [E] [redacted] (b) (6)
Cc: NIAID BUGS [redacted] (b) (6); NIAID OCGR Leg [redacted] (b) (6)
Subject: RE: Request for information: Senate Qs - Wuhan Institute of Virology

Hi Chase,
Would it be possible to find a time for one of us to talk with you tomorrow to find out what you need? Andrew has responded to previous requests about this grant. PI is Peter Daszak, and we have information on hand from previous requests.
Thanks,
Lillian

From: Crawford, Chase (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Monday, April 13, 2020 5:41 PM
To: NIAID BUGS [redacted] (b) (6)
Cc: Auchincloss, Hugh (NIH/NIAID) [E] [redacted] (b) (6); Harper, Jill (NIH/NIAID) [E] [redacted] (b) (6); NIAID OCGR Leg [redacted] (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
[redacted] (b) (6)

From: LaMontagne, Karen (NIH/OD) [E] [redacted] (b) (6)
Sent: Monday, April 13, 2020 4:23 PM
To: NIAID OCGR Leg [redacted] (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 [redacted] (b) (6)
Date: Monday, April 13, 2020 at 3:42 PM
To: Karen LaMontagne [redacted] (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

Obtained via FOIA by Judicial Watch, Inc.

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.*

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Washington, DC 20001
Phone: 860.882.2492
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Obtained via FOIA by Judicial Watch, Inc.

From: Harper, Jill (NIH/NIAID) [E]
Sent: Wed, 15 Apr 2020 14:51:17 +0000
To: Auchincloss, Hugh (NIH/NIAID) [E]
Cc: Harper, Jill (NIH/NIAID) [E]
Subject: FW: For awareness

For your awareness –

[redacted] (b) (5)

From: Haskins, Melinda (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Wednesday, April 15, 2020 8:09 AM
To: Billet, Courtney (NIH/NIAID) [E] [redacted] (b) (6); Harper, Jill (NIH/NIAID) [E] [redacted] (b) (6)
Subject: For awareness

FYI

From: Abbey, Lillian (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Wednesday, April 15, 2020 8:08 AM
To: Haskins, Melinda (NIH/NIAID) [E] [redacted] (b) (6)
Subject: Fwd: Draft response for review -- FW: Request for information: Senate Qs - Wuhan Institute of Virology

Begin forwarded message:

From: "Erbelding, Emily (NIH/NIAID) [E]" [redacted] (b) (6)
Date: April 15, 2020 at 7:45:02 AM EDT
To: "Stemmy, Erik (NIH/NIAID) [E]" [redacted] (b) (6)
Cc: "Cassetti, Cristina (NIH/NIAID) [E]" [redacted] (b) (6), "Abbey, Lillian (NIH/NIAID) [E]" [redacted] (b) (6)
Subject: FW: Draft response for review -- FW: Request for information: Senate Qs - Wuhan Institute of Virology

[redacted] (b) (5)

Erik, do you know if Peter Dazsak has a publication coming on the current outbreak?

From: Erbelding, Emily (NIH/NIAID) [E]
Sent: Wednesday, April 15, 2020 7:43 AM
To: Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6); Tabak, Lawrence (NIH/OD) [E] [redacted] (b) (6)
Subject: RE: Draft response for review -- FW: Request for information: Senate Qs - Wuhan Institute of Virology

Peter's only publication on SARS CoV2 since epidemic began is thought piece in NEJM:

https://www.nejm.org/doi/full/10.1056/NEJMp2002106?url_ver=Z39.88-2003&rfr_id=ori:rid:crossref.org&rfr_dat=cr_pub%3dpubmed

Note that all of the prior work on zoonotic reservoirs of CoV's was also supported by USAID funding through a program called PREDICT, which has since ended.

I will ask his PO if he knows of anything on the verge of submission now.
Emily

From: Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Wednesday, April 15, 2020 12:02 AM
To: Tabak, Lawrence (NIH/OD) [E] [redacted] (b) (6)
Cc: Erbelding, Emily (NIH/NIAID) [E] [redacted] (b) (6)
Subject: Re: Draft response for review -- FW: Request for information: Senate Qs - Wuhan Institute of Virology

There was this paper based on work before the outbreak but often cited with regard to animal origin: https://www.ncbi.nlm.nih.gov/pubmed/32040190

[redacted] (b) (5)

Emily might have more.

On Apr 14, 2020, at 10:27 PM, Tabak, Lawrence (NIH/OD) [E] [redacted] (b) (6) wrote:

Have they published anything seminal related to the current pandemic?

From: "Erbelding, Emily (NIH/NIAID) [E]" [redacted] (b) (6)
Date: Tuesday, April 14, 2020 at 10:11 PM
To: "Tabak, Lawrence (NIH/OD) [E]" [redacted] (b) (6)
Cc: "Marston, Hilary (NIH/NIAID) [E]" [redacted] (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]" [redacted] (b) (6)
Date: April 14, 2020 at 4:24:34 PM EDT
To: "Cassetti, Cristina (NIH/NIAID) [E]" [redacted] (b) (6), "Erbelding, Emily (NIH/NIAID) [E]" [redacted] (b) (6)
Cc: "Ford, Andrew (NIH/NIAID) [E]" [redacted] (b) (6), "Bateman, Karen (NIH/NIAID) [E]" [redacted] (b) (6), "Werner, Alyssa (NIH/NIAID) [E]" [redacted] (b) (6), "Mulach, Barbara (NIH/NIAID) [E]" [redacted] (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. [redacted] (b) (5)

[redacted] (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:

[redacted] (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.

[redacted] (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] [redacted] (b) (6)
Sent: Monday, April 13, 2020 5:41 PM
To: NIAID BUGS [redacted] (b) (6)
Cc: Auchincloss, Hugh (NIH/NIAID) [E] [redacted] (b) (6); Harper, Jill (NIH/NIAID) [E] [redacted] (b) (6); NIAID OCGR Leg [redacted] (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
[redacted] (b) (6)

From: LaMontagne, Karen (NIH/OD) [E] [redacted] (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 [redacted] (b) (6)
Date: Monday, April 13, 2020 at 3:42 PM
To: Karen LaMontagne [redacted] (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.
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White Coat Waste Project

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

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Washington, DC 20001
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From: Harper, Jill (NIH/NIAID) [E]
Sent: Thu, 16 Apr 2020 19:55:18 +0000
To: Crawford, Chase (NIH/NIAID) [E];Auchincloss, Hugh (NIH/NIAID) [E];Gilles, Sharon (NIH/NIAID) [E];Marston, Hilary (NIH/NIAID) [E];Johnson, Martin S. (NIH/NIAID) [E];Billet, Courtney (NIH/NIAID) [E]
Cc: Sullivan, Fantasia (NIH/NIAID) [C];NIAID OCGR Leg;Harper, Jill (NIH/NIAID) [E]
Subject: RE: ACTION Requested ASAP (4/16): Review draft NIAID response to Senate Qs - Wuhan Institute of Virology

Ok with me. Thanks.

From: Crawford, Chase (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Thursday, April 16, 2020 3:52 PM
To: Auchincloss, Hugh (NIH/NIAID) [E] [redacted] (b) (6); Harper, Jill (NIH/NIAID) [E] [redacted] (b) (6); Gilles, Sharon (NIH/NIAID) [E] [redacted] (b) (6); Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6); Johnson, Martin S. (NIH/NIAID) [E] [redacted] (b) (6); Billet, Courtney (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Sullivan, Fantasia (NIH/NIAID) [C] [redacted] (b) (6); NIAID OCGR Leg [redacted] (b) (6)>
Subject: ACTION Requested ASAP (4/16): Review draft NIAID response to Senate Qs - Wuhan Institute of Virology
Importance: High

Good Afternoon,

OCGR-Leg has drafted the **attached proposed response** to recent Congressional requests for information on NIAID support for research activities at the **Wuhan Institute of Virology** (additional background on Congressional interest can be found in the email chain below the signature line). As you may recall the Wuhan Institute of Virology has been supported through subawards from an NIAID-supported EcoHealth Alliance project (R01AI110964).

NIAID also has been asked [redacted] (b) (5) (b) (5)

ACTION
As soon as possible, please review the attached draft NIAID response and provide any edits in track changes.

Please let us know if you have any questions.

Thanks,
Chase

Chase Crawford, D.V.M., M.S.
Public Health Analyst

Legislative Affairs and Correspondence Management Branch
Office of Communications and Government Relations
NIAID/NIH/DHHS

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

Hi BUGS,

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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
[redacted] (b) (6)

From: LaMontagne, Karen (NIH/OD) [E] [redacted] (b) (6)
Sent: Monday, April 13, 2020 4:23 PM
To: NIAID OCGR Leg [redacted] (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

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Karen

From: Michelle Mitchell [redacted] (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

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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.*

Obtained via FOIA by Judicial Watch, Inc.

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Phone: 860.882.2492
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Obtained via FOIA by Judicial Watch, Inc.

From: Cassetti, Cristina (NIH/NIAID) [E]
Sent: Sat, 18 Apr 2020 22:22:50 +0000
To: Erbelding, Emily (NIH/NIAID) [E];Auchincloss, Hugh (NIH/NIAID) [E]
Subject: FW: Statement from Prof Edward Holmes on the SARS-CoV-2 virus
https://bit.ly/2ym1UGe

(b) (5)

From: Folkers, Greg (NIH/NIAID) [E] (b) (6)
Sent: Saturday, April 18, 2020 2:04 PM
Subject: Statement from Prof Edward Holmes on the SARS-CoV-2 virus https://bit.ly/2ym1UGe

Statement from Prof Edward Holmes on the SARS-CoV-2 virus

16 April 2020

On the origins of the virus that causes COVID-19

Share

Unfounded speculation on the origins of the SARS-CoV-2 virus that causes COVID-19 has prompted the following statement from Professor Holmes, who was involved in mapping the genome of the virus.

Professor Edward Holmes.

"There is no evidence that SARS-CoV-2, the virus that causes COVID-19 in humans, originated in a laboratory in Wuhan, China.

"Coronaviruses like SARS-CoV-2 are commonly found in wildlife species and frequently jump to new hosts. This is also the most likely explanation for the origin of SARS-CoV-2.

"The closest known relative of SARS-CoV-2 is a bat virus named RaTG13, which was kept at the Wuhan Institute of Virology. There is some unfounded speculation that this virus was the origin of SARS-CoV-2. However:

(i) RaTG13 was sampled from a different province of China (Yunnan) to where COVID-19 first appeared; and

(ii) the level of genome sequence divergence between SARS-CoV-2 and RaTG13 is equivalent to an average of 50 years (and at least 20 years) of evolutionary change.

"Hence, SARS-CoV-2 was not derived from RaTG13.

"In addition, we know that viruses related to SARS-CoV-2 are also found in pangolins. This suggests that other wildlife species are likely to carry relatives of SARS-CoV-2.

"In summary, the abundance, diversity and evolution of coronaviruses in wildlife strongly suggests that this virus is of natural origin. However, a greater sampling of animal species in nature, including bats from Hubei province, is needed to resolve the exact origins of SARS-CoV-2."

Professor Edward Holmes is an Australian Research Council Laureate Fellow, a Fellow of the Australian Academy of Science and a Fellow of the Royal Society in London.

He has published six academic papers this year on the genome and origin of SARS-CoV-2, the virus that causes COVID-19 in humans.

At the University of Sydney he is a member of the Charles Perkins Centre and the Marie Bashir Institute for Infectious Diseases and Biosecurity. He holds a joint position with the School of Life and Environmental Sciences and the Sydney Medical School.

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From: Harper, Jill (NIH/NIAID) [E]
Sent: Tue, 21 Apr 2020 19:40:39 +0000
To: Crawford, Chase (NIH/NIAID) [E];Auchincloss, Hugh (NIH/NIAID) [E];Marston, Hilary (NIH/NIAID) [E];Johnson, Martin S. (NIH/NIAID) [E];Billet, Courtney (NIH/NIAID) [E]
Cc: NIAID OCGR Leg;Harper, Jill (NIH/NIAID) [E]
Subject: RE: ACTION by COB today (4/21): Review draft NIAID response to Wuhan Institute of Virology funding question

[redacted] (b) (5)

From: Crawford, Chase (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Tuesday, April 21, 2020 3:29 PM
To: Auchincloss, Hugh (NIH/NIAID) [E] [redacted] (b) (6); Harper, Jill (NIH/NIAID) [E] [redacted] (b) (6); Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6); Johnson, Martin S. (NIH/NIAID) [E] [redacted] (b) (6); Billet, Courtney (NIH/NIAID) [E] [redacted] (b) (6)
Cc: NIAID OCGR Leg [redacted] (b) (6)
Subject: ACTION by COB today (4/21): Review draft NIAID response to Wuhan Institute of Virology funding question

Good Afternoon,

NIAID received the below follow-up question from minority staff to the House Labor-HHS Appropriations Subcommittee regarding the funding level for the EcoHealth Alliance project subaward to Wuhan Institute of Virology in FY 2019 (complete funding history in table below signature line):

> "Do we know why the subaward amount for Wuhan Institute of Virology went down in 2019? Just random fluctuation?"

OCGR-Leg has worked with the DMID to develop the following proposed NIAID response:

[redacted] (b) (5)

ACTION
By COB today (4/21), please provide any must-change edits to the proposed NIAID response.

Please let us know if you have any questions.

Thanks,
Chase

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NIAID Subawards to Wuhan Institute of Virology

Fiscal Year	Project Number/ Title	Organization	Subaward Recipient	Subaward Amount
2019	R01AI110964: Understanding the Risk of Bat Coronavirus Emergence	EcoHealth Alliance	Wuhan Institute of Virology	$76,301
2018	R01AI110964: Understanding the Risk of Bat Coronavirus Emergence	EcoHealth Alliance	Wuhan Institute of Virology	$159,122
2017	R01AI110964: Understanding the Risk of Bat Coronavirus Emergence	EcoHealth Alliance	Wuhan Institute of Virology	$159,122
2016	R01AI110964: Understanding the Risk of Bat Coronavirus Emergence	EcoHealth Alliance	Wuhan Institute of Virology	$159,122
2015	R01AI110964: Understanding the Risk of Bat Coronavirus Emergence	EcoHealth Alliance	Wuhan Institute of Virology	$139,015
2014	R01AI110964: Understanding the Risk of Bat Coronavirus Emergence	EcoHealth Alliance	Wuhan Institute of Virology	$133,595
			Total FY 14-19	**$826,277**

Obtained via FOIA by Judicial Watch, Inc.

From: Pekoc, Ken (NIH/NIAID) [E]
Sent: Mon, 26 Mar 2018 16:08:49 +0000
To: Auchincloss, Hugh (NIH/NIAID) [E];Doepel, Laurie (NIH/NIAID) [E];Folkers, Greg (NIH/NIAID) [E];Hudgings, Carole (NIH/NIAID) [E];Marston, Hilary (NIH/NIAID) [E]
Cc: Billet, Courtney (NIH/NIAID) [E];Stover, Kathy (NIH/NIAID) [E]
Subject: FOR FOG REVIEW / CoV bat study / China
Attachments: 2018 Nature Daszak new CoV MA3.docx, 2018 Nature Daszak new CoV clearance.doc, 2018 Nature Daszak new CoV revised ms.docx

I've attached a draft media availability for review regarding a newly identified coronavirus in swine from China, found in the same region where SARS originated and involving the same bat species.

Nature will publish the study; a date is not firm but the authors believe it will be soon.

Some background correspondence that BUGS shared last fall is below.

Thanks

From: Peter Daszak <daszak@ecohealthalliance.org>
Date: October 1, 2017 at 1:21:51 PM EDT
To: (b) (6)
Cc: "David Morens (b) (6), "David Morens (b) (6), (b) (6) (b) (6), (b) (6), "Stemmy, Erik (NIH/NIAID) [E]" (b) (6), Alison Andre <andre@ecohealthalliance.org>, Aleksei Chmura <chmura@ecohealthalliance.org>
Subject: Confidential - A new bat-origin coronavirus emerging in pigs in China discovered under our NIAID R01

Dear Dr Fauci and NIAID colleagues,

It was a pleasure to meet you again today. I've attached an unpublished paper, currently in the second round of review with *Nature* that describes a novel bat-origin Coronavirus (SADS-CoV: Swine Acute Diarrheal Syndrome coronavirus) that recently spilled over into pig farms in Southern China, leading to the death of over 25,000 piglets in 5+ farms in Guandong Province.

The virus originates in the same group of bats as SARS-CoV, and emerged in the same place. It's not known to be zoonotic (we've tested 35+ pig farm workers with an antibody assay and none are positive. The pig farm owners tell us the virus is now under control, thanks to culling and separation of infected herds. It's not yet known if this virus has appeared elsewhere, but we are looking. We're also doing assays to find out if it can infect human cells in the lab – so far no evidence of this.

I hope this paper is of interest. You should know that this work was supported by a NIAID R01 that Erik Stemmy is the Program Officer for, and that I'm PI on, with Zhengli Shi as co-PI.

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If you want any other information at all, please don't hesitate to email or call and I'd be happy to come over to NIAID to brief you further. I'll also let you know if/when it will be published so that we can try to foster some publicity as appropriate.

Cheers,

Peter

Peter Daszak
President

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

Tel. +1 212-380-4473
www.ecohealthalliance.org

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

Ken Pekoc
Public Affairs Officer
Rocky Mountain Laboratories
NIAID Office of Communications and Government Relations
(b) (6)

Please note that I am not a spokesperson for NIAID.

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DRAFT
FOR IMMEDIATE RELEASE
Day, XXXXXX, 2018
XXXX Eastern Time

New Coronavirus Emerges from Bats in China, Devastates Young Swine

SADS Identified in Same Region, from Same Bats, as SARS

(b) (5)

[redacted]

WHO:

NIAID's Erik Stemmy, Ph.D., Human Coronavirus Research Program Officer, is available for comment.

CONTACT:
To schedule interviews, please contact Ken Pekoc, (301) 402-1663, kpekoc@niaid.nih.gov.

This research was supported by NIAID award R01AI110964.

NIAID conducts and supports research—at NIH, throughout the United States, and worldwide—to study the causes of infectious and immune-mediated diseases, and to develop better means of preventing, diagnosing and treating these illnesses. News releases, fact sheets and other NIAID-related materials are available on the NIAID website.

About the National Institutes of Health (NIH): NIH, the nation's medical research agency, includes 27 Institutes and Centers and is a component of the U.S. Department of Health and Human Services. NIH is the primary federal agency conducting and supporting basic, clinical, and translational medical research, and is investigating the causes, treatments, and cures for both common and rare diseases. For more information about NIH and its programs, visit http://www.nih.gov/.

###

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Horseshoe bat (EcoHealth Alliance)

Obtained via FOIA by Judicial Watch, Inc.

Researchers preparing to locate bats in a Chinese cave. (EcoHealth Alliance)

Obtained via FOIA by Judicial Watch, Inc.

NIAID News and Science Writing Branch (NSWB)
Clearance Form

Media Availability

Title: New Coronavirus Emerges in China from Bats, Devastates Young Swine
SADS Identified in Same Region, from Same Bats, as SARS

Audience: general public / science writers
Distribution Date/ Embargo Date:
NSWB Contact/Writer: Ken Pekoc
Comments:

DATE	NAME
2-28-18	Scientific Reviewers: Peter Daszak and Eric Stemmy
na	Branch/Program/Lab Chief:
BUGS	Division Director:
na	Budget Officer (as needed)
3-12-18	Beat Supervisor: Kathy Stover
3-23-18	Kathy Stover, NSWB Branch Chief
3-23-18	Courtney Billet, OCGR Director
_______	Laurie Doepel, Special Assistant to the Director
_______	Carole Hudgings, Sr. Advisor to the Deputy Director
_______	Greg Folkers, NIAID Chief of Staff
_______	Hugh Auchincloss, NIAID Deputy Director
_______	Anthony S. Fauci, NIAID Director
	Other Reviewers:
11-9-17 & 2-28-18	Erik Stemmy, DMID
	Peter Daszak + EcoHealth Alliance staff

Obtained via FOIA by Judicial Watch, Inc.

Title: **Fatal Swine Acute Diarrhea Syndrome caused by an HKU2-related Coronavirus of Bat Origin**

Authors: Peng Zhou[1]*, Hang Fan[2]*, Tian Lan[3]*, Xing-Lou Yang[1], Wei-Feng Shi[4], Wei Zhang[1], Yan Zhu[1], Ya-Wei Zhang[2], Qing-Mei Xie[3], Shailendra Mani[5], Xiao-Shuang Zheng[1], Bei Li[1], Jin-Man Li[2], Hua Guo[1], Guang-Qian Pei[2], Xiao-Ping An[2], Jun-Wei Chen[3], Ling Zhou[3], Kai-Jie Mai[3], Zi-Xian Wu[3], Di Li[3], Danielle E. Anderson[5], Li-Biao Zhang[6], Shi-Yue Li[7], Zhi-Qiang Mi[2], Tong-Tong He[2], Feng Cong[8], Peng-Ju Guo[8], Ren Huang[8], Yun Luo[1], Xiang-Ling Liu[1], Jing Chen[1], Yong Huang[2], Qiang Sun[2], Xiang-Li-Lan Zhang[2], Yuan-Yuan Wang[2], Shao-Zhen Xing[2], Yan-Shan Chen[3], Yuan Sun[3], Juan Li[4], Peter Daszak[9]†, Lin-Fa Wang[5]†, Zheng-Li Shi[1]†, Yi-Gang Tong[2,10]†, Jing-Yun Ma[3]†

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Obtained via FOIA by Judicial Watch, Inc.

Cross-species transmission of viruses from wildlife animal reservoirs poses a significant threat to human and animal health. Bats have been recognized as one of the most important reservoirs for emerging viruses and the jump of a bat-origin coronavirus into humans via intermediate hosts was responsible for the high-impact emerging zoonosis, severe acute respiratory syndrome (SARS). Here, we report virological, epidemiological, evolutionary and experimental infection evidence that a novel HKU2-related bat coronavirus, Swine Acute Diarrhea Syndrome coronavirus (SADS-CoV), is the etiological agent responsible for a large scale outbreak of fatal disease in pigs in China that caused the death of 24,693 piglets across four farms. Significantly, the outbreak began in Guangdong Province in the vicinity of the origin of the SARS pandemic. Furthermore, we identified SADS-related CoVs with 96-98% sequence identity in 11.9% (71/596) of anal swabs collected from bats in Guangdong Province during 2013-16, predominantly in *Rhinolophus* spp. horseshoe bats that are known reservoirs of SARS-related CoVs. Our results demonstrated striking similarities between the SADS and SARS outbreaks in geographic, temporal, ecological and etiological settings. This study highlights the importance in identifying coronavirus diversity and distribution in bats to mitigate future outbreaks that threaten livestock, public health and economic growth.

The emergence of severe acute respiratory syndrome (SARS) in southern China in 2002, which was caused by a previously unknown coronavirus (SARS-CoV)[1-5] and led to more than 8,000 human infections and 774 deaths

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[http://www.who.int/csr/sars/en/], heralded two new frontiers in emerging infectious diseases. Firstly, it demonstrated that coronaviruses are capable of causing fatal diseases in humans. Secondly, the identification of bats as the reservoir for SARS-related coronaviruses, and likely origin of SARS-CoV[6-8] firmly established bats as an important source of highly lethal zoonotic viruses that include Hendra, Nipah, Ebola and Marburg viruses[9].

Here we report a series of fatal swine disease outbreaks in Guangdong Province, China, approximately 100 km from the location of the purported index case of SARS. Most strikingly, we found that the causative agent of this swine acute diarrhea syndrome (SADS) is a novel HKU2-related coronavirus 98.48% identical in genome sequence to a bat coronavirus we detected in 2016 from a bat cave in the vicinity of the index pig farm. This new virus (SADS-CoV) originated from the same genus of horseshoe bats (*Rhinolophus*) as SARS-CoV.

From 28 October 2016, fatal swine disease outbreaks were observed in a pig farm in Qingyuan, Guangdong Province, China, very close to the location of the first known index case of SARS which occurred in 2002 in Foshan (Extended Data Fig. 1a). Porcine epidemic diarrhea virus (PEDV, a coronavirus) had caused prior outbreaks at this farm, and was detected in the intestine of deceased piglets at the start of the outbreak. However, PEDV could no longer be detected in deceased piglets after 12th January 2017, despite accelerating mortality (Fig. 1a) and extensive testing for other common swine viruses yielded negative results (Extended Data Table 1). These findings suggested an outbreak of a novel disease. Clinical signs are similar to those

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caused by other known swine enteric coronaviruses[10,11] and include severe and acute diarrhea, and acute vomiting, leading to death due to rapid weight loss in newborn piglets less than five days of age. Infected piglets died 2-6 days following disease onset, while infected sows suffered only mild diarrhea and most recovered in two days. The disease caused no signs of febrile illness in piglets or sows. The mortality rate reached as high as 90% for piglets five days or younger, while for piglets older than eight days the mortality dropped to 5%. Subsequently, SADS-related outbreaks were found in three additional pig farms within 20-150 km of the index farm (Extended Data Fig. 1a) and, by 2nd May 2017, had resulted in the death of 24,693 piglets from four farms (Fig. 1a). In Farm A alone, 64% (4,659/7,268) of all piglets born in February died. The outbreak has abated, and measures taken to control SADS have included separation of sick sows and piglets from the rest of the herd. A qPCR test described below was used as the main diagnostic tool to confirm SADS-CoV infection.

A sample collected from the small intestine of a diseased piglet was subjected to metagenomics analysis by next generation sequencing (NGS) to identify potential etiologic agents. Of the 15,256,565 total reads obtained, 4,225 matched sequences of the bat CoV HKU2, which was first detected in Chinese horseshoe bats in Hong Kong and Guangdong Province, China[12]. By *de novo* assembly and targeted PCR we obtained a 27,173-bp CoV genome that shared 95% sequence identity to HKU2-CoV (Genbank accession number NC009988.1). Thirty-three full genome sequences of SADS-CoV were subsequently obtained (8 from farm A, 5 farm B, 11 farm C and 9

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farm D), and they are 99.9% identical to each other (Supplementary Information Table 1).

Using qPCR targeting the nucleocapsid gene (Supplementary Information Table 2), we detected SADS-CoV in acutely sick piglets and sows, but not in recovered or healthy pigs on the four farms, nor in nearby farms that showed no evidence of SADS. The virus replicated to higher titers in piglets than in sows (Fig. 1b). SADS-CoV displayed tissue tropism for small intestine (Fig.1c), as observed for other swine enteric coronaviruses[13]. Retrospective PCR analysis revealed that SADS-CoV was present on Farm A during the PEDV epidemic, where the first strongly positive SADS-CoV sample was detected on 6 December 2016. From mid-January onwards, SADS-CoV was the dominant viral agent detected in diseased animals (Extended Data Fig.1b). It is possible that the presence of PEDV early in the SADS-CoV outbreak may have somehow facilitated or enhanced spillover and amplification of SADS. However the fact that the vast majority of piglet mortality occurred after PEDV infection had become undetectable suggests that SADS-CoV itself causes a lethal infection in pigs that was responsible for these large-scale outbreaks, and that PEDV does not directly contribute to its severity in individual pigs. This was supported by the absence of PEDV and other known swine diarrhea viruses during the peak and later phases of the SADS outbreaks in the four farms (Extended Data Table 1).

We rapidly developed an antibody assay based on the S1 domain of the spike (S) protein using the Luciferase Immunoprecipitation System (LIPS)[14]. As SADS is

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acute with rapid onset in piglets, serological investigation was conducted only in sows. Among 46 recovered sows tested, 12 were seropositive for SADS-CoV within three weeks of infection (Fig. 1d). To investigate possible zoonotic transmission, serum samples from 35 farm workers who had close contact with sick pigs were subjected to the same LIPS test and none were positive for SADS-CoV.

While the overall genome identity of SADS-CoV and HKU2-CoV is 95%, the S gene sequence identity is only 86%, suggesting that previously reported HKU2-CoV is not the direct progenitor of SADS-CoV, but that they may have originated from a common ancestor. To test the hypothesis, we developed a SADS-CoV specific qPCR assay based on its RNA dependent RNA polymerase (RdRp) gene (Supplementary Information Table 2) and screened 596 bat anal swabs collected during 2013-2016 from seven different locations in Guangdong Province (Extended Data Fig. 1a). A total of 71 samples (11.9%) tested positive (Extended Data Table 2), the majority (94.3%) were from *Rhinolophus* spp. bats which are also the natural reservoir hosts of SARS-related coronaviruses[6-8, 15-18]. Four complete genome sequences with the highest RdRp PCR fragment sequence identity to that of SADS-CoV were determined by NGS. They are very similar in size (27.2 kb) to SADS-CoV (Fig. 2a) and we tentatively nominate them SADS related coronaviruses (SADSr-CoV). Overall sequence identity between SADSr-CoV and SADS-CoV ranges from 96-98%. Most importantly, the S protein of SADS-CoV shared more than 98% sequence identity with those of the two SADSr-CoVs (162149 and 141388), compared to 86% with HKU2-CoV. The major sequence differences among the four

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SADSr-CoV genomes lie in the predicted coding regions of the S and NS7a and NS7b genes (Fig. 2a). In addition, the coding region of the S protein N-terminal (S1) domain was determined from 19 bat SADSr-CoVs to aid more detailed phylogenetic analysis.

The phylogeny of S1 and full-length genome revealed a high genetic diversity of alpha coronaviruses among bats and strong coevolutionary relationships to their hosts (Fig. 2b and Extended Data Fig. 2), with SADS-CoVs more closely related to SADSr-CoVs from *Rhinolophus affinis* than from *Rhinolophus sinicus* in which HKU2-CoV was found. Both phylogenetic and haplotype network analyses demonstrated that viruses from the four farms likely originated from their reservoir hosts independently (Extended Data Fig. 3), and a few viruses might have undergone further genetic recombination (Extended Data Fig. 4). However, molecular clock analysis of the 33 SADS-CoV genome sequences failed to establish a positive association between sequence divergence and sampling date. Therefore, we speculate that either the virus was introduced into pigs from bats multiple times, or the virus was introduced into pigs once, but subsequent genetic recombination disturbed the molecular clock.

For viral isolation, we tried to culture the virus in a variety of cell lines (see Methods for detail) using intestinal tissue homogenate as starting material. Cytopathic effect was observed in Vero cells only after five passages (Extended Data Fig. 5a &b). The identity of SADS-CoV was verified in Vero cells by immunofluorescent staining (Extended Data Fig. 5c & d) and by whole genome

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sequencing (GenBank accession number MG557844). Similar results were obtained by other groups[19, 20].

Known coronavirus host cell receptors include angiotensin-converting enzyme 2 (ACE2) for SARS-related CoV, aminopeptidase N (APN) for certain alphacoronavirus like HCoV-229E, and dipeptidyl peptidase 4 (DPP4) for MERS-CoV[21-23]. To investigate the receptor usage of SADS-CoV, we tested live or pseudotyped SADS-CoV infection on HeLa cells expressing each of the three molecules, respectively. While the positive control worked for SL-CoV and MERS-CoV pseudoviruses, we found no evidence of enhanced infection or entry for SADS-CoV, suggesting that none of them is a functional receptor of SADS-CoV (Extended Data Table 3).

To fulfill Koch's postulates for SADS-CoV, two different types of animal challenge experiments were conducted (see Method for details). The first challenge experiment was conducted with SPF piglets infected with a tissue homogenate of SADS-CoV positive intestine. Two days after infection, 3/7 animals died in the challenge group whereas 4/5 survived in the control group. Incidentally, the one piglet that died in the control group was the only individual that didn't receive colostrum due to a shortage of supply. It is thus highly likely that lack of nursing and inability to access colostrum was responsible for the death (Extended Data Table 4). For the second challenge, healthy piglets were acquired from a farm in Guangdong that had been free of diarrheal disease for a number of weeks prior to the experiment, and were infected with the cultured isolate of SADS-CoV or tissue culture medium as control.

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Of those inoculated with SADS-CoV, 50% (3/6) died between 2-4 days post infection, while all control animals survived (Extended Data Table 5). All animals in the infected group suffered watery diarrhea, rapid weight loss and intestinal lesions (determined after euthanasia upon experiment termination, Extended Data Table 4 & 5). Histopathological examination revealed significant villus atrophy only in SADS-CoV inoculated farm piglets 4-days after inoculation but not in control piglets (Fig. 3a and 3b) and viral N protein-specific staining was observed mainly in small intestine epithelial cells (Fig. 3c and 3d).

The current study highlights the value of proactive viral discovery in wildlife, and targeted surveillance in response to an emerging infectious disease event, as well as the disproportionate importance of bats as reservoirs of viruses that threaten veterinary and public health[24]. It also demonstrates that by using modern technological platforms such as NGS, LIPS serology and phylogenic analysis, key experiments that traditionally rely on isolation of live virus can be performed rapidly prior to virus isolation.

Online Content Methods, along with any additional Extended Data display items and Source Data, are available in the online version of the paper, references unique to these sections appear only in the online paper.

ACKNOWLEDGEMENTS: We thank Prof. Shao-Bo Xiao for kindly providing pig cell lines, Dr. Peter Burbelo from NIH for kindly providing the LIPS vector and Dr.

Li Zhu from GenScript for great facilitation in rapid synthesis of the S gene. We thank the WIV animal facilities, and Ms Juan Min for help in preparing IHC samples, and Guang-Jian Zhu and Aleksei A. Chmura for assistance in bat sampling. This work was jointly supported by the Strategic Priority Research Program of the Chinese Academy of Sciences (XDPB0301) to ZLS, China Natural Science Foundation (81290341 and 31621061 to ZLS, 81661148058 to PZ, 31672564 and 31472217 to JYM, 81572045, 81672001 and 81621005 to TYG), National Key Research and Development Program of China (2015AA020108, 2016YFC1202705, SKLPBS1518, AWS16J020 and AWS15J006) to TYG; National Science and Technology Spark Program (2012GA780026) and Guangdong Province Agricultural Industry Technology System Project (2016LM1112) to JYM, State Key Laboratory of Pathogen and Biosecurity (SKLPBS1518) to TYG, Taishan Scholars program of Shandong province (ts201511056 to WFS), NRF grants NRF2012NRF-CRP001–056, NRF2016NRF-NSFC002-013 and NMRC grant CDPHRG/0006/2014 to L-FW, Funds for Environment Construction & Capacity Building of GDAS' Research Platform (2016GDASPT-0215) to LBZ, United States Agency for International Development Emerging Pandemic Threats PREDICT project (AID-OAA-A-14-00102), National Institute of Allergy and Infectious Diseases of the National Institutes of Health (Award Number R01AI110964) to PD and ZLS.

AUTHOR CONTRIBUTIONS: L.F.W., Z.L.S., P.Z., T.Y.G., M.J.Y. conceived the study. P.Z., W.Z., Y.Z., S.M., X.S.Z., B.L., X.L.Y., H.G., D.A., Y.L., X.L.L., J.C.

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performed qPCR, serology, histology and virus culturing. H.F., Y.W.Z., J.M.L., G.Q.P., X.P.A., Z.Q.M., T.T.H., Y.H., Q.S., Y.Y.W., S.Z.X., X.L.L.Z., W.F.S., J.L. performed genome sequencing and annotations. T.L., Q.M.X., J.W.C., L.Z., K.J.M., Z.X.W., Y.S,C., D.L., Y.S., F.C., P.J.G., R.H. prepared the samples and animal challenges. Z.L.S., P.D., L.B.Z., S.Y.L. coordinated collection of bat samples. P.Z., L.F.W., Z.L.S., P.D. played a major role in manuscript preparation.

The authors declare no competing financial interests. Correspondence and requests for materials should be addressed to ZLS (zlshi@wh.iov.cn).

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Supplementary Information is available in the online version of the paper.

Main Figure Legend

Figure 1 | Detection of SADS-CoV infection in pigs in Guangdong, China. a, Records of daily death toll on the four farms from 28 October 2016 to 2 May 2017. **b**, Detection of SADS-CoV by qPCR. Sample size: 12 sick piglets, 5 sick sows, 16 recovered sows, and 10 healthy piglets. **c**, Tissue distribution of SADS-CoV in diseased pigs (n=3). Centre values are average while bars indicate standard deviations. **d**, Detection of SADS-CoV antibodies. Sample size: 46 first bleed sera taken in the first three weeks of the outbreak, 8 second bleed sera taken >1 month post outbreak onset, 8 healthy pig control sera, 35 human sera from pig farmers.

Figure 2 | Genome and phylogenetic analysis of SADS-CoV and SADSr-CoV. a, Genome organization and comparison. Color-coding for different genomic regions: Green- nonstructural polyproteins ORF1a and 1b; Yellow- structural proteins S, E, M and N; Blue- accessory proteins NS3a, NS7a and Ns7b; Orange- UTRs. The level of sequence identity of SADSr-CoV to SADS-CoV is illustrated by different patterns of boxes: Open- highly similar; Dotted- moderately similar; Dash lined- least similar. **b**, Phylogenetic analysis of 57 S1 sequences (33 from SADS-CoV and 24 from SADSr-CoV). Different colors represent different host species as shown on the left. Scale bar indicates nucleotide substitutions per site.

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Figure 3 | Immunohistopathology of SADS-CoV infected tissues. Sections of Jejunum tissue from control (**a**, **c**) and infected farm piglets (**b**, **d**) 4-day after inoculation, respectively, were stained with hematoxylin and eosin in **a** & **b** (bar = 200 μm) or with rabbit anti- SADSr-CoV N serum (red), DAPI (blue) and mouse antibodies for epithelial cell marker cytokeratin 8, 18 and19 (green) in **c** & **d** (bar = 50 μm). SADS-CoV N protein is evident in epithelial cells and deeper in the tissue of infected piglets, which exhibit villus shortening. The experiment was conducted three times independently with similar results.

METHODS

Sample collection. Bats were captured and sampled in their natural habitat in Guangdong Province (Extended Data Fig. 1) as described previously[6]. Fecal swab samples were collected in viral transport medium (VTM) 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). Stool samples from sick pigs were collected in VTM. When appropriate and feasible, intestinal samples were also taken from deceased animals. Samples were aliquoted and stored at -80 ^{0}C until use. Blood samples were collected from recovered sows and farm workers who had close contact with sick pigs. Serum was separated by centrifugation at 3,000 *g* for 15 min within 24 h of collection and preserved at 4 ^{0}C. Human serum collection was approved by the Medical Ethics Committee of the Wuhan School of Public Health,

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Wuhan University and Hummingbird IRB. Human, pigs and bats were sampled without gender or age preference unless where indicated (e.g. piglets or sows).

Virus isolation. The following cells were used for virus isolation in this study: Vero (cultured in DMEM +10% FBS); *Rhinolophus sinicus* primary or immortalized cells generated by our laboratory (all cultured in DMEM/F12 +15% FBS): kidney primary RsKi9409, lung primary RsLu4323, lung immortalized RsLuT, brain immortalized RsBrT and heart immortalized RsHeT; and swine cell lines: two intestinal porcine enterocytes IPEC (RPMI1640+10% FBS) and SIEC (DMEM+10% FBS), three kidney PK15, LLC-PK1 (DMEM+10% FBS for all) and IBRS (MEM+10% FBS), and one pig testes cells ST (DMEM+10% FBS). All cell lines were tested free of mycoplasma contamination, applied to species identification and authenticated by microscopic morphologic evaluation. None of cell lines was on the list of commonly misidentified cell lines (by ICLAC).

Cultured cell monolayers were maintained in their respective medium. PCR-positive pig fecal or supernatant from homogenized pig intestine (in 200 μl VTM) spin at 8,000g for 15 min, filtered and diluted 1:2 with DMEM supplied with 16 μg/ml trypsin before adding to cells. After incubation at 37 ^{0}C for 1 h, the inoculum was removed and replaced with fresh culture medium containing antibiotics (below) and 16 μg/ml trypsin. The cells were incubated at 37 ^{0}C and observed daily for cytopathic effect (CPE). Four blind passages (three-day interval between every passage) were performed for each sample. After each passage, both the culture supernatant and cell pellet were examined for presence of virus by RT-PCR using the

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SADS-CoV primers listed in Supplementary Information Table 2. Penicillin (100 units/ml) and streptomycin (15 μg/ml) were included in all tissue culture media.

RNA extraction, S1 gene amplification and qPCR. Whenever commercial kits were used, manufacturer's instructions were followed without modification. RNA was extracted from 200 μl of swab samples (bat), feces or homogenized intestine (pig) with the High Pure Viral RNA Kit (Roche). RNA was eluted in 50 μl of elution buffer and used as the template for RT-PCR. Reverse transcription was performed using the SuperScript III kit (Thermo Fisher Scientific).

To amplify S1 genes from bat samples, nested PCR was performed with primers designed based on HKU2-CoV (Genbank accession number NC009988.1)[12] (Supplementary Information Table 2). The 25 μl first-round PCR mixture contained 2.5 μl 10×PCR reaction buffer, 5 pmol of each primer, 50 mM MgCl2, 0.5 mM dNTP, 0.1 μl Platinum Taq Enzyme (Thermo Fisher Scientific) and 1 μl cDNA. The 50 μl second-round PCR mixture was identical to the first-round PCR mixture except for primers. Amplification of both rounds was performed as follows: 94 ^{0}C for 5 min followed by 60 cycles consisting of 94 ^{0}C for 30 s, 50 ^{0}C for 40 s, 72 ^{0}C for 2.5 min, and a final extension of 72 ^{0}C for 10 min. PCR products were gel purified and sequenced.

For qPCR analysis, primers based on SADS-CoV RdRp and NP genes were used (Supplementary Information Table 2). RNA extracted from above was reverse-transcribed using PrimeScript RT Master Mix (Takara). The 10 μl qPCR reaction mix contained 5 μl 2×SYBR premix Ex Taq II (Takara), 0.4 μM of each primer and 1 μl

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cDNA. Amplification was performed as follows: 95 ^{0}C for 30 s followed by 40 cycles consisting of 95 ^{0}C for 5 s, 60 ^{0}C for 30 s, and a melting curve step.

Luciferase Immunoprecipitation System (LIPS) assay. The SADS-CoV S1 gene was codon optimized for eukaryotic expression, synthesized (GenScript) and cloned in frame with the Renilla luciferase gene (Rluc) and a FLAG tag in the **pREN2** vector[14]. **pREN2**-S1 plasmids were transfected into Cos-1 cells using Lipofectamine 2000 (Thermo Fisher Scientific). At 48 h post-transfection, cells were harvested, lysed and a luciferase assay was performed to determine Rluc expression for both the empty vector (**pREN2**) and the **pREN2**-S1 construct. For testing of unknown pig or human serum samples, 1 µl of serum was incubated with 10 million units of Rluc alone (vector) or Rluc-S1, respectively, together with 3.5 µl of a 30% protein A/G ultralink bead suspension (Thermo Fisher Scientific). After extensive washing to remove unbounded luciferase-tagged antigen, captured luciferase amount was determined using the commercial luciferase substrate kit (Promega). The ratio of Rluc-S1/Rluc (Vector) was used to determine the specific S1 reactivity of pig and human sera. Commercial FLAG antibody (Thermo Fisher Scientific) was used as the positive control, and various pig sera (from uninfected animals in China or Singapore; or pigs infected with PEDV, TGEV or Nipah virus) were used as a negative control.

Protein expression and antibody production. The N gene from SADSr-CoV 3755 (GenBank accession number MF094702), which shared a 98% aa sequence identity to the SADS-CoV N gene, was inserted into **pET-28a+** (Novagen) for prokaryotic expression. Transformed *E. coli* were grown at 37 ^{0}C for 12-18 h in media containing

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1 mM IPTG. Bacteria were collected by centrifugation and resuspended in 30 ml of 5 mM imidazole and lysed by sonication. The lysate, from which N protein expression was confirmed with an anti-HIS-tag antibody, was applied to the Ni^{2+} resin (Thermo Fisher Scientific). The purified N protein, at a concentration of 400 μg/ml, was used to immunize rabbits for antibody production following published methods[25]. After immunization and two boosts, rabbits were euthanized and sera were collected. Rabbit anti-N protein serum was used 1:10,000 for subsequent Western blots.

Amplification, cloning and expression of human and swine genes. Construction of expression clones for human ACE2 in **pcDNA3.1** has been described previously[8, 26]. Human DPP4 was amplified from human cell lines. Human APN gene was commercially synthesized. Swine APN, DPP4 and ACE2 genes were amplified from piglet intestine. Full-length gene fragments were amplified using specific primers (provided upon request). The human ACE2 gene was cloned into **pCDNA3.1** fused with HIS tag. Human APN, DPP4, Swine APN, DPP4 and ACE2 genes were cloned into **pCAGGS** fused with S tag. Purified plasmids were transfected to HeLa cells. After 24 h, HeLa cells expressing human or swine genes were confirmed by immunofluorescence assay (IFA) using mouse anti-HIS tag or mouse anti-S tag monoclonal antibodies (produced in house) followed by cyanin 3-labeled goat anti-mouse/rabbit IgG (Proteintech Group).

Pseudovirus preparation. The codon-humanized S protein genes of SADS-CoV or MERS-CoV cloned into **pcDNA3.1** were used for pseudovirus construction as described previously[8, 26]. Briefly, 15 μg of each pHIV-Luc (**pNL4.3.Luc.R$^-$E$^-$Luc**)

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and the S protein expressing plasmids (or empty vector control) were co-transfected into 4 × 10^6 293T cells using Lipofectamine 3000 (Thermo Fisher Scientific). After 4 h, the medium was replaced with fresh medium. Supernatants were harvested at 48 h post transfection and clarified by centrifugation at 3,000g, then passed through a 0.45µm filter (Millipore). The filtered supernatants were stored at -80°C in aliquots until use. To evaluate the incorporation of S proteins into the core of HIV virions, pseudoviruses in supernatant (20 ml) were concentrated by ultracentrifugation through a 20% sucrose cushion (5ml) at 80,000g for 90 min using a SW41 rotor (Beckman). Pelleted pseudoviruses were dissolved in 50µl phosphate-buffered saline (PBS) and examined by electron microscopy (EM).

Pseudovirus infection. HeLa cells transiently expressing APN, ACE2 or DPP4 were prepared using Lipofectamine 2000 (Thermo Fisher Scientific). Pseudoviruses prepared above were added to APN, ACE2 or DPP4 overexpressed HeLa cells at 24h post transfection. The unabsorbed viruses were removed and replaced with fresh medium at 3 hpi. The infection was monitored by measuring the luciferase activity conferred by the reporter gene carried by the pseudovirus, using the Luciferase Assay System (Promega) as follows: cells were lysed at 48 hpi, and 20 µl of the lysates was taken for determining luciferase activity by the addition of 50 µl of luciferase substrate.

Examination of known CoV receptors for SADS-CoV entry/infection. HeLa cells transiently expressing APN, ACE2 or DPP4 were prepared by a lipofectamine 2000 system (Thermo Fisher Scientific) in 96-well plate, with mock-transfected cells as

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controls. SADS-CoV grown from Vero cells was used to infect Hela cells transiently expressing APN, ACE2 or DPP4. The inoculum was removed after 1h absorption and washed twice with PBS and supplemented with medium. SARS-related-CoV WIV16[18] and MERS-CoV HIV-pseudovirus were used as positive control for human/swine ACE2 or human/swine DPP4, respectively. At 24 hpi, cells were washed with PBS and fixed with 4% formaldehyde in PBS (pH 7.4) for 20 min at room temperature. SL-CoV WIV16 replication was detected using rabbit antibody against the SL-CoV Rp3 nucleocapsid protein (made in house, 1:100) followed by cyanin 3-conjugated goat anti-rabbit IgG (1:50, Proteintech)[18]. SADS-CoV replication was monitored using rabbit antibody against the SADSr-CoV 3755 N protein (made in house, 1:50) followed by FITC-conjugated goat anti-rabbit IgG (1:50, Proteintech). Nucleus was stained with DAPI (Beyotime). Staining patterns were examined using the FV1200 confocal microscopy (Olympus). Infection of MERS-CoV HIV-pseudovirus was monitored by luciferase at 48 hpi.

High throughput sequencing, pathogen screening and genome assembly. Tissue from the small intestine of deceased pigs was homogenized and filtered through 0.45 μm filters before nucleic acid was extracted and ribosomal RNA were depleted using NEBNext rRNA Depletion Kit (New England Biolabs). Metagenomics analysis of both RNA and DNA viruses was performed. For the RNA virus screening, the sequencing library was constructed using Ion Total RNA-Seq Kit v2 (Thermo Fisher Scientific). For the DNA virus screening, NEBNext Fast DNA Fragmentation & Library Prep Set for Ion Torrent (New England Biolabs) was used for library

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preparation. Both libraries were sequenced on an Ion S5 sequencer (Thermo Fisher Scientific). An analysis pipeline was applied on the sequencing data which perform the following analysis steps: 1) raw data quality filtering, 2) host genomic sequence filtering, 3) blastn against virus nucleotide database using BLAST, 4) blastx against virus protein database using DIAMOND v0.9.0; 5) contig assembling and blastx against virus protein database. For whole viral genome sequencing, amplicon primers (To be provided upon request) were designed using the Thermo Fisher Scientific online tool with HKU2-CoV and SADS-CoV Farm A genome as reference, and the sequencing libraries were constructed using NEBNext Ultra II DNA Library Prep Kit for Illumina and sequenced on an MiSeq sequencer. PCR and Sanger sequencing was performed to fill gaps in the genome. Genome sequences were assembled using CLC Genomic Workbench v9.0. 5'-RACE was performed to determine the 5'-end of the genomes using SMARTer RACE 5'/3' Kit (Takara). Genomes were annotated using Clone Manager Professional Suite 8 (Sci-Ed Software).

Phylogenetic analysis. SADS-CoV genome sequences and other representative coronavirus sequences (obtained from GenBank) were aligned using MAFFT v7.221. Phylogenetic analyses with full-length genome, S gene and RdRp were performed using MrBayes v3.2. Twenty million to fifty million steps were run, with GTR+G+I model (General Time Reversible model of nucleotide substitution with a proportion of invariant sites and γ-distributed rates among sites). The first 10% were removed as burn-in. The association between phylogenies and phenotypes (e.g. host species and farms) was assessed by BaTS beta-build2, with the trees obtained in the previous step

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used as input. For SADS-CoVs, a median-joining network analysis was performed using PopART v1.7, with $\varepsilon = 0$. Phylogenetic analysis of the 33 full-length SADS-CoV genome sequences was performed using RAxML v8.2.11, with GTRGAMMA as the nucleotide substitution model and 1,000 bootstrap replicates. The maximum likelihood tree was used to test the molecular clock by TempEst v1.5. Potential genetic recombination events in our datasets were detected using RDP v4.72.

Animal infection studies. Experiments were carried out strictly in accordance with the recommendations of the Guide for the Care and Use of Laboratory Animals of the National Institutes of Health. The use of animals in this study was approved by the South China Agricultural University Committee of Animal Experiments (approval ID: 201004152).

Two different animal challenge experiments were conducted. Pigs were used without gender preference. In the first experiment, which was conducted before the virus was isolated, we used 3-day old specific pathogen free (SPF) piglets of the same breeding line, cared at a specific pathogen free (SPF) facility, supplied by colostrum (except one). These are bred and reared to be free of PEDV, CSFV, SIV, PCV2 and PPV, and are routinely tested using PCR. We also conducted NGS to further confirm this before the animal experiment, and to demonstrate freedom from SADS-CoV infection. The intestinal tissue samples from diseased and healthy animals, respectively (intestinal samples excised from euthanized piglets, then ground to make slurry for the inoculum. NGS was performed to confirm no other pig pathogens exist), were used to feed two groups of 5 (as control) and 7 (infection) animals, respectively.

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For the second experiment, isolated SADS-CoV was used to infect healthy piglets from a farm in Guangdong which had been free of diarrheal disease for a number of weeks previously. These piglets were from the same breed as those on SADS-affected farms, to eliminate potential host factor differences and to more accurately reproduce the conditions that occurred during the outbreak in the region. Both groups of piglets were cared at a known pig disease free facility. Again, qPCR and NGS were used to make sure that there was no other known swine diarrhea virus present in the virus inoculum or any of the experimental animals. Two groups (6 for each group) of 3-day old piglets were inoculated with SADS-CoV culture supernatant or normal cell culture medium as control. NGS and qPCR was used to confirm that there were no other known swine pathogens in the inoculum.

For both experiments, animals were recorded daily for signs of diseases, such as diarrhea, weight loss and death. Fecal swabs were collected daily from all animals and screened for known swine diarrhea viruses by qPCR. Weight loss was calculated as >5% loss from original weight at day 0. It is important to point out that piglets at three days old tend to suffer from diarrhea and weight loss when they are taken away from sows and the natural breast-feeding environment without infection. At experimental endpoints, piglets were humanely euthanized and necropsies performed. Pictures were taken to record gross pathological changes to the intestines. Ileal, jejunal and duodenal tissues were taken from selected animals and stored at -80 ^{0}C for further analysis.

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Hematoxylin and eosin (H&E) and immunohistochemistry (IHC) analysis. Frozen (-80 ^{0}C) small intestinal tissues including duodenum, jejunum, and ileum taken from the above experimentally infected pigs were pre-frozen at -20 ^{0}C for 10 min. Tissues were then embedded in optimal cutting temperature compound and cut into 8-μm sections using the Cryotome FSE machine (Thermo Fisher Scientific). Mounted microscope slides were fixed with paraformaldehyde and stained with H&E for histopathological examination.

For IHC analysis, the rabbit antibody raised against the SADSr-CoV 3755 N protein was used for specific staining of SADS-CoV antigen. Slides were blocked by incubating with 10% goat serum (Beyotime) at 37 ^{0}C for 30 min, followed by overnight incubation at 4 ^{0}C with the rabbit anti-3755 N protein serum (1:1000) and mouse anti-Cytokeratin 8+18+19 mAb (Abcam) 1:100 diluted in PBST buffer containing 5% goat serum. After washing, slides were then incubated for 50 min at room temperature with Cy3 conjugated goat-anti-rabbit IgG (Proteintech) and FITC conjugated goat-anti-mouse IgG (Proteintech) diluted 1:100 in PBST buffer containing 5% goat serum. Slides were stained with DAPI (Beyotime) and observed under fluorescence microscope (Nikon).

Data Availability statement. Sequence data that support the findings of this study have been deposited in GenBank with the accession codes listed: MF094681-MF094688, MF769416-MF769444, MF094697-MF094701, MF769406-MF769415, and MG557844 (e.g. http://www.ncbi.nlm.nih.gov/nuccore/MF094861). Raw sequencing data that support the findings of this study have been deposited in

Sequence Read Achieve (SRA) with the accession codes listed: SRR5991652, SRR5991654, SRR5991649, SRR5991656, SRR5991651, SRR5995595, SRR5991657, SRR5991648, SRR5991650, SRR5991658, SRR5991657 and SRR5991655 （e.g. https://www.ncbi.nlm.nih.gov/sra/?term=SRR5991652).

25. E. Harlow, D. Lane, Antibodies: A Laboratory Manual. (Cold Spring Harbor Laboratory Press, New York, 1988).

26. Ren, W. et al. Difference in receptor usage between severe acute respiratory syndrome (SARS) coronavirus and SARS-like coronavirus of bat origin. J Virol 82, 1899-1907 (2008).

EXTENDED DATA LEGEND

Extended Data Figure 1 | Map of outbreak locations and sampling sites in Guangdong Province, China (a) and the co-circulation of PEDV and SADS-CoV during the initial outbreak on Farm A (b). a, SADS-affected farms are labeled A to D with blue swine symbols following the temporal sequence of the outbreaks. Bat sampling sites are indicated by black bat symbols. The bat SADSr-CoV that is most closely related to SADS-CoV (sample 162140) originated in Conghua. The red flag marks Foshan city, site of the SARS index case. **b**, Pooled intestinal samples (n=5 or more biological independent samples) were collected at dates given on the x-axis from deceased piglets and analyzed by qPCR. The viral load for each piglet is shown as copy number per milligram of intestine tissue (y-axis).

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Extended Data Figure 2 | Bayesian phylogenetic tree of the full-length genome (a) or ORF1ab sequences (b) of SADS-CoV and related coronaviruses. Trees were constructed using MrBayes with the average standard deviation of split frequencies under 0.01. The host of each sequence is represented pictorially. Newly sequenced SADS-CoVs are highlighted in red, bat SADSr-CoVs in blue and previously published sequences in black. Scale bar indicates nucleotide substitutions per site.

Extended Data Figure 3 | Phylogeny and haplotype network analyses of the 33 SADS-CoV strains from the four farms. **a**, phylogenetic tree constructed using MrBayes. The GTR+GAMMA model was applied and 20 million steps were run, with the first 10% of which were removed as burn in. Viruses from different farms are labeled with different colors. Scale bar indicates nucleotide substitutions per site. **b**, median-joining haplotype network constructed using ProART. In this analysis $\varepsilon = 0$ was applied. Size of the circles represents the number of samples. The larger the circle, the more samples it includes.

Extended Data Figure 4 | Recombination analysis for SADS-CoV and related CoVs. The potential genetic recombination events were detected using RDP. For each virus strain, different colors represent different sources of the genomes.

Extended Data Figure 5 | Isolation and antigenic characterization of SADS-CoV. Vero cells are shown at 20 hours post infection with mock (**a**) or SADS-CoV (**b**). **c** and **d** are mock or SADS-CoV infected samples stained with rabbit serum raised

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against the recombinant SADSr-CoV N protein (red) and DAPI (blue). The experiment was conducted three times independently with similar results.

Extended Data Table 1 | List of all known swine viruses tested by PCR at the beginning of the of SADS outbreak investigation on the four farms[*†]. Feces, intestine or fecal swabs collected from January to April 2017 were subjected for testing. Dash indicates a negative PCR result. ND, not done.

[*]Virus abbreviations: PEDV- Porcine Epidemic Diarrhea Virus; PDCoV- Porcine Delta Coronavirus; TGEV-Porcine Transmissible Gastroenteritis Virus; RV- Porcine Rotavirus; PBV- Porcine Picobirnavirus; PSV- Porcine Sapelovirus; SVA- Porcine Senecavirus A; SIV- Swine Influenza Virus; NADC30- Porcine Reproductive and Respiratory Syndrome Virus, strain NADC30; PRV- Porcine Pseudorabies Virus; FMDV- Foot and Mouth Disease Virus; CSFV- Classical Swine Fever Virus; PCV2- Porcine Circovirus 2; PCV3- Porcine Circovirus 3; APPV- Atypical Porcine Pestivirus; PPV- Porcine Parvovirus. [†]Sampling type and size for each farm: Farm A: 1 feces, 20 intestines and 6 fecal swabs; Farm B: 1 feces and 15 intestines; Farm C: 2 intestines and 1 fecal swab; Farm D: 5 feces and 1 fecal swab.

Extended Data Table 2 | List of SADSr-CoVs detected in bats in Guangdong, China. See Extended Data Figure 1 for sampling sites in relation to SARS and SADS outbreak locations.

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Extended Data Table 3 | Test of SADS-CoV entry and infection in Hela cells expressing known coronavirus receptors.

[*] Gene accession numbers for the genes used in this study: human APN, M22324.1; human ACE2, NM_021804; human DPP4, NM_001935.3; SwAPN (swine APN), NM_214277.1; SwACE2 (swine ACE2), NM_001116542.1; SwDPP4 (swine DPP4), NM_214257.1. [†] For MERS-CoV infection, HIV-pseudovirus was used. [‡] Expression of APN, ACE2 and DPP4 was confirmed by antibodies against fused tags.

Extended Data Table 4 | Experimental infection of SPF piglets using intestine tissue homogenate. Experimental details can be found in Methods. **a**, Animals were recorded every day for sign of diseases including weight loss, diarrhea and death. PCR on fecal swabs was conducted to monitor the presence of SADS-CoV or other pig viruses. **b**, Daily body weight record of all piglets. Unit = kg.

[*] Euthanized on the day indicated for further analysis. [†] Animals died during the experiment. [‡] The only animal which didn't receive colostrum in this experiment due to supply shortage.

Extended Data Table 5 | Experimental animal infection of farm piglets using cultured SADS-CoV. Experimental details can be found in Methods. **a**, Animals were recorded every day for sign of diseases including weight loss, diarrhea and

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death. PCR on fecal swabs was conducted to monitor the presence of SADS-CoV or other pig viruses. **b**, Daily body weight record of all piglets. Unit = kg.

[*]Euthanized on the day indicated for further analysis. [†]Animals died during the experiment.

From: Folkers, Greg (NIH/NIAID) [E]
Sent: Mon, 26 Mar 2018 17:14:54 +0000
To: Doepel, Laurie (NIH/NIAID) [E];Pekoc, Ken (NIH/NIAID) [E];Auchincloss, Hugh (NIH/NIAID) [E];Hudgings, Carole (NIH/NIAID) [E];Marston, Hilary (NIH/NIAID) [E]
Cc: Billet, Courtney (NIH/NIAID) [E];Stover, Kathy (NIH/NIAID) [E]
Subject: RE: FOR FOG REVIEW / CoV bat study / China
Attachments: 2018 Nature Daszak new CoV MA3 ld gf.docx

Here are my suggestions to consider

From: Doepel, Laurie (NIH/NIAID) [E]
Sent: Monday, March 26, 2018 12:53 PM
To: Pekoc, Ken (NIH/NIAID) [E] [redacted] (b) (6); Auchincloss, Hugh (NIH/NIAID) [E] [redacted] (b) (6); Folkers, Greg (NIH/NIAID) [E] [redacted] (b) (6); Hudgings, Carole (NIH/NIAID) [E] [redacted] (b) (6); Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Billet, Courtney (NIH/NIAID) [E] [redacted] (b) (6); Stover, Kathy (NIH/NIAID) [E] [redacted] (b) (6)
Subject: RE: FOR FOG REVIEW / CoV bat study / China

Nicely done, Ken. Minor comments/suggestions for your consideration.

From: Pekoc, Ken (NIH/NIAID) [E]
Sent: Monday, March 26, 2018 12:09 PM
To: Auchincloss, Hugh (NIH/NIAID) [E] [redacted] (b) (6); Doepel, Laurie (NIH/NIAID) [E] [redacted] (b) (6); Folkers, Greg (NIH/NIAID) [E] [redacted] (b) (6); Hudgings, Carole (NIH/NIAID) [E] [redacted] (b) (6); Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Billet, Courtney (NIH/NIAID) [E] [redacted] (b) (6); Stover, Kathy (NIH/NIAID) [E] [redacted] (b) (6)
Subject: FOR FOG REVIEW / CoV bat study / China

I've attached a draft media availability for review regarding a newly identified coronavirus in swine from China, found in the same region where SARS originated and involving the same bat species.

Nature will publish the study; a date is not firm but the authors believe it will be soon.

Some background correspondence that BUGS shared last fall is below.

Thanks

From: Peter Daszak <daszak@ecohealthalliance.org>
Date: October 1, 2017 at 1:21:51 PM EDT
To: [redacted] (b) (6)

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Cc: "David Morens [redacted] (b) (6), "David Morens [redacted] (b) (6), [redacted] (b) (6)" [redacted] (b) (6), [redacted] (b) (6), "Stemmy, Erik (NIH/NIAID) [E]" [redacted] (b) (6), Alison Andre <andre@ecohealthalliance.org>, Aleksei Chmura <chmura@ecohealthalliance.org>
Subject: Confidential - A new bat-origin coronavirus emerging in pigs in China discovered under our NIAID R01

Dear Dr Fauci and NIAID colleagues,

It was a pleasure to meet you again today. I've attached an unpublished paper, currently in the second round of review with *Nature* that describes a novel bat-origin Coronavirus (SADS-CoV: Swine Acute Diarrheal Syndrome coronavirus) that recently spilled over into pig farms in Southern China, leading to the death of over 25,000 piglets in 5+ farms in Guandong Province.

The virus originates in the same group of bats as SARS-CoV, and emerged in the same place. It's not known to be zoonotic (we've tested 35+ pig farm workers with an antibody assay and none are positive. The pig farm owners tell us the virus is now under control, thanks to culling and separation of infected herds. It's not yet known if this virus has appeared elsewhere, but we are looking. We're also doing assays to find out if it can infect human cells in the lab – so far no evidence of this.

I hope this paper is of interest. You should know that this work was supported by a NIAID R01 that Erik Stemmy is the Program Officer for, and that I'm PI on, with Zhengli Shi as co-PI.

If you want any other information at all, please don't hesitate to email or call and I'd be happy to come over to NIAID to brief you further. I'll also let you know if/when it will be published so that we can try to foster some publicity as appropriate.

Cheers,

Peter

Peter Daszak
President

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

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www.ecohealthalliance.org

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

Ken Pekoc
Public Affairs Officer
Rocky Mountain Laboratories
NIAID Office of Communications and Government Relations
(b) (6)

Please note that I am not a spokesperson for NIAID.

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DRAFT

FOR IMMEDIATE RELEASE
Day, XXXXXX, 2018
XXXX Eastern Time

(b) (5)

[redacted]

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(b) (5)

[redacted]

Obtained via FOIA by Judicial Watch, Inc.

Horseshoe bat (EcoHealth Alliance)

Researchers preparing to locate bats in a Chinese cave. (EcoHealth Alliance)

From: Hudgings, Carole (NIH/NIAID) [E]
Sent: Mon, 26 Mar 2018 17:39:23 +0000
To: Folkers, Greg (NIH/NIAID) [E];Doepel, Laurie (NIH/NIAID) [E];Pekoc, Ken (NIH/NIAID) [E];Auchincloss, Hugh (NIH/NIAID) [E];Marston, Hilary (NIH/NIAID) [E]
Cc: Billet, Courtney (NIH/NIAID) [E];Stover, Kathy (NIH/NIAID) [E];Hudgings, Carole (NIH/NIAID) [E]
Subject: RE: FOR FOG REVIEW / CoV bat study / China
Attachments: 2018 Nature Daszak new CoV MA3 ld gf ch.docx

A couple of suggestions on the attached.
Thanks, Carole

From: Folkers, Greg (NIH/NIAID) [E]
Sent: Monday, March 26, 2018 1:15 PM
To: Doepel, Laurie (NIH/NIAID) [E] (b) (6); Pekoc, Ken (NIH/NIAID) [E] (b) (6); Auchincloss, Hugh (NIH/NIAID) [E] (b) (6); Hudgings, Carole (NIH/NIAID) [E] (b) (6); Marston, Hilary (NIH/NIAID) [E] (b) (6)
Cc: Billet, Courtney (NIH/NIAID) [E] (b) (6); Stover, Kathy (NIH/NIAID) [E] (b) (6)
Subject: RE: FOR FOG REVIEW / CoV bat study / China

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Sent: Monday, March 26, 2018 12:53 PM
To: Pekoc, Ken (NIH/NIAID) [E] (b) (6); Auchincloss, Hugh (NIH/NIAID) [E] (b) (6); Folkers, Greg (NIH/NIAID) [E] (b) (6); Hudgings, Carole (NIH/NIAID) [E] (b) (6); Marston, Hilary (NIH/NIAID) [E] (b) (6)
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Nicely done, Ken. Minor comments/suggestions for your consideration.

From: Pekoc, Ken (NIH/NIAID) [E]
Sent: Monday, March 26, 2018 12:09 PM
To: Auchincloss, Hugh (NIH/NIAID) [E] (b) (6); Doepel, Laurie (NIH/NIAID) [E] (b) (6); Folkers, Greg (NIH/NIAID) [E] (b) (6); Hudgings, Carole (NIH/NIAID) [E] (b) (6); Marston, Hilary (NIH/NIAID) [E] (b) (6)
Cc: Billet, Courtney (NIH/NIAID) [E] (b) (6); Stover, Kathy (NIH/NIAID) [E] (b) (6)
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Nature will publish the study; a date is not firm but the authors believe it will be soon.

Some background correspondence that BUGS shared last fall is below.

Thanks

From: Peter Daszak <daszak@ecohealthalliance.org>
Date: October 1, 2017 at 1:21:51 PM EDT
To: "[redacted] (b) (6)
Cc: "David Morens [redacted] (b) (6), "David Morens [redacted] (b) (6), [redacted] (b) (6) [redacted] (b) (6), [redacted] (b) (6), "Stemmy, Erik (NIH/NIAID) [E]" [redacted] (b) (6), Alison Andre <andre@ecohealthalliance.org>, Aleksei Chmura <chmura@ecohealthalliance.org>
Subject: Confidential - A new bat-origin coronavirus emerging in pigs in China discovered under our NIAID R01

Dear Dr Fauci and NIAID colleagues,

It was a pleasure to meet you again today. I've attached an unpublished paper, currently in the second round of review with *Nature* that describes a novel bat-origin Coronavirus (SADS-CoV: Swine Acute Diarrheal Syndrome coronavirus) that recently spilled over into pig farms in Southern China, leading to the death of over 25,000 piglets in 5+ farms in Guandong Province.

The virus originates in the same group of bats as SARS-CoV, and emerged in the same place. It's not known to be zoonotic (we've tested 35+ pig farm workers with an antibody assay and none are positive. The pig farm owners tell us the virus is now under control, thanks to culling and separation of infected herds. It's not yet known if this virus has appeared elsewhere, but we are looking. We're also doing assays to find out if it can infect human cells in the lab – so far no evidence of this.

I hope this paper is of interest. You should know that this work was supported by a NIAID R01 that Erik Stemmy is the Program Officer for, and that I'm PI on, with Zhengli Shi as co-PI.

If you want any other information at all, please don't hesitate to email or call and I'd be happy to come over to NIAID to brief you further. I'll also let you know if/when it will be published so that we can try to foster some publicity as appropriate.

Cheers,

Peter

Obtained via FOIA by Judicial Watch, Inc.

Peter Daszak
President

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

Tel. +1 212-380-4473
www.ecohealthalliance.org

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

Ken Pekoc
Public Affairs Officer
Rocky Mountain Laboratories
NIAID Office of Communications and Government Relations
(b) (6)

Please note that I am not a spokesperson for NIAID.

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Obtained via FOIA by Judicial Watch, Inc.

DRAFT

FOR IMMEDIATE RELEASE
Day, XXXXXX, 2018
XXXX Eastern Time

(b) (5)

[redacted]

Obtained via FOIA by Judicial Watch, Inc.

[redacted]

(b) (5)

Obtained via FOIA by Judicial Watch, Inc.

Horseshoe bat (EcoHealth Alliance)

Researchers preparing to locate bats in a Chinese cave. (EcoHealth Alliance)

From: Pekoc, Ken (NIH/NIAID) [E]
Sent: Wed, 28 Mar 2018 19:46:40 +0000
To: Hudgings, Carole (NIH/NIAID) [E];Folkers, Greg (NIH/NIAID) [E];Doepel, Laurie (NIH/NIAID) [E];Auchincloss, Hugh (NIH/NIAID) [E];Marston, Hilary (NIH/NIAID) [E]
Cc: Billet, Courtney (NIH/NIAID) [E];Stover, Kathy (NIH/NIAID) [E]
Subject: RE: FOR FOG REVIEW / CoV bat study / China
Attachments: 2018 Nature Daszak new CoV MA5.docx

Thanks all; good suggestions and questions. Updated version attached: HM and GF, I ran your Qs past Dr. Daszak … [redacted] (b) (5) (b) (5) (b) (5)

Anything further?

I also just learned this will be coming out April 12.

Thanks

From: Hudgings, Carole (NIH/NIAID) [E]
Sent: Monday, March 26, 2018 11:39 AM
To: Folkers, Greg (NIH/NIAID) [E] [redacted] (b) (6); Doepel, Laurie (NIH/NIAID) [E] [redacted] (b) (6); Pekoc, Ken (NIH/NIAID) [E] [redacted] (b) (6); Auchincloss, Hugh (NIH/NIAID) [E] [redacted] (b) (6); Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Billet, Courtney (NIH/NIAID) [E] [redacted] (b) (6); Stover, Kathy (NIH/NIAID) [E] [redacted] (b) (6); Hudgings, Carole (NIH/NIAID) [E] [redacted] (b) (6)
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Obtained via FOIA by Judicial Watch, Inc.

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The virus originates in the same group of bats as SARS-CoV, and emerged in the same place. It's not known to be zoonotic (we've tested 35+ pig farm workers with an antibody assay and none are positive. The pig farm owners tell us the virus is now under control, thanks to culling and separation of infected herds. It's not yet known if this virus has appeared elsewhere, but we are looking. We're also doing assays to find out if it can infect human cells in the lab – so far no evidence of this.

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If you want any other information at all, please don't hesitate to email or call and I'd be happy to come over to NIAID to brief you further. I'll also let you know if/when it will be published so that we can try to foster some publicity as appropriate.

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Peter Daszak
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Ken Pekoc
Public Affairs Officer
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DRAFT

FOR IMMEDIATE RELEASE

Thursday, April 12, 2018

XXXX Eastern Time

(b) (5)

[redacted]

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[redacted]

(b) (5)

Obtained via FOIA by Judicial Watch, Inc.

Horseshoe bat (EcoHealth Alliance)

Researchers preparing to locate bats in a Chinese cave. (EcoHealth Alliance)

From:	Lane, Cliff (NIH/NIAID) [E]
Sent:	Tue, 24 Apr 2018 15:04:41 +0000
To:	McNay, Laura (NIH/NIAID) [E]
Subject:	Re: MCB Cables for HHS U.S 19Apr18

Thanks

From: McNay, Laura (NIH/NIAID) [E]
Sent: Tuesday, April 24, 2018 10:58:44 AM
To: Lane, Cliff (NIH/NIAID) [E]
Subject: FW: MCB Cables for HHS U.S 19Apr18

fyi

From: Curtis, Holly (NIH/NIAID) [E]
Sent: Tuesday, April 24, 2018 9:48 AM
To: McNay, Laura (NIH/NIAID) [E] [redacted] (b) (6); Higgs, Elizabeth (NIH/NIAID) [E] [redacted] (b) (6); Orsega, Susan (NIH/NIAID) [E] [redacted] (b) (6); Sow, Ydrissa (NIH/NIAID) [E] [redacted] (b) (6); Siddiqui, Sophia (NIH/NIAID) [E] [redacted] (b) (6); Pineda, Mark (NIH/NIAID) [E] [redacted] (b) (6); Aboulhab, Jamila (NIH/NIAID) [E] [redacted] (b) (6); Feldmann, Heinrich (NIH/NIAID) [E] [redacted] (b) (6); Hensley, Lisa (NIH/NIAID) [E] [redacted] (b) (6); Jahrling, Peter (NIH/NIAID) [E] [redacted] (b) (6); Munster, Vincent (NIH/NIAID) [E] [redacted] (b) (6)
Subject: FW: MCB Cables for HHS U.S 19Apr18

Hi all,

Attached is a cable on the destruction of Ebola samples in Guinea. Please share with others who may be interested.

Warm regards,

Holly Curtis, PhD
Sub-Saharan Africa Regional Program Officer
NIAID Office of Global Research
5601 Fishers Lane, 1E63A, MSC 9802
Bethesda, MD 20892-9802
Phone: [redacted] (b) (6)
Cell: [redacted] (b) (6)
Fax: (301) 480-4447
[redacted] (b) (6)

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From: Handley, Gray (NIH/NIAID) [E]
Sent: Sunday, April 22, 2018 6:30 PM
To: Bernabe, Gayle (NIH/NIAID) [E] [redacted] (b) (6); Meegan, James (NIH/NIAID) [E] [redacted] (b) (6); Chen, Ping (NIH/NIAID) [E] [redacted] (b) (6); Curtis, Holly (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Western, Karl (NIH/NIAID) [C] [redacted] (b) (6)
Subject: FW: MCB Cables for HHS U.S 19Apr18

Please distribute these interesting cables on BSL-4 in China and Ebola in Guinea to anyone potentially interested.

Thanks. g

China Virus Institute Welcomes More U.S. Cooperation on Global Health Security

(b) (5)
[redacted]

Obtained via FOIA by Judicial Watch, Inc.

From: Higgs, Elizabeth (NIH/NIAID) [E]
Sent: Tue, 24 Apr 2018 14:41:41 +0000
To: Lane, Cliff (NIH/NIAID) [E];Siddiqui, Sophia (NIH/NIAID) [E]
Subject: FW: MCB Cables for HHS U.S 19Apr18
Attachments: China Virus Institute Welcomes More U.S. Cooperation onGlobal Health Security, Guinea: Inactivation and Destruction of 18,000 Ebola Samples

FYI

From: "Curtis, Holly (NIH/NIAID) [E]" (b) (6)
Date: Tuesday, April 24, 2018 at 9:48 AM
To: (b) (6), (b) (6) (b) (6), "Orsega, Susan (NIH/NIAID) [E]" (b) (6), Ydrissa Sow (b) (6), (b) (6), (b) (6), Jamila Aboulhab (b) (6), "Feldmann, Heinrich (NIH/NIAID) [E]" (b) (6), Lisa Hensley (b) (6), (b) (6), "Munster, Vincent (NIH/NIAID) [E]" (b) (6)
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<u>China Virus Institute Welcomes More U.S. Cooperation on Global Health Security</u>

(b) (5)

[redacted]

Obtained via FOIA by Judicial Watch, Inc.

From: [redacted] (b) (6)
Sent: Thu, 19 Apr 2018 11:43:31 +0000
Cc: International Cables (HHS/OS)
Subject: China Virus Institute Welcomes More U.S. Cooperation onGlobal Health Security

[redacted] (b) (6)

SENSITIVE

E.O. 13526: N/A
TAGS: SHLH, PGOV, CN, PREL, TBIO, KGHI, CDC, EAID, KHIV, IN, JP, TW, TSPL, PINS, SENV
SUBJECT: China Virus Institute Welcomes More U.S. Cooperation on Global Health Security

REF: 18 BEIJING 138
17 BEIJING 2458
11 MUMBAI 630
17 TOKYO 716
13 SEOUL 790

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).
[redacted] (b) (5)

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(b) (5) [redacted] (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 HYPERLINK "https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5404250/"one P4 lab. South Korea was close to HYPERLINK "http://www.koreaherald.com/view.php?ud=20170316000902"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

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

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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 HYPERLINK "http://science.sciencemag.org/content/359/6378/872.full"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) 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) (6), recently planned to visit Wuhan to meet with (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 Chinas 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) The workshop explored opportunities for U.S.-China research cooperation in areas like using "big data" to predict emerging infectious diseases, climate changes effect on

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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 GVPs 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.
FOUSS
BT
#8609

NNNN

Obtained via FOIA by Judicial Watch, Inc.

From: Morens, David (NIH/NIAID) [E]
Sent: Wed, 29 Jan 2020 22:19:47 +0000
To: Cassetti, Cristina (NIH/NIAID) [E]
Subject: RE: Wuhan novel coronavirus - NIAID's role in bat-origin CoVs

OK, talk to ya then

David

David M. Morens, M.D.
CAPT, United States Public Health Service
Senior Advisor to the Director
Office of the Director
National Institute of Allergy and Infectious Diseases
National Institutes of Health
Building 31, Room 7A-03
31 Center Drive, MSC 2520
Bethesda, MD 20892-2520
☎ [redacted] (b) (6) (assistants: Kimberly Barasch; Whitney Robinson)
📠 301 496 4409
💻 [redacted] (b) (6)

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[redacted] (b) (6)

From: Cassetti, Cristina (NIH/NIAID) [E] [redacted] (b) (6)>
Sent: Wednesday, January 29, 2020 5:18 PM
To: Morens, David (NIH/NIAID) [E] [redacted] (b) (6)
Subject: RE: Wuhan novel coronavirus - NIAID's role in bat-origin CoVs

Ok, let's try to connect tomorrow

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Cheers,
Cristina

From: Morens, David (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Wednesday, January 29, 2020 5:16 PM
To: Cassetti, Cristina (NIH/NIAID) [E] [redacted] (b) (6)
Subject: RE: Wuhan novel coronavirus - NIAID's role in bat-origin CoVs

C, [redacted] (b) (6). I'll be in tomorrow and also tonight will eventually be reachable on cell phone [redacted] (b) (6)

David

David M. Morens, M.D.
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Senior Advisor to the Director
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[redacted] (b) (6)

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From: Cassetti, Cristina (NIH/NIAID) [E] (b) (6)
Sent: Wednesday, January 29, 2020 4:15 PM
To: Morens, David (NIH/NIAID) [E] (b) (6)
Subject: FW: Wuhan novel coronavirus - NIAID's role in bat-origin CoVs

Hi David,

I hope you are doing well. Do you have few minutes to talk?

Cheers,

Cristina

Cristina Cassetti, Ph.D.
Deputy Director
Division of Microbiology and Infectious Diseases
National Institute of Allergy and Infectious Diseases, NIH
5601 Fishers Lane, Room 7G51
Rockville, MD 20852
Tel: (b) (6)
(b) (6)

Administrative Assistant:
Ms. Roshawn Treadwell-Hyde
Tel: (b) (6)
(b) (6)

From: "Morens, David (NIH/NIAID) [E]" (b) (6)
Date: January 27, 2020 at 4:53:54 PM EST
To: Peter Daszak <daszak@ecohealthalliance.org>
Cc: "Stemmy, Erik (NIH/NIAID) [E]" (b) (6), Alison Andre <andre@ecohealthalliance.org>
Subject: RE: Wuhan novel coronavirus - NIAID's role in bat-origin CoVs

Great info, thanks. Tony doesn't maintain awareness of these things and doesn't know unless program officers tell him, which they rarely do, since they are across town and may not see him more than once a year, or less....

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[redacted] (b) (4)

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<image002.jpg>

From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Monday, January 27, 2020 1:36 PM
To: Morens, David (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Stemmy, Erik (NIH/NIAID) [E] [redacted] (b) (6); Alison Andre <andre@ecohealthalliance.org>
Subject: Wuhan novel coronavirus - NIAID's role in bat-origin CoVs
Importance: High

Hi David – Happy to have a phone call re. the Wuhan CoV, but just wanted to mentioned a few things for your information and hopefully to pass on to Tony Fauci for when he's being interviewed re. the new CoV:

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Also – FYI, prior to the R01, we worked under an R01 with Eun-Chung Park as Program Officer on viral discovery in bats, where originally identified SARS-CoV as having a likely origin in bats (published in Science)

As I mentioned, I'm now part of a group that's meeting by phone weekly with CEIRS to discuss the nCoV and Erik's part of that.

Cheers,

Peter

Peter Daszak
President

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

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Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

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From: Morens, David (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Thursday, January 9, 2020 1:36 PM
To: Peter Daszak; Ian Lipkin (wil2001@columbia.edu); Jon Epstein
Subject: RE: Wuhan virus

Thanks, the excitement never ends, right?

<image001.gif>

David M. Morens, M.D.
CAPT, United States Public Health Service
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<image002.jpg>

From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Thursday, January 9, 2020 12:57 PM
To: Morens, David (NIH/NIAID) [E] (b) (6); Ian Lipkin (wil2001@columbia.edu) <wil2001@columbia.edu>; Jon Epstein <epstein@ecohealthalliance.org>
Subject: RE: Wuhan virus
Importance: High

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To: W. Ian Lipkin (wil2001@columbia.edu); Peter Daszak; Jon Epstein
Subject: Wuhan virus

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From: Morens, David (NIH/NIAID) [E]
Sent: Wed, 29 Jan 2020 21:51:02 +0000
To: Cassetti, Cristina (NIH/NIAID) [E]
Subject: RE: Wuhan novel coronavirus - NIAID's role in bat-origin CoVs

Yes, you can call me at [redacted] (b) (6)

David

David M. Morens, M.D.
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5601 Fishers Lane, Room 7G51
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Tel: [redacted] (b) (6)
[redacted] (b) (6)

Administrative Assistant:
Ms. Roshawn Treadwell-Hyde
Tel: [redacted] (b) (6)
[redacted] (b) (6)

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Subject: RE: Wuhan novel coronavirus - NIAID's role in bat-origin CoVs

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From: Morens, David (NIH/NIAID) [E]
Sent: Mon, 10 Feb 2020 14:21:27 +0000
To: Taubenberger, Jeffery (NIH/NIAID) [E] [redacted] (b) (6)
Subject: FW: Wuhan novel coronavirus - NIAID's role in bat-origin CoVs

[redacted] (b) (5)

David

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[redacted] (b) (6)

From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Monday, February 10, 2020 9:12 AM
To: Morens, David (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Aleksei Chmura <chmura@ecohealthalliance.org>; Alison Andre <andre@ecohealthalliance.org>
Subject: RE: Wuhan novel coronavirus - NIAID's role in bat-origin CoVs

Delighted to join you on a paper. Let me know when/what specifics to contribute and I'll get ready.

Also sad to see Ellen move on (our PREDICT project ended), but she'll still be involved and we're already writing grants to keep her working with us….

Cheers,

Peter

Peter Daszak
President

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From: Morens, David (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Tuesday, February 4, 2020 11:29 AM
To: Peter Daszak
Subject: RE: Wuhan novel coronavirus - NIAID's role in bat-origin CoVs

Peter, circling back, as even I, despite heroic efforts, am having trouble hiding from this corona epidemic…. We are being bombarded, to put it mildly.

[redacted] (b) (4)

We both wondered whether you'd consider joining as a co-author, allowing your input on certain key issues such as the relevance of the human-wildlife interface,

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zoonotic host-switching, and all the things you do. Assuming you were in general agreement. If not that's fine although I am sure we'll ref at least one of your papers.

Shocked to hear that Ellen C has left EcoHealth, a loss for you guys. Hopefully she will stay connected with you....

David

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📠 301 496 4409
💻 [redacted] (b) (6)

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From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Thursday, January 9, 2020 12:57 PM
To: Morens, David (NIH/NIAID) [E] [redacted] (b) (6); Ian Lipkin (wil2001@columbia.edu) <wil2001@columbia.edu>; Jon Epstein <epstein@ecohealthalliance.org>
Subject: RE: Wuhan virus
Importance: High

Yes – lots of information and I spoke with Erik Stemmy and Alan Embry yesterday before the news was released. Erik is my program officer on our coronavirus grant specifically focused on China.

I've been talking with reporters today and happy to fill you in on any further information…

Cheers,

Peter

Peter Daszak
President

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Twitter: @PeterDaszak

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From: Morens, David (NIH/NIAID) [E] (b) (6)
Sent: Thursday, January 9, 2020 12:50 PM
To: W. Ian Lipkin (wil2001@columbia.edu); Peter Daszak; Jon Epstein
Subject: Wuhan virus

Hi guys, do any of you have any inside info on this new coronavirus that isn't yet in the public domain? Or any thoughts?

TY,

David

David M. Morens, M.D.
CAPT, United States Public Health Service
Senior Advisor to the Director
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National Institute of Allergy and Infectious Diseases
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From: Morens, David (NIH/NIAID) [E]
Sent: Fri, 14 Feb 2020 22:24:21 +0000
To: Taubenberger, Jeffery (NIH/NIAID) [E] [redacted] (b) (6)
Subject: FW: Wuhan novel coronavirus - NIAID's role in bat-origin CoVs
Attachments: NEJM Perspective nCoV Morens Taubenberger 02-06-2020 final draft + dmm edits PD comments.docx

David

David M. Morens, M.D.
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[redacted] (b) (6)

From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Friday, February 14, 2020 5:07 PM
To: Morens, David (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Aleksei Chmura <chmura@ecohealthalliance.org>; Alison Andre <andre@ecohealthalliance.org>

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Subject: RE: Wuhan novel coronavirus - NIAID's role in bat-origin CoVs
Importance: High

Sorry about that - I was at the WHO meeting on the R&D Blueprint research agenda for COVID-19 so had to go to Geneva this week, and spent every other spare minute on phone calls and talking with journalists. I didn't realize it would be accelerated, but I think all papers are at this point!

I read through it and really like the historical perspective and Pandora's box references – as I've come to expect from your writing. I've made some light edits and suggestions – if it's worthy of authorship, great! If not, no problem.

Cheers,

Peter

Peter Daszak
President

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New York, NY 10001

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Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

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From: Morens, David (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Monday, February 10, 2020 2:51 PM
To: Peter Daszak
Cc: Aleksei Chmura; Alison Andre
Subject: RE: Wuhan novel coronavirus - NIAID's role in bat-origin CoVs

Peter, good news and bad news story.... Aiming for good news. Not hearing from you for several days the New England Journal aggressively bugged us to send something in, which we did (attached). We had planned to wait until we heard from you but figured you may be away or tied up with more important things or whatever.

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Of course we don't know if they will accept it, but if they do we can request they add you as a co-author, particularly since your papers and experience are cited. The downside of this is that once accepted we have little ability to do any major edits. This all happened because the Deputy Editor Lindsey Baden asked me to review a different ms., I sometimes have down rapid turn around reviews for him and Marty Hirsch in the past, but in our correspondence he then asked if we could send in something asap from us.

[redacted] (b) (4)

David

David M. Morens, M.D.
CAPT, United States Public Health Service
Senior Advisor to the Director
Office of the Director
National Institute of Allergy and Infectious Diseases
National Institutes of Health
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💻 [redacted] (b) (6)

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[redacted] (b) (6)

From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Monday, February 10, 2020 9:12 AM
To: Morens, David (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Aleksei Chmura <chmura@ecohealthalliance.org>; Alison Andre <andre@ecohealthalliance.org>
Subject: RE: Wuhan novel coronavirus - NIAID's role in bat-origin CoVs

Delighted to join you on a paper. Let me know when/what specifics to contribute and I'll get ready.

Also sad to see Ellen move on (our PREDICT project ended), but she'll still be involved and we're already writing grants to keep her working with us….

Cheers,

Peter

Peter Daszak
President

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

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Website: www.ecohealthalliance.org
Twitter: @PeterDaszak

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From: Morens, David (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Tuesday, February 4, 2020 11:29 AM
To: Peter Daszak
Subject: RE: Wuhan novel coronavirus - NIAID's role in bat-origin CoVs

Peter, circling back, as even I, despite heroic efforts, am having trouble hiding from this corona epidemic…. We are being bombarded, to put it mildly.

[redacted] (b) (4)

We both wondered whether you'd consider joining as a co-author, allowing your input on certain key issues such as the relevance of the human-wildlife interface, zoonotic host-switching, and all the things you do. Assuming you were in general agreement. If not that's fine although I am sure we'll ref at least one of your papers.

Shocked to hear that Ellen C has left EcoHealth, a loss for you guys. Hopefully she will stay connected with you….

David

David M. Morens, M.D.
CAPT, United States Public Health Service
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Office of the Director
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[redacted] (b) (6)

From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Monday, January 27, 2020 1:36 PM
To: Morens, David (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Stemmy, Erik (NIH/NIAID) [E] [redacted] (b) (6); Alison Andre <andre@ecohealthalliance.org>
Subject: Wuhan novel coronavirus - NIAID's role in bat-origin CoVs
Importance: High

Hi David – Happy to have a phone call re. the Wuhan CoV, but just wanted to mentioned a few things for your information and hopefully to pass on to Tony Fauci for when he's being interviewed re. the new CoV:

NIAID has been funding coronavirus work in China for the past 5 years through an R01 to me (1R01AI110964: "Understanding the Risk of Bat Coronavirus Emergence"). That's now been renewed, with a specific focus that we identify cohorts of people highly exposed to bats in China, and work out if they're getting sick from CoVs. Erik Stemmy is the Program Officer (cc'd here). Collaborators include Wuhan Institute of Virology (currently working on the nCoV), and Ralph Baric. The results of our work to date include:

[redacted] (b) (4)

- Discovered Swine Acute Diarrheal Syndrome Virus (SADS-CoV) killing >25,000 pigs in Guangdong Province (Published in Nature)
- Found SARS-related CoVs that can bind to human cells (Published in Nature), and that cause SARS-like disease in humanized mouse models.

[redacted] (b) (4)

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Also – FYI, prior to the R01, we worked under an R01 with Eun-Chung Park as Program Officer on viral discovery in bats, where originally identified SARS-CoV as having a likely origin in bats (published in Science)

As I mentioned, I'm now part of a group that's meeting by phone weekly with CEIRS to discuss the nCoV and Erik's part of that.

Cheers,

Peter

Peter Daszak
President

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From: Morens, David (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Thursday, January 9, 2020 1:36 PM
To: Peter Daszak; Ian Lipkin (wil2001@columbia.edu); Jon Epstein
Subject: RE: Wuhan virus

Thanks, the excitement never ends, right?

David

David M. Morens, M.D.
CAPT, United States Public Health Service
Senior Advisor to the Director
Office of the Director
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Building 31, Room 7A-03

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From: Peter Daszak <daszak@ecohealthalliance.org>
Sent: Thursday, January 9, 2020 12:57 PM
To: Morens, David (NIH/NIAID) [E] (b) (6); Ian Lipkin (wil2001@columbia.edu) <wil2001@columbia.edu>; Jon Epstein <epstein@ecohealthalliance.org>
Subject: RE: Wuhan virus
Importance: High

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From: Morens, David (NIH/NIAID) [E] (b) (6)
Sent: Thursday, January 9, 2020 12:50 PM
To: W. Ian Lipkin (wil2001@columbia.edu); Peter Daszak; Jon Epstein
Subject: Wuhan virus

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TY,

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(b) (4)

[redacted]

Obtained via FOIA by Judicial Watch, Inc.

(b) (4)

[redacted]

Obtained via FOIA by Judicial Watch, Inc.

(b) (4)

[redacted]

From: Morens, David (NIH/NIAID) [E]
Sent: Tue, 14 Apr 2020 19:17:02 +0000
To: Taubenberger, Jeffery (NIH/NIAID) [E]
Subject: Re: WaPo: State Department cables warned of safety issues at Wuhan lab studying bat coronaviruses

[redacted] (b) (5). D

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

On Apr 14, 2020, at 15:08, Taubenberger, Jeffery (NIH/NIAID) [E]
[redacted] (b) (6) wrote:

From: "Vandalen, Kaci (NIH/NIAID) [E]" [redacted] (b) (6)
Date: Tuesday, April 14, 2020 at 3:06 PM
To: NIAID HCTF [redacted] (b) (6)
Subject: FW: WaPo: State Department cables warned of safety issues at Wuhan lab studying bat coronaviruses

Good afternoon,
Marshall asked that I distribute this to the HCTF. I hope everyone is staying safe and sane!

Kaci VanDalen | *Health Specialist (BioRisk)*
National Institutes of Health (NIH)
National Institute of Allergy and Infectious Diseases (NIAID)
Surety & Preparedness Coordination Branch
5601 Fishers Lane RM 1G56B, Rockville, MD 20852
C: [redacted] (b) (4) E: [redacted] (b) (6)

Remote Work Address
[redacted] (b) (6)

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From: Bloom, Marshall (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Tuesday, April 14, 2020 8:47 AM
To: Vandalen, Kaci (NIH/NIAID) [E] [redacted] (b) (6)

Obtained via FOIA by Judicial Watch, Inc.

Subject: FW: WaPo: State Department cables warned of safety issues at Wuhan lab studying bat coronaviruses

Kaci,

Please send to the HCTF. Thanks!
Marshall

State Department cables warned of safety issues at Wuhan lab studying bat coronaviruses

A woman wearing a protective suit at a hospital in Wuhan, China. (Aly Song/Reuters)

By
Josh Rogin
Columnist
April 14, 2020 at 6:00 a.m. EDT

Two years before the novel coronavirus pandemic upended the world, U.S. Embassy officials visited a Chinese research facility in the city of Wuhan several times and sent two official warnings back to Washington about inadequate safety at the lab, which was conducting risky studies on coronaviruses from bats. The cables have fueled discussions inside the U.S. government about whether this or another Wuhan lab was the source of the virus — even though conclusive proof has yet to emerge.

In January 2018, the U.S. Embassy in Beijing took the unusual step of repeatedly sending U.S. science diplomats to the Wuhan Institute of Virology (WIV), which had in 2015 become China's first laboratory to achieve the highest level of international bioresearch safety (known as BSL-4). WIV issued a news release in English about the last of these visits, which occurred on March 27, 2018. The U.S. delegation was led by Jamison Fouss, the consul general in Wuhan, and Rick Switzer, the embassy's counselor of environment, science, technology and health. Last week, WIV erased that statement from its website, though it remains archived on the Internet.

What the U.S. officials learned during their visits concerned them so much that they dispatched two diplomatic cables categorized as Sensitive But Unclassified back to Washington. The cables warned about safety and management weaknesses at the WIV lab and proposed more attention and help. The first cable, which I obtained, also warns that the lab's work on bat coronaviruses and their potential human transmission represented a risk of a new SARS-like pandemic.

"During interactions with scientists at the WIV laboratory, they noted the new lab has a serious shortage of appropriately trained technicians and investigators needed to safely operate this high-containment laboratory," states the Jan. 19, 2018, cable, which was drafted by two officials from the embassy's environment, science and health sections who met with the WIV scientists. (The State Department declined to comment on this and other details of the story.)

The Chinese researchers at WIV were receiving assistance from the Galveston National Laboratory at the University of Texas Medical Branch and other U.S. organizations, but the Chinese requested additional help. The cables argued that the United States should give the Wuhan lab further support, mainly because its research on bat coronaviruses was important but also dangerous.

As the cable noted, the U.S. visitors met with Shi Zhengli, the head of the research project, who had been publishing studies related to bat coronaviruses for many years. In November 2017, just before the U.S. officials' visit, Shi's team had published research showing that horseshoe bats they had collected from a cave in Yunnan province were very likely from the same bat population that spawned the SARS coronavirus in 2003.

"Most importantly," the cable states, "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 diseases. 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."

The research was designed to prevent the next SARS-like pandemic by anticipating how it might emerge. But even in 2015, other scientists questioned whether Shi's team was taking unnecessary risks. In October 2014, the U.S. government had imposed a moratorium on funding of any research that makes a virus more deadly or contagious, known as "gain-of-function" experiments.

As many have pointed out, there is no evidence that the virus now plaguing the world was engineered; scientists largely agree it came from animals. But that is not the same as saying it didn't come from the lab, which spent years testing bat coronaviruses in animals, said Xiao

Obtained via FOIA by Judicial Watch, Inc.

Qiang, a research scientist at the School of Information at the University of California at Berkeley.

"The cable tells us that there have long been concerns about the possibility of the threat to public health that came from this lab's research, if it was not being adequately conducted and protected," he said.

There are similar concerns about the nearby Wuhan Center for Disease Control and Prevention lab, which operates at biosecurity level 2, a level significantly less secure than the level-4 standard claimed by the Wuhan Insititute of Virology lab, Xiao said. That's important because the Chinese government still refuses to answer basic questions about the origin of the novel coronavirus while suppressing any attempts to examine whether either lab was involved.

Sources familiar with the cables said they were meant to sound an alarm about the grave safety concerns at the WIV lab, especially regarding its work with bat coronaviruses. The embassy officials were calling for more U.S. attention to this lab and more support for it, to help it fix its problems.

"The cable was a warning shot," one U.S. official said. "They were begging people to pay attention to what was going on."

No extra assistance to the labs was provided by the U.S. government in response to these cables. The cables began to circulate again inside the administration over the past two months as officials debated whether the lab could be the origin of the pandemic and what the implications would be for the U.S. pandemic response and relations with China.

Inside the Trump administration, many national security officials have long suspected either the WIV or the Wuhan Center for Disease Control and Prevention lab was the source of the novel coronavirus outbreak. According to the New York Times, the intelligence community has provided no evidence to confirm this. But one senior administration official told me that the cables provide one more piece of evidence to support the possibility that the pandemic is the result of a lab accident in Wuhan.

"The idea that is was just a totally natural occurrence is circumstantial. The evidence it leaked from the lab is circumstantial. Right now, the ledger on the side of it leaking from the lab is packed with bullet points and there's almost nothing on the other side," the official said.

As my colleague David Ignatius noted, the Chinese government's original story — that the virus emerged from a seafood market in Wuhan — is shaky. Research by Chinese experts published in the Lancet in January showed the first known patient, identified on Dec. 1, had no connection to the market, nor did more than one-third of the cases in the first large cluster. Also, the market didn't sell bats.

Shi and other WIV researchers have categorically denied this lab was the origin for the novel coronavirus. On Feb. 3, her team was the first to publicly report the virus known as 2019-nCoV was a bat-derived coronavirus.

The Chinese government, meanwhile, has put a total lockdown on information related to the virus origins. Beijing has yet to provide U.S. experts with samples of the novel coronavirus

Obtained via FOIA by Judicial Watch, Inc.

collected from the earliest cases. The Shanghai lab that published the novel coronavirus genome on Jan. 11 was quickly shut down by authorities for "rectification." Several of the doctors and journalists who reported on the spread early on have disappeared.

On Feb. 14, Chinese President Xi Jinping called for a new biosecurity law to be accelerated. On Wednesday, CNN reported the Chinese government has placed severe restrictions requiring approval before any research institution publishes anything on the origin of the novel coronavirus.

The origin story is not just about blame. It's crucial to understanding how the novel coronavirus pandemic started because that informs how to prevent the next one. The Chinese government must be transparent and answer the questions about the Wuhan labs because they are vital to our scientific understanding of the virus, said Xiao.

We don't know whether the novel coronavirus originated in the Wuhan lab, but the cable pointed to the danger there and increases the impetus to find out, he said.

"I don't think it's a conspiracy theory. I think it's a legitimate question that needs to be investigated and answered," he said. "To understand exactly how this originated is critical knowledge for preventing this from happening in the future."

Josh Rogin is a columnist for the Global Opinions section of The Washington Post. He writes about foreign policy and national security. Rogin is also a political analyst for CNN. He previously worked for Bloomberg View, the Daily Beast, Foreign Policy, Congressional Quarterly, Federal Computer Week and Japan's Asahi Shimbun newspaper.

Obtained via FOIA by Judicial Watch, Inc.

From: Taubenberger, Jeffery (NIH/NIAID) [E]
Sent: Fri, 28 Feb 2020 17:41:44 +0000
To: Athota, Rani (NIH/NIAID) [C];Batchenkova, Natalia (NIH/NIAID) [F];Bean, Rachel (NIH/NIAID) [E];Cervantes-Medina, Adriana (NIH/NIAID) [C];Czajkowski, Lindsay (NIH/NIAID) [E];Fong, Sharon (NIH/NIAID) [E];Freeman, Ashley (NIH/NIAID) [C];Giurgea, Luca (NIH/NIAID) [E];Gouzoulis, Monica (NIH/NIAID) [C];Han, Alison (NIH/NIAID) [E];Kash, John (NIH/NIAID) [E];Matthews, Alexis (NIH/NIAID) [C];Memoli, Matthew (NIH/NIAID) [E];Morens, David (NIH/NIAID) [E];Park, Jaekeun (NIH/NIAID) [F];Qi, Li (NIH/NIAID) [E];Reed, Susan (NIH/NIAID) [C];Rosas, Luz Angela (NIH/NIAID) [E];Sheng, Zong-mei (NIH/NIAID) [E];Taubenberger, Jeffery (NIH/NIAID) [E];Williams, Stephanie (NIH/NIAID) [F];Xiao, Yongli (NIH/NIAID) [E]
Subject: FW: SCMP: Chinese laboratory that first shared coronavirus genome with world ordered to close for 'rectification', hindering its Covid-19 research

---

From: Folkers, Greg (NIH/NIAID) [E] (b) (6)
Sent: Friday, February 28, 2020 12:41 PM
Subject: SCMP: Chinese laboratory that first shared coronavirus genome with world ordered to close for 'rectification', hindering its Covid-19 research

Chinese laboratory that first shared coronavirus genome with world ordered to close for 'rectification', hindering its Covid-19 research

- No reason was given for the closure of Shanghai facility, which released information about the virus ahead of authorities
- One source at the laboratory said the closure has hampered scientists' research when they should be 'racing against the clock'

Zhuang Pinghui in Beijing
Published: 11:00pm, 28 Feb, 2020
Updated: 12:49am, 29 Feb, 2020

The genome sequence was released on open platforms for scientists. Photo: Handout

Obtained via FOIA by Judicial Watch, Inc.

The Shanghai laboratory where researchers published the world's first genome sequence of the deadly coronavirus that causes Covid-19 has been shut down.

The laboratory at the Shanghai Public Health Clinical Centre was ordered to close for "rectification" on January 12, a day after Professor Zhang Yongzhen's team published the genome sequence on open platforms. It closed temporarily the following day.

The release of the data helped researchers develop test kits for the virus.

"The centre was not given any specific reasons why the laboratory was closed for rectification. [We have submitted] four reports [asking for permission] to reopen but we have not received any replies," a source with the centre said, requesting anonymity because of the matter's sensitivity.

"The closure has greatly affected the scientists and their research when they should be racing against the clock to find the means to help put the novel coronavirus outbreak under control," the source said.

The laboratory is a Level 3 biosafety facility, the second highest level, and passed an annual inspection by the China National Accreditation Service for Conformity Assessment on January 5. It also obtained the required credentials to conduct research on the coronavirus on January 24.

It was not clear whether the closure was related to the publishing of the sequencing data before the authorities.

The closure order was issued by the Shanghai Health Commission. Five telephone calls to officials at the commission seeking comment on the closure were not picked up. A fax sent to the commission requesting comment was not answered.

China's National Health Commission announced hours after the release by Zhang's team that it would share the genome sequence with the World Health Organisation. It later emerged that the information had been sent through the officially designated Wuhan Institute of Virology.

Zhang's team isolated and finished the genome sequence of the then-unknown virus on January 5, two days before China's official announcement that mysterious pneumonia cases in Wuhan were caused by a hitherto unknown coronavirus.

The Shanghai centre reported its discovery to the National Health Commission on the same day and recommended "relevant prevention and control measures" be taken in public places, because the patient from whom the sample was collected had suffered very severe symptoms and the virus resembled a group previously found in bats.

The laboratory at the Shanghai Public Health Clinical Centre Shanghai was ordered to close a day after sharing the genome sequence. Photo: AFP

The team made the finding public on January 11 after it saw that the authorities had taken no obvious action to warn the public about the coronavirus.

At the time, the public was told that no new cases had been reported in Wuhan since January 3 and there was no clear evidence of human-to-human transmission.

"It was not about any individual's achievements. It's about having biological test kits ready in face of a previously unknown respiratory disease, especially when a large part of the population [was] moving [across the country] during the Lunar New Year holidays," said a source close to Zhang's team, who spoke on condition of anonymity.

It shared the data on virological.org, an open platform for discussions, and GenBank, an open-access data repository, and said researchers were welcome to download, share, use and analyse the data.

Within a week of its publication, several companies in China announced that they had developed diagnosis kits for the virus.

The findings by Zhang's team were published in the scientific journal *Nature* on February 3. The research said the virus sample was collected from a patient who showed symptoms of fever, dizziness and coughing and was admitted to a Wuhan hospital on December 26.

The Shanghai centre has a long-term cooperation relationship with Wuhan Central Hospital. The patient was identified as a 41-year-old male vendor who worked at the Huanan Wholesale Seafood Market in Wuhan, which was believed to be a key link of infections at the early stage of the outbreak.

The lab's closure not only affected Zhang's research but also studies by other scientists since it is an open facility, according to another researcher with knowledge of the matter.

"There have been applications from research institutes and universities to try drugs and compare the effects of different treatment and the development of vaccines, but [all these will have] to be turned down. Closing down the laboratory also affects the studying of the virus," the researcher said.

Zhuang Pinghui

Based in Beijing, Zhuang Pinghui joined the Post in 2004 to report on China. She covers a range of issues including policy, healthcare, culture and society.

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Obtained via FOIA by Judicial Watch, Inc.

From: Memoli, Matthew (NIH/NIAID) [E]
Sent: Tue, 14 Apr 2020 19:51:30 +0000
To: Xiao, Yongli (NIH/NIAID) [E];Taubenberger, Jeffery (NIH/NIAID) [E];Kash, John (NIH/NIAID) [E];Qi, Li (NIH/NIAID) [E];Gygli, Sebastian (NIH/NIAID) [F];Morens, David (NIH/NIAID) [E]
Subject: Re: WaPo: State Department cables warned of safety issues at Wuhan lab studying bat coronaviruses

[redacted] (b) (5)

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Matthew J. Memoli, M.D., M.S.
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From: Yongli Xiao [redacted] (b) (6)
Date: Tuesday, April 14, 2020 at 3:50 PM
To: Jeffery Taubenberger [redacted] (b) (6), John Kash [redacted] (b) (6), "Memoli, Matthew (NIH/NIAID) [E]" [redacted] (b) (6), "Qi, Li (NIH/NIAID) [E]" [redacted] (b) (6), "Gygli, Sebastian (NIH/NIAID) [F]" [redacted] (b) (6), David Morens [redacted] (b) (6)
Subject: Re: WaPo: State Department cables warned of safety issues at Wuhan lab studying bat coronaviruses

[redacted] (b) (5)

From: "Taubenberger, Jeffery (NIH/NIAID) [E]" [redacted] (b) (6)
Date: Tuesday, April 14, 2020 at 3:08 PM

To: "Kash, John (NIH/NIAID) [E]" [redacted] (b) (6), "Memoli, Matthew (NIH/NIAID) [E]" [redacted] (b) (6), "Qi, Li (NIH/NIAID) [E]" [redacted] (b) (6), "Xiao, Yongli (NIH/NIAID) [E]" [redacted] (b) (6), "Gygli, Sebastian (NIH/NIAID) [F]" [redacted] (b) (6), "Morens, David (NIH/NIAID) [E]" [redacted] (b) (6)
Subject: FW: WaPo: State Department cables warned of safety issues at Wuhan lab studying bat coronaviruses

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From: "Vandalen, Kaci (NIH/NIAID) [E]" [redacted] (b) (6)
Date: Tuesday, April 14, 2020 at 3:06 PM
To: NIAID HCTF <NIAIDHCTF@mail.nih.gov>
Subject: FW: WaPo: State Department cables warned of safety issues at Wuhan lab studying bat coronaviruses

Good afternoon,
Marshall asked that I distribute this to the HCTF. I hope everyone is staying safe and sane!

Kaci VanDalen | *Health Specialist (BioRisk)*
National Institutes of Health (NIH)
National Institute of Allergy and Infectious Diseases (NIAID)
Surety & Preparedness Coordination Branch
5601 Fishers Lane RM 1G56B, Rockville, MD 20852
C: [redacted] (b) (6) E: [redacted] (b) (6)

Remote Work Address
[redacted] (b) (6)

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From: Bloom, Marshall (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Tuesday, April 14, 2020 8:47 AM
To: Vandalen, Kaci (NIH/NIAID) [E] [redacted] (b) (6)
Subject: FW: WaPo: State Department cables warned of safety issues at Wuhan lab studying bat coronaviruses

Kaci,

Please send to the HCTF. Thanks!
Marshall

Obtained via FOIA by Judicial Watch, Inc.

State Department cables warned of safety issues at Wuhan lab studying bat coronaviruses

A woman wearing a protective suit at a hospital in Wuhan, China. (Aly Song/Reuters)

By

Josh Rogin

Columnist

April 14, 2020 at 6:00 a.m. EDT

Two years before the novel coronavirus pandemic upended the world, U.S. Embassy officials visited a Chinese research facility in the city of Wuhan several times and sent two official warnings back to Washington about inadequate safety at the lab, which was conducting risky studies on coronaviruses from bats. The cables have fueled discussions inside the U.S. government about whether this or another Wuhan lab was the source of the virus — even though conclusive proof has yet to emerge.

In January 2018, the U.S. Embassy in Beijing took the unusual step of repeatedly sending U.S. science diplomats to the Wuhan Institute of Virology (WIV), which had in 2015 become China's first laboratory to achieve the highest level of international bioresearch safety (known as BSL-4). WIV issued a news release in English about the last of these visits, which occurred on March 27, 2018. The U.S. delegation was led by Jamison Fouss, the consul general in Wuhan, and Rick Switzer, the embassy's counselor of environment, science, technology and health. Last week, WIV erased that statement from its website, though it remains archived on the Internet.

What the U.S. officials learned during their visits concerned them so much that they dispatched two diplomatic cables categorized as Sensitive But Unclassified back to Washington. The cables

Obtained via FOIA by Judicial Watch, Inc.

warned about safety and management weaknesses at the WIV lab and proposed more attention and help. The first cable, which I obtained, also warns that the lab's work on bat coronaviruses and their potential human transmission represented a risk of a new SARS-like pandemic.

"During interactions with scientists at the WIV laboratory, they noted the new lab has a serious shortage of appropriately trained technicians and investigators needed to safely operate this high-containment laboratory," states the Jan. 19, 2018, cable, which was drafted by two officials from the embassy's environment, science and health sections who met with the WIV scientists. (The State Department declined to comment on this and other details of the story.)

The Chinese researchers at WIV were receiving assistance from the Galveston National Laboratory at the University of Texas Medical Branch and other U.S. organizations, but the Chinese requested additional help. The cables argued that the United States should give the Wuhan lab further support, mainly because its research on bat coronaviruses was important but also dangerous.

As the cable noted, the U.S. visitors met with Shi Zhengli, the head of the research project, who had been publishing studies related to bat coronaviruses for many years. In November 2017, just before the U.S. officials' visit, Shi's team had published research showing that horseshoe bats they had collected from a cave in Yunnan province were very likely from the same bat population that spawned the SARS coronavirus in 2003.

"Most importantly," the cable states, "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 diseases. 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."

The research was designed to prevent the next SARS-like pandemic by anticipating how it might emerge. But even in 2015, other scientists questioned whether Shi's team was taking unnecessary risks. In October 2014, the U.S. government had imposed a moratorium on funding of any research that makes a virus more deadly or contagious, known as "gain-of-function" experiments.

As many have pointed out, there is no evidence that the virus now plaguing the world was engineered; scientists largely agree it came from animals. But that is not the same as saying it didn't come from the lab, which spent years testing bat coronaviruses in animals, said Xiao Qiang, a research scientist at the School of Information at the University of California at Berkeley.

"The cable tells us that there have long been concerns about the possibility of the threat to public health that came from this lab's research, if it was not being adequately conducted and protected," he said.

There are similar concerns about the nearby Wuhan Center for Disease Control and Prevention lab, which operates at biosecurity level 2, a level significantly less secure than the level-4 standard claimed by the Wuhan Insititute of Virology lab, Xiao said. That's important because the Chinese government still refuses to answer basic questions about the origin of the novel coronavirus while suppressing any attempts to examine whether either lab was involved.

Sources familiar with the cables said they were meant to sound an alarm about the grave safety concerns at the WIV lab, especially regarding its work with bat coronaviruses. The embassy officials were calling for more U.S. attention to this lab and more support for it, to help it fix its problems.

“The cable was a warning shot,” one U.S. official said. “They were begging people to pay attention to what was going on.”

No extra assistance to the labs was provided by the U.S. government in response to these cables. The cables began to circulate again inside the administration over the past two months as officials debated whether the lab could be the origin of the pandemic and what the implications would be for the U.S. pandemic response and relations with China.

Inside the Trump administration, many national security officials have long suspected either the WIV or the Wuhan Center for Disease Control and Prevention lab was the source of the novel coronavirus outbreak. According to the New York Times, the intelligence community has provided no evidence to confirm this. But one senior administration official told me that the cables provide one more piece of evidence to support the possibility that the pandemic is the result of a lab accident in Wuhan.

“The idea that is was just a totally natural occurrence is circumstantial. The evidence it leaked from the lab is circumstantial. Right now, the ledger on the side of it leaking from the lab is packed with bullet points and there’s almost nothing on the other side,” the official said.

As my colleague David Ignatius noted, the Chinese government’s original story — that the virus emerged from a seafood market in Wuhan — is shaky. Research by Chinese experts published in the Lancet in January showed the first known patient, identified on Dec. 1, had no connection to the market, nor did more than one-third of the cases in the first large cluster. Also, the market didn’t sell bats.

Shi and other WIV researchers have categorically denied this lab was the origin for the novel coronavirus. On Feb. 3, her team was the first to publicly report the virus known as 2019-nCoV was a bat-derived coronavirus.

The Chinese government, meanwhile, has put a total lockdown on information related to the virus origins. Beijing has yet to provide U.S. experts with samples of the novel coronavirus collected from the earliest cases. The Shanghai lab that published the novel coronavirus genome on Jan. 11 was quickly shut down by authorities for “rectification.” Several of the doctors and journalists who reported on the spread early on have disappeared.

On Feb. 14, Chinese President Xi Jinping called for a new biosecurity law to be accelerated. On Wednesday, CNN reported the Chinese government has placed severe restrictions requiring approval before any research institution publishes anything on the origin of the novel coronavirus.

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The origin story is not just about blame. It's crucial to understanding how the novel coronavirus pandemic started because that informs how to prevent the next one. The Chinese government must be transparent and answer the questions about the Wuhan labs because they are vital to our scientific understanding of the virus, said Xiao.

We don't know whether the novel coronavirus originated in the Wuhan lab, but the cable pointed to the danger there and increases the impetus to find out, he said.

"I don't think it's a conspiracy theory. I think it's a legitimate question that needs to be investigated and answered," he said. "To understand exactly how this originated is critical knowledge for preventing this from happening in the future."

Josh Rogin is a columnist for the Global Opinions section of The Washington Post. He writes about foreign policy and national security. Rogin is also a political analyst for CNN. He previously worked for Bloomberg View, the Daily Beast, Foreign Policy, Congressional Quarterly, Federal Computer Week and Japan's Asahi Shimbun newspaper.

Obtained via FOIA by Judicial Watch, Inc.

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sun, 1 Oct 2017 20:15:27 +0000
To: Folkers, Greg (NIH/NIAID) [E]
Subject: FW: Confidential - A new bat-origin coronavirus emerging in pigs in China discovered under our NIAID R01
Attachments: Nature 2017-05-06890-main text with figures and tables.pdf
Importance: High

Confidential, but FYI for you

From: Peter Daszak [mailto:daszak@ecohealthalliance.org]
Sent: Sunday, October 01, 2017 1:22 PM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Cc: Morens, David (NIH/NIAID) [E] (b) (6); David Morens (b) (6) (b) (6); Kurilla, Michael (NIH/NIAID) [E] (b) (6); (b) (6); Stemmy, Erik (NIH/NIAID) [E] (b) (6); Alison Andre <andre@ecohealthalliance.org>; Aleksei Chmura <chmura@ecohealthalliance.org>
Subject: Confidential - A new bat-origin coronavirus emerging in pigs in China discovered under our NIAID R01
Importance: High

Dear Dr Fauci and NIAID colleagues,

It was a pleasure to meet you again today. I've attached an unpublished paper, currently in the second round of review with *Nature* that describes a novel bat-origin Coronavirus (SADS-CoV: Swine Acute Diarrheal Syndrome coronavirus) that recently spilled over into pig farms in Southern China, leading to the death of over 25,000 piglets in 5+ farms in Guandong Province.

The virus originates in the same group of bats as SARS-CoV, and emerged in the same place. It's not known to be zoonotic (we've tested 35+ pig farm workers with an antibody assay and none are positive. The pig farm owners tell us the virus is now under control, thanks to culling and separation of infected herds. It's not yet known if this virus has appeared elsewhere, but we are looking. We're also doing assays to find out if it can infect human cells in the lab – so far no evidence of this.

I hope this paper is of interest. You should know that this work was supported by a NIAID R01 that Erik Stemmy is the Program Officer for, and that I'm PI on, with Zhengli Shi as co-PI.

If you want any other information at all, please don't hesitate to email or call and I'd be happy to come over to NIAID to brief you further. I'll also let you know if/when it will be published so that we can try to foster some publicity as appropriate.

Cheers,

Obtained via FOIA by Judicial Watch, Inc.

Peter

Peter Daszak
President

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

Tel. +1 212-380-4473
www.ecohealthalliance.org

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

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Obtained via FOIA by Judicial Watch, Inc.

(b) (4)

[redacted]

Obtained via FOIA by Judicial Watch, Inc.

From: Conrad, Patricia (NIH/NIAID) [E]
Sent: Fri, 1 Nov 2013 08:16:50 -0400
To: Folkers, Greg (NIH/NIAID) [E]
Subject: RE: Virologica Sinica: Bats as animal reservoirs for the #SARS coronavirus: hypothesis proved after 10 years of virus hunting http://bit.ly/1cu0V4R

I think we need more slides like this…its too cute!

Patricia L. Conrad
Special Assistant to the DIrector

From: Folkers, Greg (NIH/NIAID) [E]
Sent: Friday, November 01, 2013 7:43 AM
Subject: Virologica Sinica: Bats as animal reservoirs for the #SARS coronavirus: hypothesis proved after 10 years of virus hunting http://bit.ly/1cu0V4R

Virologica Sinica
October 2013

Bats as animal reservoirs for the SARS coronavirus: hypothesis proved after 10 years of virus hunting

- Manli Wang,
- Zhihong Hu

Download PDF (347 KB)

Abstract

Recently, the team led by Dr. Zhengli Shi from Wuhan Institute of Virology, Chinese Academy of Sciences, and Dr. Peter Daszak from Ecohealth Alliance identified SL-CoVs in Chinese horseshoe bats that were 95% identical to human SARS-CoV and were able to use human angiotensin-converting enzyme 2 (ACE2) receptor for docking and entry. Remarkably, they isolated the first known live bat SL-CoV that replicates in human and related cells. Their findings provide clear evidence that some SL-CoVs circulating in bats are capable of infecting and replicating in human (Ge X Y, et al., 2013).

Obtained via FOIA by Judicial Watch, Inc.

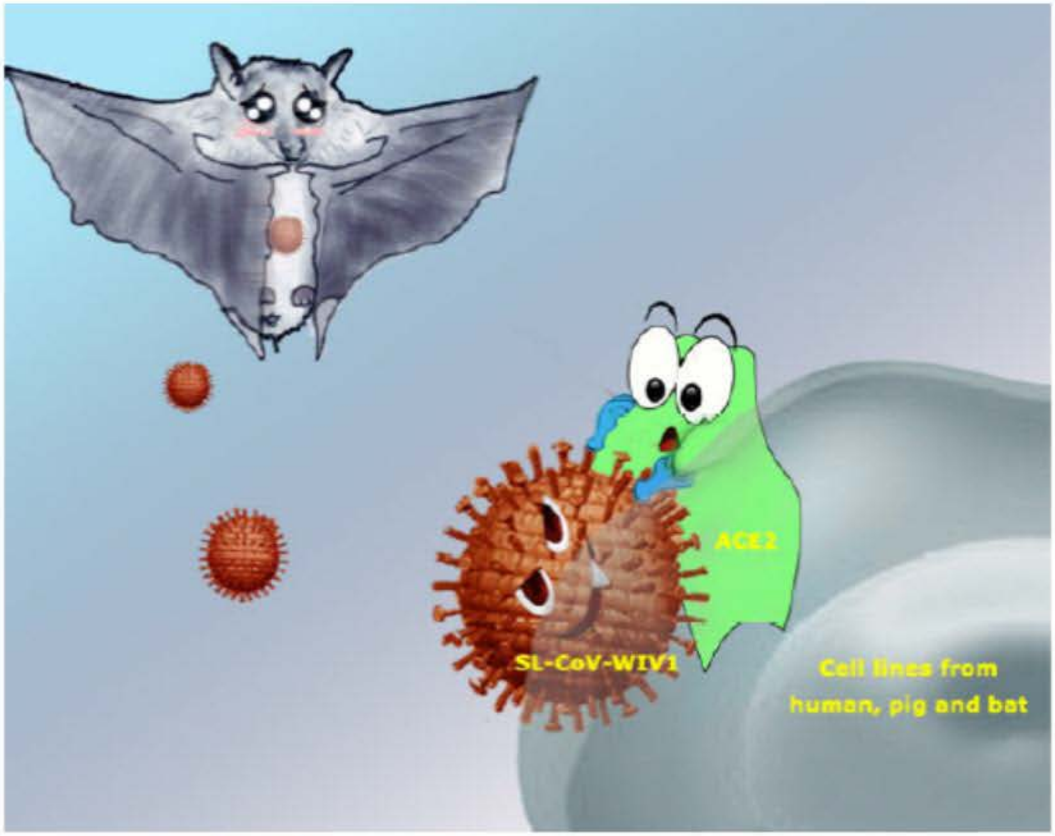

Fig. 1 Bat SL-CoV-WIV1 uses ACE2 to directly infect human cells.

A newly isolated wild-type bat SL-CoV-WIV1 is found to use ACE2 as a cellular entry receptor and replicate in human alveolar basal epithelial cells (A549), pig kidney-15 cells (PK15) and Chinese horseshoe bat kidney cells (RSKT). (Figure provided by Meng Wang, Wuhan Institute of Virology.)

From: Folkers, Greg (NIH/NIAID) [E]
Sent: Tue, 3 Nov 2015 18:02:02 +0000
To: Doepel, Laurie (NIH/NIAID) [E]
Subject: RE: Forthcoming Nature Medicine paper

Thanks
Looks interesting

From: Doepel, Laurie (NIH/NIAID) [E]
Sent: Tuesday, November 03, 2015 12:56 PM
To: Folkers, Greg (NIH/NIAID) [E] (b) (6)
Subject: FW: Forthcoming Nature Medicine paper

Not sure if you are in this long list, but in case not, just fyi

---

From: Barnstone, David [mailto:David.Barnstone@us.nature.com]
Sent: Monday, November 02, 2015 6:30 PM
To: endeavors@unc.edu; katie_obrien@med.unc.edu; spurrk@email.unc.edu; Mark.Derewicz@unch.unc.edu; bulletin@mail.casipm.ac.cn; david_cameron@hms.harvard.edu; (b) (6); Jake_Miller@hms.harvard.edu; susan_karcz@hms.harvard.edu; Elizabeth_Cooney@hms.harvard.edu; stephanie_dutchen@hms.harvard.edu; Stover, Kathy (NIH/NIAID) [E] (b) (6); Hoffman, Hillary (NIH/NIAID) [E] (b) (6); Huynh, Linda (NIH/NICHD) [E] (b) (6); Routh, Jennifer (NIH/NIAID) [E] (b) (6); Doepel, Laurie (NIH/NIAID) [E] (b) (6); Pekoc, Ken (NIH/NIAID) [E] (b) (6); Leifman, Laura Sivitz (NIH/NIAID) [E] (b) (6); NIAID NEWS (NIH/NIAID) (b) (6); Oplinger, Anne (NIH/NIAID) [E] (b) (6); Rancourt, Anne (NIH/NIAID) [E] (b) (6); NIAINFO (NIH/NIA) <niainfo@mail.nih.gov>; Cahan, Vicky (NIH/NIA) [E] (b) (6); Vaughn, Margaret (NIH/NIA/ERP) [E] (b) (6); Burklow, John (NIH/OD) [E] (b) (6); Myles, Renate (NIH/OD) [E] (b) (6); Fine, Amanda (NIH/OD) [E] (b) (6); Fritz, Craig (NIH/OD) [E] (b) (6); Jackson, Calvin (NIH/OD) [E] (b) (6); (b) (6); Harris, Mary (NIH/NIDDK) [E] (b) (6)
Subject: Forthcoming Nature Medicine paper

Dear Colleague,

I am writing to inform you that **'SARS-like cluster of circulating bat coronaviruses pose threat for human emergence' has been scheduled for Advance Online Publication (AOP) on *Nature Medicine*'s website at 1600 London time / 1100 US Eastern Time on 09 November 2015**. If you wish to see the paper, the author(s) should be able to provide you with a copy, and also to confirm that this title (taken from an early proof of the paper) remains unaltered.

You are receiving this letter because one or more of the authors are affiliated to your institution and/or because your organization provided funding for the research.

Obtained via FOIA by Judicial Watch, Inc.

The full listing of authors and their affiliations for this paper is as follows:

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[9]Department of Medicine, Harvard Medical School, Boston, Massachusetts, USA

The following funding acknowledgements from the authors appear at the end of the paper:

Research in this manuscript was supported by grants from the National Institute of Allergy & Infectious Disease and the National Institute of Aging of the US National Institutes of Health (NIH) under awards U19AI109761 (R.S.B.), U19AI107810 (R.S.B.), AI085524 (W.A.M.), F32AI102561 (V.D.M.) and K99AG049092 (V.D.M.), and by the National Natural Science Foundation of China awards 81290341 (Z.-L.S.) and 31470260 (X.-Y.G.). Human airway epithelial cultures were supported by the National Institute of Diabetes and Digestive and Kidney Disease of the NIH under award NIH DK065988 (S.H.R.).

The introduction of regular AOP means that selected papers will be subedited and formatted and then published online as soon as they are ready. Papers published online before they have been allocated to a print issue will be citable via a digital object identifier (DOI) number. The DOI for the above paper will be **10.1038/nm.3985**. Once the paper is published electronically, the DOI can be used to retrieve the abstract and full text from the *Nature* website by adding it to the following url: http://dx.doi.org/. Embargos for papers published in this way will lift at the time of electronic publication.

Every Tuesday, the Nature research journals distribute a press release of papers to be published AOP the following Monday. Within this release, a few papers of particular newsworthiness are highlighted with author contact details, and the rest are listed. Journalists are given the name of the author(s) to contact, together with phone numbers and e-mail addresses. At this time, journalists are also given online access not only to the papers on the press release, but to all the papers due to appear, plus any supplementary

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materials, such as images or videos, so they can follow up stories of interest. The authors for all papers are indexed geographically so journalists can report on research from their own region.

We would be delighted to cooperate with you in ensuring maximum publicity for this paper. You may send out an embargoed press release to trusted contacts from Tuesday (six days before publication).

Please do not post to third-party internet journalist resource sites (such as EurekAlert or AlphaGalileo) until 96 hours before publication.

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Yours sincerely,
David Barnstone
Press Officer, *Nature*

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From: Folkers, Greg (NIH/NIAID) [E]
Sent: Mon, 27 Jan 2020 23:24:58 +0000
To: Routh, Jennifer (NIH/NIAID) [E];Fauci, Anthony (NIH/NIAID) [E]
Cc: Billet, Courtney (NIH/NIAID) [E];Stover, Kathy (NIH/NIAID) [E];Conrad, Patricia (NIH/NIAID) [E];Marston, Hilary (NIH/NIAID) [E];Lerner, Andrea (NIH/NIAID) [E]
Subject: RE: For review (due to HHS for White House by 8:30 tonight): press conference talking points
Attachments: Talking Points for NIAID Director Dr. Fauci.docx

As a place folder looks good to me.
+ Andrea who is the lead on a CoV talk ASF is giving on Tuesday

Also --- when talking about CoV (not necessarily in this venue) we have on our team (Vincent and folks we fund, Peter Daszak, Ralph Baric, Ian Lipkin, etc.) probably the world's experts non-human coronaviruses.

From David M -- EcoHealth group (Peter Daszak et al), has for years been among the biggest players in coronavirus work, also in collaboration with Ralph Baric, Ian Lipkin and others.

NIAID has funded Peter's group for coronavirus work in China for the past 5 years through R01 1R01AI110964: "Understanding the Risk of Bat Coronavirus Emergence". That's now been renewed, with a specific focus to identify cohorts of people highly exposed to bats in China, and work out if they're getting sick from CoVs. Erik Stemmy is the Program Officer. Collaborators include Wuhan Institute of Virology (currently working on the nCoV), and Ralph Baric. The results of the work to date include:

(b) (5)
[redacted]

- Discovered Swine Acute Diarrheal Syndrome Virus (SADS-CoV) killing >25,000 pigs in Guangdong Province (Published in *Nature*)
- Found SARS-related CoVs that can bind to human cells (Published in *Nature*), and that cause SARS-like disease in humanized mouse models.

(b) (5)
[redacted]

Also – prior to the above R01, Peter's folks worked under an R01 with Eun-Chung Park as Program Officer on viral discovery in bats, and originally identified SARS-CoV as having a likely origin in bats (published in *Science*)

From: Routh, Jennifer (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Monday, January 27, 2020 6:14 PM
To: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Billet, Courtney (NIH/NIAID) [E] [redacted] (b) (6); Stover, Kathy (NIH/NIAID) [E] [redacted] (b) (6); Folkers, Greg (NIH/NIAID) [E] [redacted] (b) (6); Conrad, Patricia (NIH/NIAID) [E] [redacted] (b) (6); Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6)
Subject: For review (due to HHS for White House by 8:30 tonight): press conference talking points

Dr. Fauci –

You will be making brief remarks at the HHS press conference tomorrow. HHS has requested your talking points by 8:30 tonight. (They are really just a placeholder for the White House to have something and so they are not surprised by any news). I have attached proposed points and pasted them below.

Please let me know if you have edits. I will send the final version to HHS tonight.

Thanks,
Jen

Talking Points for NIAID Director Anthony S. Fauci, M.D.
HHS Press Conference on Coordinated Public Health Response to 2019 Novel Coronavirus

(b) (5)
[redacted]

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[redacted] (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: [redacted] (b) (6)
[redacted] (b) (6)

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Talking Points for NIAID Director Anthony S. Fauci, M.D.

HHS Press Conference on Coordinated Public Health Response to 2019 Novel Coronavirus

(b) (5)

[redacted]

From: Handley, Gray (NIH/NIAID) [E]
Sent: Tue, 10 Mar 2020 02:54:57 +0000
To: Chen, Ping (NIH/NIAID) [E]
Subject: FW: China sample sharing

Ping, can we have a conversation about this in the morning sometime? Thanks. Gray

---

From: Chandrasekera, Ruvani (OS/ASPR/SPPR) [redacted] (b) (6)
Sent: Monday, March 9, 2020 8:26 PM
To: Handley, Gray (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6)
Subject: RE: China sample sharing

[redacted] (b) (5)

Ruvani

Ruvani Chandrasekera

HHS/ASPR/ International Policy
Office: [redacted] (b) (6) | Cell: [redacted] (b) (6)

From: Handley, Gray (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Monday, March 9, 2020 4:20 PM
To: Chandrasekera, Ruvani (OS/ASPR/SPPR) [redacted] (b) (6)
Cc: Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6)
Subject: RE: China sample sharing

Ruvani, [redacted] (b) (5)

[redacted] Gray

From: Chandrasekera, Ruvani (OS/ASPR/SPPR) [redacted] (b) (6)
Sent: Monday, March 9, 2020 2:48 PM
To: Handley, Gray (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6)
Subject: RE: China sample sharing

Good afternoon Dr. Handley,
It was nice to meet you in person today. [redacted] (b) (5)
[redacted] (b) (5)

What are your thoughts on this?
Ruvani

Ruvani Chandrasekera
HHS/ASPR/ International Policy
Office: [redacted] (b) (6) | Cell: [redacted] (b) (6)

-----Original Appointment-----
From: [redacted] (b) (6)
Sent: Thursday, March 5, 2020 10:12 AM
To: [redacted] (b) (6); Chandrasekera, Ruvani (OS/ASPR/SPPR)
Subject: FW: China sample sharing
When: Monday, March 9, 2020 9:00 AM-10:00 AM (UTC-05:00) Eastern Time (US & Canada).
Where: SA-22, 1800 G St NW, suite [redacted] (b) (6)

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-----Original Appointment-----
From: (b) (6)
Sent: Thursday, March 5, 2020 8:53 AM
To: (b) (6); Handley, Gray (NIH/NIAID) [E]; Black, Jodi (NIH/OD) [E]; Koo, Han (OS/OGA) (CTR); Seedorff, Jennifer E; Lucera, Mark B; Frisk, Megan L; MacDonald, David L; Warner, (b) (6) (b) (6); (b) (6); Gulati, Neetu; Elvander, Erika (OS/OGA); Stewart, Jessica L. (HHS/OS/OGA)
Cc: Williams, Nekisha (NIH/NIAID) [C]; Adomako, Melissa (NIH/NIAID) [C]
Subject: China sample sharing
When: Monday, March 9, 2020 9:00 AM-10:00 AM (UTC-05:00) Eastern Time (US & Canada).
Where: SA-22, 1800 G St NW, suite (b) (6)

We are located at SA-22, 1800 G St NW, suite (b) (6). Please bring a valid form of government issued ID as you will need to go through security. Please call (b) (6) if you have any issues when arriving to the building.

Lucia

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From:	Handley, Gray (NIH/NIAID) [E]
Sent:	Wed, 11 Mar 2020 13:36:48 +0000
To:	Chen, Ping (NIH/NIAID) [E]
Subject:	FW: 18-WUHAN-38.eml (002).pdf
Attachments:	18-WUHAN-38.eml (002).pdf

[redacted] (b) (5)

Thanks. G

From: Sizemore, Christine (NIH/FIC) [E] [redacted] (b) (6)
Sent: Tuesday, March 10, 2020 4:58 PM
To: Dominique, Joyelle (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Handley, Gray (NIH/NIAID) [E] [redacted] (b) (6)
Subject: 18-WUHAN-38.eml (002).pdf

Hi Joyelle, you have seen that cable, right?
C

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SBU

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). [redacted] (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] (b) (6) 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)

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(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), 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) (6), recently planned to visit Wuhan to meet with (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

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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.

Signature: FOUSS

(b) (6)

Drafted By: [redacted]
Cleared By:

Approved By:
Released By:
Info:

Dissemination Rule: Archive Copy

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From: Chen, Ping (NIH/NIAID) [E]
Sent: Tue, 10 Mar 2020 04:15:32 +0000
To: Handley, Gray (NIH/NIAID) [E]
Subject: Re: China sample sharing
Attachments: image001.png

Sure. I usually get in around 9 am.

Sent from my iPhone

On Mar 9, 2020, at 10:55 PM, Handley, Gray (NIH/NIAID) [E] [redacted] (b) (6) wrote:

Ping, can we have a conversation about this in the morning sometime? Thanks. Gray

---

From: Chandrasekera, Ruvani (OS/ASPR/SPPR) [redacted] (b) (6)
Sent: Monday, March 9, 2020 8:26 PM
To: Handley, Gray (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6)
Subject: RE: China sample sharing

[redacted] (b) (5)

Ruvani

Ruvani Chandrasekera

HHS/ASPR/ International Policy
Office: [redacted] (b) (6) | Cell: [redacted] (b) (6)

From: Handley, Gray (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Monday, March 9, 2020 4:20 PM
To: Chandrasekera, Ruvani (OS/ASPR/SPPR) [redacted] (b) (6)
Cc: Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6)
Subject: RE: China sample sharing

Ruvani, [redacted] (b) (5)

[redacted] Gray

From: Chandrasekera, Ruvani (OS/ASPR/SPPR) [redacted] (b) (6)
Sent: Monday, March 9, 2020 2:48 PM
To: Handley, Gray (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Marston, Hilary (NIH/NIAID) [E] [redacted] (b) (6)
Subject: RE: China sample sharing

Good afternoon Dr. Handley,
It was nice to meet you in person today. [redacted] (b) (5)

[redacted] (b) (5)

What are your thoughts on this?
Ruvani

Ruvani Chandrasekera
HHS/ASPR/ International Policy
Office: [redacted] (b) (6) | Cell: [redacted] (b) (6)

-----Original Appointment-----
From: [redacted] (b) (6)
Sent: Thursday, March 5, 2020 10:12 AM
To: [redacted] (b) (6); Chandrasekera, Ruvani (OS/ASPR/SPPR)
Subject: FW: China sample sharing
When: Monday, March 9, 2020 9:00 AM-10:00 AM (UTC-05:00) Eastern Time (US & Canada).
Where: SA-22, 1800 G St NW, suite [redacted] (b) (6)

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-----Original Appointment-----
From: [redacted] (b) (6)
Sent: Thursday, March 5, 2020 8:53 AM
To: Hebbeler, Andrew M; Handley, Gray (NIH/NIAID) [E]; Black, Jodi (NIH/OD) [E]; Koo, Han (OS/OGA) (CTR); Seedorff, Jennifer E; Lucera, Mark B; Frisk, Megan L; MacDonald, David L; [redacted] (b) (6) [redacted] (b) (6); [redacted] (b) (6); Gulati, Neetu; Elvander, Erika (OS/OGA); Stewart, Jessica L. (HHS/OS/OGA)
Cc: Williams, Nekisha (NIH/NIAID) [C]; Adomako, Melissa (NIH/NIAID) [C]
Subject: China sample sharing
When: Monday, March 9, 2020 9:00 AM-10:00 AM (UTC-05:00) Eastern Time (US & Canada).
Where: SA-22, 1800 G St NW, suite [redacted] (b) (6)

We are located at SA-22, 1800 G St NW, suite [redacted] (b) (6) Please bring a valid form of government issued ID as you will need to go through security. Please call [redacted] (b) (6) if you have any issues when arriving to the building.

Lucia

[redacted] (b) (5)

(b) (5)

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[redacted]

Obtained via FOIA by Judicial Watch, Inc.

From: Chen, Ping (NIH/NIAID) [E]
Sent: Wed, 11 Mar 2020 14:00:43 +0000
To: Handley, Gray (NIH/NIAID) [E]
Subject: Re: 18-WUHAN-38.eml (002).pdf

Gray,

[redacted] (b) (5)

Hope this is helpful.

Ping

From: "Handley, Gray (NIH/NIAID) [E]" [redacted] (b) (6)
Date: Wednesday, March 11, 2020 at 9:36 AM
To: "Chen, Ping (NIH/NIAID) [E]" [redacted] (b) (6)
Subject: FW: 18-WUHAN-38.eml (002).pdf

[redacted] (b) (5)

Obtained via FOIA by Judicial Watch, Inc.

[redacted] (b) (5)

Thanks. G

From: Sizemore, Christine (NIH/FIC) [E] [redacted] (b) (6)
Sent: Tuesday, March 10, 2020 4:58 PM
To: Dominique, Joyelle (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Handley, Gray (NIH/NIAID) [E] [redacted] (b) (6)
Subject: 18-WUHAN-38.eml (002).pdf

Hi Joyelle, you have seen that cable, right?
C

Obtained via FOIA by Judicial Watch, Inc.

From: Touchette, Nancy (NIH/NIAID) [E]
Sent: Wed, 15 Apr 2020 01:00:21 +0000
To: Handley, Gray (NIH/NIAID) [E];Marston, Hilary (NIH/NIAID) [E];Higgs, Elizabeth (NIH/NIAID) [E];Bushar, Nicholas (NIH/NIAID) [E];NIAID OGR CORE;Siddiqui, Sophia (NIH/NIAID) [E];Aboulhab, Jamila (NIH/NIAID) [E];Juompan, Laure (NIH/NIAID) [E];Reynolds, Steven (NIH/NIAID) [E];Babu, Subbaraman (NIH) [E];Chopra, Nandita (NIH/NIAID) [E];Kagan, Jonathan M. (NIH/NIAID) [E];Ossorio Goldman, Margarita (NIH/NIAID) [E];Taylor, Robert (NIH/NIAID) [C];Chen, Ping (NIH/NIAID) [E];NIAID BUGS
Subject: 4-14-2020 COVID-19 Daily Update
Attachments: April 14 2020 COVID-19 update FINAL.docx

COVID-19 Daily News Summary
Office of Global Research
April 14, 2020; Current as of 4:00 p.m., EST

Compiled by Nancy Touchette

The information in this summary, which is compiled from publicly sourced information, is for internal USG use only. The information in this report does not reflect the opinions of the National Institute of Allergy and Infectious Diseases (NIAID). NIAID shall not accept liability for any statements made that are the sender's own and not expressly made on behalf of the NIAID by one of its representatives.

WHO Situation Report (compiled daily): April 14

- ***1,844,863 confirmed cases globally (71,779 new)***
- ***117,021 deaths globally (5,369 new)***

U.S. CDC Update:

- ***Total U.S. Cases: 579,005***
- ***Total U.S. deaths: 22,252***

Johns Hopkins Coronavirus Resource Center

- **Globally**
  - ***1,956,077 confirmed cases***
  - ***125,123 deaths***
  - ***471,469 cases recovered***
- **United States**
  - ***572,689 confirmed cases***
  - ***23,134 deaths***
  - ***43,482 cases recovered***

RESEARCH NEWS

Epidemiology/modeling

- NIAID-supported scientists have developed a SARS-CoV-2 transmission model that predicts recurrent wintertime outbreaks of SARS-CoV-2 after the initial, most severe pandemic wave. Prolonged or intermittent social distancing may be necessary into 2022, according to findings published in the

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April 14, 2020 issue of *Science*. Even if the virus is eliminated, SARS-CoV-2 surveillance should be maintained since a resurgence in contagion could be possible as late as 2024, according to authors. (*Science*, April 14, 2020; DOI: 10.1126/science.abb5793).

Clinical

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- Researchers collected data from 181 patients with SARS-CoV-2 pneumonia and requiring oxygen in four French hospitals to emulate a target trial aimed at assessing the effectiveness of hydroxychloroquine (HCQ) at 600 mg/day. 84 patients received HCQ within 48 hours of admission (HCQ group) and 97 did not (no-HCQ group). 20.2% patients in the HCQ group were transferred to the ICU or died within 7 days vs 22.1% in the no-HCQ. In the HCQ group, 2.8% of the patients died within 7 days vs 4.6% in the no-HCQ group and 27.4% vs. 24.1%, respectively, developed acute respiratory distress syndrome within 7 days. Eight patients receiving HCQ (9.5%) experienced electrocardiogram modifications requiring HCQ discontinuation. The researchers state that the results do not support the use of HCQ in patients hospitalized for SARS-CoV-2-positive hypoxic pneumonia (*medRxiv* https://doi.org/10.1101/2020.04.10.20060699)
- Researchers in China conducted a multicenter, open-label, randomized hydroxychloroquine (HCQ) controlled trial involving 150 patients hospitalized with COVID-19 at 16 treatment centers in China. 75 patients were assigned to HCQ plus standard of care (SOC) and 75 were assigned to SOC alone (control group). HCQ was administered with a loading dose of 1,200 mg daily for three days followed by a maintained dose of 800 mg daily for the remaining 2 or 3 weeks for mild/moderate or severe patients, respectively. The researchers conclude that HCQ did not result in a higher negative conversion rate but did result in a greater alleviation of clinical symptoms compared to patients receiving no drug. Adverse events were significantly increased in HCQ recipients but there was no apparent increase of serious adverse events. (*medRxiv;* https://doi.org/10.1101/2020.04.10.20060558)

Treatments

- HHS's Biomedical Advanced Research and Development Authority (BARDA) is providing support to several non-government organizations to develop convalescent plasma and hyperimmune globulin immunotherapies from COVID-19 survivors:
    - The American Red Cross will collect, store, and distribute convalescent plasma donated by COVID-19 survivors.
    - Emergent Biosolutions will develop and manufacture COVID-19 hyperimmune globulin (COVID-HIG) and work with NIAID to include the COVID-HIG in future clinical trials.
    - Grifols will collect plasma through a network of more than 250 U.S. plasma donor centers to manufacture COVID-19 convalescent plasma and hyperimmune globulin.
    - SAb Biotherapeutics will develop SAB-185, an immunotherapy that relies on a platform technology to produce human antibodies without donated blood; BARDA may support a Phase 1 trial. (HHS, April 14, 2020).

Obtained via FOIA by Judicial Watch, Inc.

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Vaccines

- NIAID has begun enrolling subjects to receive the highest dose of the mRNA-1273 vaccine, developed by NIAID and Moderna. The Phase I study, led by NIAID, has three arms that are administering doses of 25 mcg, 100 mcg and 250 mcg. NIAID began dosing the first patients on March 16. (Fierce Biotech, April 14, 2020).
- Sanofi and GSK announced April 14 an agreement to collaborate on developing an adjuvanted COVID-19 vaccine. Sanofi will contribute its recombinant SARS-CoV-2 protein antigen in a baculovirus expression platform. GSK will contribute its pandemic adjuvant, which could reduce the amount of vaccine required per dose. The companies plan to initiate Phase I clinical trials in the second half of 2020. (GSK, Sanofi, April 14, 2020).
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- The SARS-CoV-2 spike (S) protein mediates entry of SARS-CoV-2 into cells expressing the angiotensin-converting enzyme 2 (ACE2) through its receptor-binding domain (RBD). Antibodies to the RBD domain of SARS-CoV which emerged in 2002-2003, potently neutralize SARS-CoV S-protein-mediated entry, and the presence of anti-RBD antibodies correlates with neutralization in SARS-CoV-2 convalescent sera. Researchers at Scripps and their collaborators show that immunization with the SARS-CoV-2 S-protein receptor binding protein (RBD) elicits a robust neutralizing antibody response in rodents. Importantly, anti-sera from immunized animals did not mediate antibody-dependent enhancement (ADE) of S-protein-mediated entry under conditions in which Zika virus ADE was readily observed. These data suggest that an RBD-based vaccine for SARS-CoV-2 could be safe and effective. (*bioRxiv*, April 14, 2020; **doi:** https://doi.org/10.1101/2020.04.10.036418)

Resources

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PubMed Query:

- April 14, 2020: https://www.ncbi.nlm.nih.gov/pubmed/?cmd=historysearch&querykey=1

Non-peer-reviewed Publications:

- ***MedRxiv* and *BioRxiv* Query**
    - April 13-14, 2020: https://bit.ly/3a8G2Lt

OTHER REFERENCES:

- WHO situation report: https://www.who.int/docs/default-source/coronaviruse/situation-reports/20200413-sitrep-84-covid-19.pdf?sfvrsn=44f511ab_2
- WHO Dashboard ARC GIS MAP: https://who.sprinklr.com/

- JHU Coronavirus Resource Center: https://coronavirus.jhu.edu/map.html
- CDC Coronavirus Web Page: https://www.cdc.gov/coronavirus/2019-ncov/whats-new-all.html
- CDC Travel COVID-19 Recommendations by Country: https://www.cdc.gov/coronavirus/2019-ncov/travelers/map-and-travel-notices.html
- Milken COVID-19 vaccine and treatment tracker: https://milkeninstitute.org/covid-19-tracker
- New York times Coronavirus deaths by U.S. state and country over time: Daily tracking https://www.nytimes.com/interactive/2020/03/21/upshot/coronavirus-deaths-by-country.html
- FDA EUAs related to COVID-19: https://www.fda.gov/emergency-preparedness-and-response/mcm-legal-regulatory-and-policy-framework/emergency-use-authorization#2019-ncov
- GHTC tracker for U.S. government-funded COVID-19 R&D: https://www.ghtcoalition.org/resources-item/covid-19-r-d-tracker
- CEIRS Contributions to the COVID-19 Response http://www.niaidceirs.org/covid-19/

Nancy
Nancy Touchette, Ph.D.
Health Research Program and Policy Analyst
Office of Global Research
National Institute of Allergy and Infectious Diseases
National Institutes of Health
Department of Health and Human Services
5601 Fishers Lane Rm 1E51B MSC 9802
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Fax: 301-480-2954
E-mail: (b) (6)

Obtained via FOIA by Judicial Watch, Inc.

COVID-19 Daily News Summary
Office of Global Research
April 14, 2020; Current as of 4:00 p.m., EST

Compiled by Nancy Touchette

The information in this summary, which is compiled from publicly sourced information, is for internal USG use only. The information in this report does not reflect the opinions of the National Institute of Allergy and Infectious Diseases (NIAID). NIAID shall not accept liability for any statements made that are the sender's own and not expressly made on behalf of the NIAID by one of its representatives.

WHO Situation Report (compiled daily): April 14

- ***1,844,863 confirmed cases globally (71,779 new)***
- ***117,021 deaths globally (5,369 new)***

U.S. CDC Update:

- ***Total U.S. Cases: 579,005***
- ***Total U.S. deaths: 22,252***

Johns Hopkins Coronavirus Resource Center

- **Globally**
  - ***1,956,077 confirmed cases***
  - ***125,123 deaths***
  - ***471,469 cases recovered***
- **United States**
  - ***572,689 confirmed cases***
  - ***23,134 deaths***
  - ***43,482 cases recovered***

RESEARCH NEWS

Epidemiology/modeling

- NIAID-supported scientists have developed a SARS-CoV-2 transmission model that predicts recurrent wintertime outbreaks of SARS-CoV-2 after the initial, most severe pandemic wave. Prolonged or intermittent social distancing may be necessary into 2022, according to findings published in the April 14, 2020 issue of *Science*. Even if the virus is eliminated, SARS-CoV-2 surveillance should be maintained since a resurgence in contagion could be possible as late as 2024, according to authors. (*Science*, April 14, 2020; DOI: 10.1126/science.abb5793).

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- WHO Dashboard ARC GIS MAP: https://who.sprinklr.com/
- JHU Coronavirus Resource Center: https://coronavirus.jhu.edu/map.html
- CDC Coronavirus Web Page: https://www.cdc.gov/coronavirus/2019-ncov/whats-new-all.html
- CDC Travel COVID-19 Recommendations by Country: https://www.cdc.gov/coronavirus/2019-ncov/travelers/map-and-travel-notices.html
- Milken COVID-19 vaccine and treatment tracker: https://milkeninstitute.org/covid-19-tracker
- New York times Coronavirus deaths by U.S. state and country over time: Daily tracking https://www.nytimes.com/interactive/2020/03/21/upshot/coronavirus-deaths-by-country.html
- FDA EUAs related to COVID-19: https://www.fda.gov/emergency-preparedness-and-response/mcm-legal-regulatory-and-policy-framework/emergency-use-authorization#2019-ncov
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- CEIRS Contributions to the COVID-19 Response http://www.niaidceirs.org/covid-19/

Obtained via FOIA by Judicial Watch, Inc.

From: Chen, Ping (NIH/NIAID) [E]
Sent: Wed, 15 Apr 2020 21:24:39 +0000
To: Handley, Gray (NIH/NIAID) [E]
Subject: Re: Info for 5:30 call about the WIV cable

I tried to search for messages in my outlook for Oct 2017 and later, my inbox doesn't go that far. Will need to get IT help.

Ping

From: "Chen, Ping (NIH/NIAID) [E]" [redacted] (b) (6)
Date: Wednesday, April 15, 2020 at 5:02 PM
To: "Handley, Gray (NIH/NIAID) [E]" [redacted] (b) (6)
Subject: Info for 5:30 call about the WIV cable

Here is the conference call information: USA Toll-Free: [redacted] (b) (4), (b) (5), (b) (6) International Toll: [redacted] (b) (4), (b) (5), (b) (4) / Access Code: [redacted] (b) (4), (b) (5), (b) (6)
Adrienne, Ron (CDC country director before R.J.), me, Rick, don't know who else Rick might have included. He said it is OK for you to join the call.

Talk to you soon.

Ping

Obtained via FOIA by Judicial Watch, Inc.

From: Bernabe, Gayle (NIH/NIAID) [E]
Sent: Wed, 15 Apr 2020 22:00:31 +0000
To: Handley, Gray (NIH/NIAID) [E]
Subject: RE: Wuhan Lab
Attachments: Re: trip report

Attached is Ping's trip report. I'll keep looking for more info.

From: Bernabe, Gayle (NIH/NIAID) [E]
Sent: Wednesday, April 15, 2020 5:48 PM
To: Handley, Gray (NIH/NIAID) [E] [redacted] (b) (6)
Subject: RE: Wuhan Lab

Will do.

From: Handley, Gray (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Wednesday, April 15, 2020 5:26 PM
To: Bernabe, Gayle (NIH/NIAID) [E] [redacted] (b) (6)
Subject: Wuhan Lab

Gayle, please check your files for messages from Ping back in October 2017 when she visited the Wuhan lab and sent us by e-mail information on it. Basically anything we can find on that grant and that lab.

Thanks much.

Gray

Obtained via FOIA by Judicial Watch, Inc.

From: Chen, Ping (NIH/NIAID) [E]
Sent: Wed, 22 Nov 2017 07:03:29 +0000
To: Handley, Gray (NIH/NIAID) [E]
Cc: Bernabe, Gayle (NIH/NIAID) [E];Meegan, James (NIH/NIAID) [E];Rosa, William (NIH/NIAID) [E]
Subject: Re: trip report
Attachments: WIV P4 lab Summary.docx

I drafted the following report for my visit to the P4 lab as you requested. [redacted] (b) (5) (b) (5) (b) (5) (b) (5)
Anyway I want to get it out before the holiday starts now in the embassy (early release).
Have a nice Thanksgiving! I won't eat any turkeys but will try to find chicken in Gulangyu Island.
Ping
Ping Chen, PhD
Director of NIAID Office in China
Office of Global Research, NIAID, NIH
Bethesda Office: [redacted] (b) (6)
BB: [redacted] (b) (5)
Beijing Office: [redacted] (b) (5)
Cell: [redacted] (b) (5)
U.S. Cell: [redacted] (b) (5)
U.S. Embassy Beijing
#55 An Jia Lou Road
ChaoYang District, 100600
Beijing, China
[redacted] (b) (6)
(b) (6)

From: Chen, Ping (NIH/NIAID) [E]
Sent: Monday, November 6, 2017 21:24
To: Handley, Gray (NIH/NIAID) [E]
Cc: Bernabe, Gayle (NIH/NIAID) [E]; Meegan, James (NIH/NIAID) [E]; Rosa, William (NIH/NIAID) [E]
Subject: Re: trip report
OK.

Sent from my iPhone

On Nov 6, 2017, at 9:21 PM, Handley, Gray (NIH/NIAID) [E] [redacted] (b) (6) wrote:

Please send us by e-mail your full report on the visit and then we can decide what to do with that information. Gray

---

From: Chen, Ping (NIH/NIAID) [E]
Sent: Thursday, October 26, 2017 11:28 PM

Obtained via FOIA by Judicial Watch, Inc.

To: Handley, Gray (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Bernabe, Gayle (NIH/NIAID) [E] [redacted] (b) (6); Meegan, James (NIH/NIAID) [E] [redacted] (b) (6); Rosa, William (NIH/NIAID) [E] [redacted] (b) (6)
Subject: Re: trip report

[redacted] (b) (5)

Let me know what you would like me to do.
Ping

Ping Chen, PhD
Director of NIAID Office in China
Office of Global Research, NIAID, NIH
Bethesda Office: [redacted] (b) (6)
BB: [redacted] (b) (6)
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U.S. Embassy Beijing
#55 An Jia Lou Road
ChaoYang District, 100600
Beijing, China
[redacted] (b) (6)
[redacted] (b) (6)

From: Handley, Gray (NIH/NIAID) [E]
Sent: Friday, October 27, 2017 1:40:04 AM
To: Chen, Ping (NIH/NIAID) [E]
Cc: Bernabe, Gayle (NIH/NIAID) [E]; Meegan, James (NIH/NIAID) [E]; Rosa, William (NIH/NIAID) [E]
Subject: RE: trip report

Thanks for this report, Ping. [redacted] (b) (5)
[redacted] (b) (5)

[redacted] (b) (5)

Gray

From: Chen, Ping (NIH/NIAID) [E]
Sent: Thursday, October 26, 2017 5:01 AM
To: Handley, Gray (NIH/NIAID) [E] [redacted] (b) (6); Bernabe, Gayle (NIH/NIAID) [E] [redacted] (b) (6); Meegan, James (NIH/NIAID) [E] [redacted] (b) (6); Rosa, William (NIH/NIAID) [E] [redacted] (b) (6)
Subject: trip report

Hi,

This week I went to Wuhan to visit the Bio safety lab 4 in Wuhan Institute of Virology (WIV), an institute under the Chinese Academy of Sciences (CAS). My contact who helped arrange the visit is Dr. Zhengli Shi, who is a Chinese collaborator on a NIAID grant to EcoHealth for SARS like corona virus project.

[redacted] (b) (5)

Obtained via FOIA by Judicial Watch, Inc.

(b) (5) [redacted]

Please let me know if you have any questions.

Thanks

Ping

Ping Chen, PhD
Director of NIAID Office in China
Office of Global Research, NIAID, NIH
Bethesda Office: [redacted] (b) (6)
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#55 An Jia Lou Road
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[redacted] (b) (6)

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From: Chen, Ping (NIH/NIAID) [E]
Sent: Wed, 15 Apr 2020 23:02:55 +0000
To: Handley, Gray (NIH/NIAID) [E]
Subject: FW: 2018 cable
Attachments: 18-BEIJING-138.eml.pdf

Rick forwarded the cable. I was listed as a drafter. About half of the content was taken from my summary.

[redacted] (b) (5)

Talk to you in the morning.

Ping

From: [redacted] (b) (6)
Date: Wednesday, April 15, 2020 at 6:18 PM
To: "Chen, Ping (NIH/NIAID) [E]" [redacted] (b) (6)
Cc: Ronald Moolenaar [redacted] (b) (6)
Subject: 2018 cable

Get Outlook for iOS

Obtained via FOIA by Judicial Watch, Inc.

UNCLASSIFIED
SBU

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. [redacted] (b) (5) (b) (5) (b) (5) **End Summary and Comment.**

<u>China Investing in Infectious Disease Control</u>

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

Obtained via FOIA by Judicial Watch, Inc.

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.

[redacted] (b) (6)

[redacted] (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.

[redacted] (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, [redacted] (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 [redacted] (b) (6) the training for technicians and investigators working on dangerous pathogens will certainly be in demand.

Despite Limitations, WIV Researchers Produce SARS Discoveries

Obtained via FOIA by Judicial Watch, Inc.

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, [redacted] (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. [redacted] (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

Signature:	BRANSTAD
Drafted By: **Cleared By:** **Approved By:** **Released By:**	[redacted] (b) (6)
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Obtained via FOIA by Judicial Watch, Inc.

From: Chen, Ping (NIH/NIAID) [E]
Sent: Thu, 16 Apr 2020 12:17:53 +0000
To: Handley, Gray (NIH/NIAID) [E]
Subject: Re: UTMB

Thanks Gray.
Her phone number is [redacted] (b) (6)
I will let her know you are going to call her. I did tell her I will contact her in the morning.
Talk to you at noon.

Ping

From: "Handley, Gray (NIH/NIAID) [E]" [redacted]
Date: Thursday, April 16, 2020 at 8:11 AM
To: "Chen, Ping (NIH/NIAID) [E]" [redacted] (b) (6)
Subject: RE: UTMB

[redacted] (b) (5) I will call her this morning because you are busy. I really appreciate your reach out to her and her willingness to talk to Jim at UTMB. We will talk at noon. Thanks again for engaging with this.

From: Chen, Ping (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Wednesday, April 15, 2020 11:54 PM
To: Handley, Gray (NIH/NIAID) [E] [redacted] (b) (6)
Subject: UTMB

Gray,

Talked to Nancy Boyd this evening. She would be happy to reach out to UTMB tomorrow.

Rick sent me the following questions for UTMB. I want to bring these questions by you before I ask Nancy. Talk to you tomorrow. I have an appointment with IT to fix my password renewal problem at 8:30 and my COR training starts at 9. I will try to call you a few minute before 8 if that is OK.

In addition to the questions Rick has below, [redacted] (b) (5)

[redacted] (b) (5)

Obtained via FOIA by Judicial Watch, Inc.

(b) (5)

Thanks

Ping

From: Chen, Ping (NIH/NIAID) [E]
Sent: Thu, 16 Apr 2020 14:13:32 +0000
To: Handley, Gray (NIH/NIAID) [E]
Subject: Re: 2018 cable

You remember this one well because most content was taken from the visit summary I wrote. The other cable (in the first email Rick sent to me and I forwarded to you) was written after they visited the institute. Definitely that Cable was obtained by the reporter because Rick and Wuhan CG's names were in the newspaper article. I don't know if the cable based on my summary was also obtained by the press.

I visited WIV on Oct. 24, 2017. I must have shared the information within the health group in the embassy. ESTH decided to make it into a cable (that is probably you remember I wrote a cable about the visit). This cable was before Rick and Wuhan CG visited WIV. They visited WIV in early 2018.

Ping

From: "Handley, Gray (NIH/NIAID) [E]" [redacted] (b) (6)
Date: Thursday, April 16, 2020 at 9:55 AM
To: "Chen, Ping (NIH/NIAID) [E]" [redacted] (b) (6)
Subject: RE: 2018 cable

I recall this cable very well. How does it relate to the other cable text that you sent yesterday or the day before? g

---

From: Chen, Ping (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Wednesday, April 15, 2020 7:03 PM
To: Handley, Gray (NIH/NIAID) [E] [redacted] (b) (6)
Subject: FW: 2018 cable

Rick forwarded the cable. I was listed as a drafter. About half of the content was taken from my summary.

[redacted] (b) (5)

Talk to you in the morning.

Ping

From: [redacted] (b) (6)
Date: Wednesday, April 15, 2020 at 6:18 PM
To: "Chen, Ping (NIH/NIAID) [E]" [redacted] (b) (6)
Cc: Ronald Moolenaar [redacted] (b) (6)
Subject: 2018 cable

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From: Boyd, Nancy (NIH/NIAID) [E]
Sent: Thu, 16 Apr 2020 16:11:22 +0000
To: Handley, Gray (NIH/NIAID) [E]
Subject: Re: Sources believe coronavirus outbreak originated in Wuhan lab as part of China's efforts to compete with US

https://science.sciencemag.org/content/362/6410

Sorry if you already got this twice before. If so, my mail did not track it.

Nancy

From: "Boyd, Nancy (NIH/NIAID) [E]" [redacted] (b) (6)
Date: Thursday, April 16, 2020 at 11:57 AM
To: "Handley, Gray (NIH/NIAID) [E]" [redacted] (b) (6)
Subject: Fwd: Fox: Sources believe coronavirus outbreak originated in Wuhan lab as part of China's efforts to compete with US

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From: Folkers, Greg (NIH/NIAID) [E] [redacted] (b) (6)
Sent: Thursday, April 16, 2020 10:34 AM
Subject: Fox: Sources believe coronavirus outbreak originated in Wuhan lab as part of China's efforts to compete with US

Sources believe coronavirus outbreak originated in Wuhan lab as part of China's efforts to compete with US

By Bret Baier, Gregg Re | Fox News

Sources tell Fox News that the belief is now is that the coronavirus originated in a Wuhan lab, not as a bio weapon, but as China's effort to find and deal with viruses.

EXCLUSIVE: There is increasing confidence that the COVID-19 outbreak likely originated in a Wuhan laboratory, though not as a bioweapon but as part of China's attempt to demonstrate that its efforts to identify and combat viruses are equal to or greater than the capabilities of the United States, multiple sources who have been briefed on the details of early actions by China's government and seen relevant materials tell Fox News.

This may be the "costliest government cover-up of all time," one of the sources said.

The sources believe the initial transmission of the virus – a naturally occurring strain that was being studied there – was bat-to-human and that "patient zero" worked at the laboratory, then went into the population in Wuhan.

The “increasing confidence” comes from classified and open-source documents and evidence, the sources said. Fox News has requested to see the evidence directly. Sources emphasized -- as is often the case with intelligence -- that it’s not definitive and should not be characterized as such. Some inside the administration and the intelligence and epidemiological communities are more skeptical, and the investigation is continuing.

What all of the sources agree about is the extensive cover-up of data and information about COVID-19 orchestrated by the Chinese government.

Asked by Fox News' John Roberts about the reporting, President Trump remarked at Wednesday's coronavirus press briefing, "More and more we're hearing the story...we are doing a very thorough examination of this horrible situation."

Documents detail early efforts by doctors at the lab and early efforts at containment. The Wuhan wet market initially identified as a possible point of origin never sold bats, and the sources tell Fox News that blaming the wet market was an effort by China to deflect blame from the laboratory, along with the country's propaganda efforts targeting the U.S. and Italy.

U.S. Embassy officials warned in January 2018 about inadequate safety at the Wuhan Institute of Virology lab and passed on information about scientists conducting risky research on coronavirus from bats, The Washington Post reported Tuesday.

Responding to the report, Gen. Mark Milley, the chairman of the Joint Chiefs of Staff, said on Tuesday afternoon: "It should be no surprise to you that we have taken a keen interest in that and we've had a lot of intelligence take a hard look at that. I would just say at this point, it's inconclusive, although the weight of evidence seems to indicate natural, but we don't know for certain."

“Even today, I see them withholding information and I think we need to do more to continue to press them to share,” Secretary of Defense Mark Esper told “America’s Newsroom" on Wednesday, referring to China. Esper added that he wouldn't speak to "intelligence reporting," but that "most people believe it began naturally — it was organic, if you will. I think in due course, once we get through the pandemic we're in right now, there'll be time to look back and really ascertain what happened and make sure we have a better understanding so we can prevent this in the future."

Speaking to "The Story" Wednesday evening, Secretary of State Mike Pompeo remarked: "What we do know is we know that this virus originated in Wuhan, China. We know there is the Wuhan Institute of Virology just a handful of miles away from where the wet market was. There is still lots to learn. You should know that the United States government is working diligently to figure it out."

Secretary of State Mike Pompeo sits down with Martha MaCallum on 'The Story' to discuss the coronavirus pandemic and U.S.-China relations.

Concerning the State Department cables warning about the Wuhan laboratory, Pompeo said the installation "contained highly contagious materials — we knew that, we knew that they were working on this program, many countries have programs like this. In countries that are open and transparent, they have the ability to control them and keep them safe, and they allow outside observers in to make sure all the processes and procedures are right. I only wish that that had happened in this place."

On Thursday, China's foreign ministry pushed back on the suspicion that the virus escaped from the facility, by citing statements from the World Health Organization that there is no evidence the coronavirus came from a laboratory.

Americans were originally helping train the Chinese in a program called PREVENT well before the Chinese started working on this virus. The French government helped the Chinese set up the Wuhan lab.

China "100 percent" suppressed data and changed data, the sources tell Fox News. Samples were destroyed, contaminated areas scrubbed, some early reports erased, and academic articles stifled.

There were doctors and journalists who were "disappeared" warning of the spread of the virus and its contagious nature and human to human transmission. China moved quickly to shut down travel domestically from Wuhan to the rest of China, but did not stop international flights from Wuhan. Additionally, the sources tell Fox News the World Health Organization (WHO) was complicit from the beginning in helping China cover its tracks.

Trump announced at the White House coronavirus news briefing in the Rose Garden on Tuesday that the United States will immediately halt all funding for the WHO, saying it had put "political correctness over lifesaving measures." The United States is the WHO's largest single donor, and the State Department had previously planned to provide the agency $893 million in the current two-year funding period.

Senior administrations separately tell Fox News the rollout of the president's "blueprint for reopening the U.S. economy" will happen Thursday afternoon, first for governors and then briefed to the press.

Meanwhile, Trump's own handling of the crisis has come into focus. On January 24, for example, Trump tweeted in praise of China's "transparency" on coronavirus.

Though they were not speaking for the president, the sources ventured an explanation, saying it was diplomatic talk to make the Chinese "feel good". while the investigation was ongoing, with trade and other talks happening simultaneously.

In the six days after top Chinese officials secretly determined they likely were facing a pandemic from a new coronavirus, the city of Wuhan at the epicenter of the disease hosted a mass banquet for tens of thousands of people; millions began traveling through for Lunar New Year celebrations.

President Xi Jinping warned the public on the seventh day, Jan. 20. But by that time, more than 3,000 people had been infected during almost a week of public silence, according to internal documents obtained by The Associated Press and expert estimates based on retrospective infection data.

"This is tremendous," said Zuo-Feng Zhang, an epidemiologist at the University of California, Los Angeles. "If they took action six days earlier, there would have been much fewer patients and medical facilities would have been sufficient. We might have avoided the collapse of Wuhan's medical system."

Fox News' Barnini Chakraborty and The Associated Press contributed to this report.

Bret Baier is the chief political anchor of Fox News Channel, and the anchor and executive editor of "Special Report with Bret Baier." He is the author of "Three Days in January: Dwight Eisenhower's Final Mission," and "Three Days in Moscow: Ronald Reagan and the Fall of the Soviet Empire." His third presidential book, "Three Days at the Brink: FDR's Daring Gamble to win World War II," will be released on Oct. 22, 2019.

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