



**United States Department of State**

*Washington, D.C. 20520*

September 19, 2025

Case No. FL-2022-00062

Mr. Gary Ruskin  
U.S. Right to Know  
4096 Piedmont Avenue, #963  
Oakland, CA 94611

Dear Mr. Ruskin:

As we noted in our letter dated August 8, 2025, we are processing your request for material under the Freedom of Information Act ("FOIA"), 5 U.S.C. § 552. The Department of State ("Department") has identified an additional five responsive records subject to the FOIA. Upon review, we have determined that all five records may be released in part.

An enclosure explains the FOIA exemptions and other grounds for withholding material. Where we have made redactions, the applicable FOIA exemptions are marked on each record. Where applicable, the Department has considered the foreseeable harm standard when reviewing these records and applying FOIA exemptions. All non-exempt material that is reasonably segregable from the exempt material has been released and is enclosed.

We will keep you informed as your case progresses. If you have any questions, your attorney may contact Assistant United States Attorney Stephanie Johnson at [stephanie.johnson5@usdoj.gov](mailto:stephanie.johnson5@usdoj.gov) or (202) 252-7874. Please refer to the case number, FL-2022-00062, and the civil action number, 22-cv-01130, in all correspondence about this case.

Sincerely,

A handwritten signature in black ink, appearing to read 'D. Hickson', with a large, stylized initial 'D' and a horizontal flourish extending to the right.

Diamonece Hickson  
Supervisory Government Information Specialist  
Litigation and Appeals Office

Enclosures: As stated.

## **The Freedom of Information Act (5 USC 552)**

### **FOIA Exemptions**

- (b)(1) Information specifically authorized by an executive order to be kept secret in the interest of national defense or foreign policy. Executive Order 13526 includes the following classification categories:
- 1.4(a) Military plans, systems, or operations
  - 1.4(b) Foreign government information
  - 1.4(c) Intelligence activities, sources or methods, or cryptology
  - 1.4(d) Foreign relations or foreign activities of the US, including confidential sources
  - 1.4(e) Scientific, technological, or economic matters relating to national security, including defense against transnational terrorism
  - 1.4(f) U.S. Government programs for safeguarding nuclear materials or facilities
  - 1.4(g) Vulnerabilities or capabilities of systems, installations, infrastructures, projects, plans, or protection services relating to US national security, including defense against transnational terrorism
  - 1.4(h) Weapons of mass destruction
- (b)(2) Related solely to the internal personnel rules and practices of an agency
- (b)(3) Specifically exempted from disclosure by statute (other than 5 USC 552), for example:
- |                |   |
|----------------|---|
| ARMSEXP        | Arms Export Control Act, 50a USC 2411(c)                    |
| CIA PERS/ORG   | Central Intelligence Agency Act of 1949, 50 USC 403(g)      |
| EXPORT CONTROL | Export Administration Act of 1979, 50 USC App. Sec. 2411(c) |
| FS ACT         | Foreign Service Act of 1980, 22 USC 4004                    |
| INA            | Immigration and Nationality Act, 8 USC 1202(f), Sec. 222(f) |
| IRAN           | Iran Claims Settlement Act, Public Law 99-99, Sec. 505      |
- (b)(4) Trade secrets and confidential commercial or financial information
- (b)(5) Interagency or intra-agency communications forming part of the deliberative process, attorney-client privilege, or attorney work product
- (b)(6) Personal privacy information
- (b)(7) Law enforcement information whose disclosure would:
- (A) interfere with enforcement proceedings
  - (B) deprive a person of a fair trial
  - (C) constitute an unwarranted invasion of personal privacy
  - (D) disclose confidential sources
  - (E) disclose investigation techniques
  - (F) endanger life or physical safety of an individual
- (b)(8) Prepared by or for a government agency regulating or supervising financial institutions
- (b)(9) Geological and geophysical information and data, including maps, concerning wells

### **Other Grounds for Withholding**

- NR Material not responsive to a FOIA request excised with the agreement of the requester

<b>From:</b>	(b)(6)
<b>To:</b>	Paulopol, Andreea I (b)(6)@state.gov>
<b>Subject:</b>	Wuhan lab article
<b>Date:</b>	Wed, 15 Apr 2020 13:01:17 +0000

Not sure if you all saw this article yesterday....

<https://www.washingtonpost.com/opinions/2020/04/14/state-department-cables-warned-safety-issues-wuhan-lab-studying-bat-coronaviruses/>

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

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.

*Full coverage of the coronavirus pandemic*

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 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 Institute 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 it 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.

*The Opinions section is looking for stories of how the coronavirus has affected people of all walks of life. Write to us.*

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.

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.”

(b)(6)

Senior Science Advisor

Office of the Assistant Secretary for Preparedness and Response (ASPR)

Office of Strategy, Policy, Planning & Requirements (SPPR)

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**U.S. DEPARTMENT OF HEALTH AND HUMAN SERVICES (DHHS) |**

O’Neill House Office Building, Office #5306 |

200 C Street SW | Washington, DC 20515

o. (b)(6) | m. (b)(6)

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

<http://www.phe.gov/s3>

**Sender:** (b)(6)

**Recipient:** Paulopol, Andreea I (b)(6)@state.gov>

<b>From:</b>	"Paulopol, Andreea I" (b)(6)@state.gov>
<b>To:</b>	(b)(6)
<b>Subject:</b>	thoughts on this?
<b>Date:</b>	Fri, 9 Oct 2020 11:30:59 +0000

Hi (b)(6)

Wondering if you have seen the article below and if you have any thoughts on it from your end. I'm also attaching one of her papers. (b)(5) DPP

(b)(5) DPP

**The Chinese government intentionally manufactured and released the COVID-19 virus that led to mass shutdowns and deaths across the world, a top virologist and whistleblower told Fox News host Tucker Carlson.**

<https://www.foxnews.com/media/chinese-virologist-government-intentionally-coronavirus>

Curious about your thoughts here.

Thanks,

Andreea

*Physical Scientist  
Office of Chemical and Biological Weapons Affairs  
Bureau of Arms Control, Compliance and Verification  
U.S. Department of State  
2201 C Street, N.W.  
Washington, DC 20520  
Desk: (b)(6)  
(b)(6)@state.gov*

<b>Sender:</b>	"Paulopol, Andreea I" (b)(6)@state.gov>
<b>Recipient:</b>	(b)(6)



<b>From:</b>	"Yu, Miles" (b)(6)@state.gov>
<b>To:</b>	Paulopol, Andreea I (b)(6)@state.gov>
<b>Subject:</b>	Re: your paper
<b>Date:</b>	Fri, 11 Dec 2020 21:01:06 +0000

Andrea,  
Here it is. It needs updating.  
Miles

Dr. M. Miles Yu  
Policy Planning Staff  
Office of the Secretary of State  
Washington, DC

(b)(6) (office)  
(b)(6) (mobile)

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From: Yu, Miles  
Sent: Friday, December 11, 2020 1:58 PM  
To: Paulopol, Andreea I  
Subject: Re: your paper

Sure. Give me an hour or so.

[state seal]  
Dr. M. Miles Yu  
Policy Planning Staff  
Office of the Secretary  
U.S. Department of State

(b)(6)

On Dec 11, 2020, at 1:06 PM, Paulopol, Andreea I (b)(6)@state.gov> wrote:

Hi Miles—

(b)(5) DPP

If you can do so today, that would be great.

Many thanks in advance,  
Andreea

Andreea Paulopol  
Physical Scientist  
Office of Chemical and Biological Weapons Affairs  
Bureau of Arms Control, Compliance and Verification  
U.S. Department of State  
2201 C Street, N.W.  
Washington, DC 20520  
Desk: (b)(6)  
(b)(6)@state.gov<mailto:(b)(6)@state.gov>

~~SENSITIVE BUT UNCLASSIFIED~~

<b>Sender:</b>	"Yu, Miles" (b)(6)@state.gov>
<b>Recipient:</b>	Paulopol, Andreea I (b)(6)@state.gov>

**From:** (b)(6)@state.gov>  
**To:** (b)(6)@state.gov>;  
(b)(6)@state.gov>  
**CC:** (b)(6)@state.gov>;  
Feith, David (b)(6)@state.gov>;  
(b)(6)@state.gov>;  
Gross, Laura J (b)(6)@state.gov>;  
(b)(6)@state.gov>;  
Paulopol, Andreea I (b)(6)@state.gov>  
**Subject:** RE: CBM Technical Question  
**Date:** Fri, 4 Dec 2020 22:14:30 +0000

(b)(6) if you are in next week, would like to discuss a couple of issues related to this.

(b)(5) DPP

(b)(6)

SENIOR ADVISOR

AVC BUREAU

DEPARTMENT OF STATE

(b)(6)

OFFICE

CELL

---

**From:** (b)(6)@state.gov>  
**Sent:** Friday, December 4, 2020 4:23 PM  
**To:** (b)(6)@state.gov>  
**Cc:** (b)(6)@state.gov>; Feith, David (b)(6)@state.gov>; (b)(6)@state.gov>; Gross, Laura J (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>; Paulopol, Andreea I (b)(6)@state.gov>  
**Subject:** Re: CBM Technical Question

(b)(6)

Thanks --

(b)(5) DPP; (b)(5) ACP

Best,

(b)(6)

**From:** (b)(6)@state.gov>

**Sent:** Friday, December 4, 2020 3:09 PM

**To:** (b)(6)@state.gov>

**Cc:** (b)(6)@state.gov>; Feith, David (b)(6)@state.gov>; (b)(6)

(b)(6)@state.gov>; Gross, Laura J (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)

(b)(6)@state.gov>; Paulopol, Andreea I (b)(6)@state.gov>

**Subject:** RE: CBM Technical Question

Many thanks. (b)(5) DPP; (b)(5) ACP

(b)(5) DPP; (b)(5) ACP

---

**From:** (b)(6)@state.gov>

**Sent:** Friday, December 4, 2020 2:58 PM

**To:** Gross, Laura J (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)

(b)(6)@state.gov>; (b)(6)@state.gov>; Paulopol, Andreea I

(b)(6)@state.gov>

**Cc:** (b)(6)@state.gov>; Feith, David (b)(6)@state.gov>; (b)(6)

(b)(6)@state.gov>

**Subject:** Re: CBM Technical Question

Thanks, (b)(6) (b)(5) ACP

(b)(5) ACP

Best,

(b)(6)

---

**From:** Gross, Laura J (b)(6)@state.gov>

**Sent:** Friday, December 4, 2020 2:38 PM

**To:** (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)

(b)(6)@state.gov>; (b)(6)@state.gov>; Paulopol, Andreea I

(b)(6)@state.gov>

**Cc:** (b)(6)@state.gov>; Feith, David (b)(6)@state.gov>; (b)(6)

(b)(6)@state.gov>

**Subject:** RE: CBM Technical Question

Many thanks!

---

Sent from Workspace ONE Boxer

On December 4, 2020 at 2:37:10 PM EST, (b)(6)@state.gov wrote:

Said list in work.

---

**From:** Gross, Laura J (b)(6)@state.gov

**Sent:** Friday, December 4, 2020 2:35 PM

**To:** (b)(6)@state.gov; (b)(6)@state.gov (b)(6)

(b)(6)@state.gov; (b)(6)@state.gov; Paulopol, Andreea I

(b)(6)@state.gov

**Cc:** (b)(6)@state.gov; Feith, David (b)(6)@state.gov; (b)(6)

(b)(6)@state.gov

**Subject:** Re: CBM Technical Question

Hi David, (b)(6) - Many thanks.

(b)(5) DPP

We're with you. The next step is to write it up.

Best - Laura

---

Sent from Workspace ONE Boxer

On December 4, 2020 at 1:16:06 PM EST, (b)(6)@state.gov wrote:

(b)(5) DPP; (b)(6)

(b)(5) DPP

---

**From:** (b)(6)@state.gov>

**Sent:** Friday, December 4, 2020 12:43 PM

**To:** Gross, Laura J (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)

(b)(6)@state.gov>; Paulopol, Andreea I (b)(6)@state.gov>

**Cc:** (b)(6)@state.gov>; (b)(6)@state.gov>; Feith, David

(b)(6)@state.gov>; (b)(6)@state.gov>

**Subject:** Re: CBM Technical Question

(b)(5) DPP

(b)(6)

Senior Adviser AVC

SSD/AVC

c: (b)(6)

---

**From:** Gross, Laura J (b)(6)@state.gov>

**Sent:** Friday, December 4, 2020 12:12 PM

**To:** (b)(6)@state.gov>; (b)(6)@state.gov>; Paulopol,

Andreea I (b)(6)@state.gov>

**Cc:** (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)

(b)(6)@state.gov>; Feith, David (b)(6)@state.gov>; (b)(6)@state.gov>

**Subject:** Re: CBM Technical Question

Looping in (b)(6) and Andreea

Hi (b)(6) (b)(5) DPP (b)(6) (b)(5) DPP

(b)(5) DPP

I'm not sure how to respond to your last comment. (b)(5) DPP

(b)(5) DPP

Best - Laura

---

**From:** (b)(6)@state.gov>

**Sent:** Friday, December 4, 2020 11:15 AM

**To:** Gross, Laura J (b)(6)@state.gov>

**Cc:** (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>; Feith, David (b)(6)@state.gov>; (b)(6)@state.gov>

**Subject:** CBM Technical Question

Laura,

(U//~~FOUO~~) (b)(5) DPP

(b)(5) DPP

(U) (b)(5) DPP

(b)(5) DPP

(b)(5) DPP

(b)(6)

*Bureau of Arms Control, Verification and Compliance  
US Department of State*

(b)(6)

NSTS: (b)(6)

JWICS: (b)(6)@state.ic.gov

SIPR: (b)(6)@state.sgov.gov

~~SENSITIVE BUT UNCLASSIFIED~~

~~SENSITIVE BUT UNCLASSIFIED~~

~~SENSITIVE BUT UNCLASSIFIED~~

~~SENSITIVE BUT UNCLASSIFIED~~

<b>Sender:</b>	(b)(6)@state.gov>
<b>Recipient:</b>	(b)(6)@state.gov>;
	(b)(6)@state.gov>;
	(b)(6)@state.gov>;
	Feith, David (b)(6)@state.gov>;
	(b)(6)@state.gov>;
	Gross, Laura J (b)(6)@state.gov>;
	(b)(6)@state.gov>;
	Paulopol, Andreea I (b)(6)@state.gov>



<b>From:</b>	(b)(6)@state.gov>
<b>To:</b>	DiNanno, Thomas G (b)(6)@state.gov>; (b)(6)@state.gov>
<b>CC:</b>	(b)(6)@state.gov>; Stilwell, David R (b)(6)@state.gov>; Feith, David (b)(6)@state.gov>; Keshap, Atul (b)(6)@state.gov>; (b)(6)@state.gov>; Switzer, Bryan R (Rick) (b)(6)@state.gov>; (b)(6)@state.gov>; Gross, Laura J (b)(6)@state.gov>; Yu, Miles (b)(6)@state.gov>; (b)(6)@state.gov>
<b>Subject:</b>	Fw: Fw: RaTG13 (shared in confidence)—DR. QUAY'S PAPER on why SARS COVID19 was optimally engineered
<b>Date:</b>	Mon, 30 Nov 2020 14:56:34 +0000

Sorry that the attachment didn't transmit.

(b)(6)  
**From:** (b)(6)@state.gov>  
**Sent:** Sunday, November 29, 2020 5:58 PM  
**To:** DiNanno, Thomas G (b)(6)@state.gov>  
**Cc:** (b)(6)@state.gov>; Stilwell, David R (b)(6)@state.gov>; Feith, David (b)(6)@state.gov>; (b)(6)@state.gov>; Switzer, Bryan R (Rick) (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>; Gross, Laura J (b)(6)@state.gov>; Yu, Miles (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>; Keshap, Atul (b)(6)@state.gov>  
**Subject:** FRaTG13 (shared in confidence)—

Tom,

The attached note from Dr. Quay seems important. I asked Dr. Quay to respond specifically to Anderson et al who were among the early proponents that COVID 19, undoubtedly, was of natural zoonotic origin. This assertion in various forms gets repeated like is serious scientific fact based truth—when it may be the opposite based on some of the very evidence they put forward.

Bizarrely Anderson et al also were among the main proponents of the view that Gain of Function for virological spread prediction was a waste of money (see below). This said, Anderson et al never contemplate that someone could genetically engineer a bio threat vector with the exact characteristics they observe as "natural." Since many of us have dealt with unconventional warfare and weapons designed to scare, maim, destroy economic resilience, etc the type of analysis presented by Quay resonates from that perspective. Like IEDS and mines, the most effective weapons in UW are hiding and plain site. Same rules apply to BW, in theory. This genetic sequence analysis doesn't confirm BW research as a possible origin but it

does further highlight that the COVID 19 vector could have been bio-engineered for unknown reasons and somehow got out into the wild. So Quay's independent analysis does seem to conform with Segreto and

Deigin. <https://onlinelibrary.wiley.com/doi/epdf/10.1002/bies.202000240>

### Prospects&Overviews

### ThegeneticstructureofSARS-CoV-2doesnotruleouta laboratoryorigin

2of9 SEGRETOANDDEIGIN adaptation to human cells. We here describe how the two main SARS-CoV-2 features,(1)thepresenceofafurincleavagesitemissinginthe r ...

[onlinelibrary.wiley.com](https://onlinelibrary.wiley.com)

(b)(5) DPP (b)(6)

(b)(6) (b)(5) DPP We are broadening the inquiry within AVC to include outreach to the science community as well as a more head on discussion with the "community."

Thanks.

(b)(6)

**From:** Steven Quay (b)(6)

**Sent:** Sunday, November 29, 2020 8:24 AM

**To:** (b)(6)@state.gov>

**Subject:** Re: Fw: RaTG13 (shared in confidence)

(b)(6)

Here is my response to the Andersen argument that CoV-2 was not ideal for the receptor binding and so should have come from nature. The facts show the exact opposite.

Regards, Steve

On Sun, 29 Nov 2020 at 03:45, (b)(6)@state.gov> wrote:

Steve, Here are the same authors laying out why COV-19 had to be natural. Have you considered a response letter? (b)(6)

<https://www.nature.com/articles/s41591-020-0820-9.pdf>

**From:** Steven Quay (b)(6)

**Sent:** Sunday, November 29, 2020 8:24 AM

**To:** (b)(6)@state.gov>  
**Subject:** Re: Fw: RaTG13 (shared in confidence)

(b)(6)

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<https://www.nature.com/articles/s41591-020-0820-9.pdf>

**From:** (b)(6)@state.gov>  
**Sent:** Saturday, November 28, 2020 2:32 PM  
**To:** Steven Quay (b)(6)  
**Subject:** Re: Fw: RaTG13 (shared in confidence)

*Below: Nature commentary pointing out the futility, waste, and opportunity costs associated projects pursued by Ecohealth, WIV, NIAID, et al, in the name of "predicting the next outbreak". Though they don't address the grave hazards, and BW dual use issues, involved with the gain of function work in WIV's prediction research, they laid out other important fundamental flaws with Ecohealth and WIV's approach. The authors go on to make the more compelling case for better bio surveillance instead.* <https://www.nature.com/articles/d41586-018-05373-w>



**COMMENT**

07 JUNE 2018

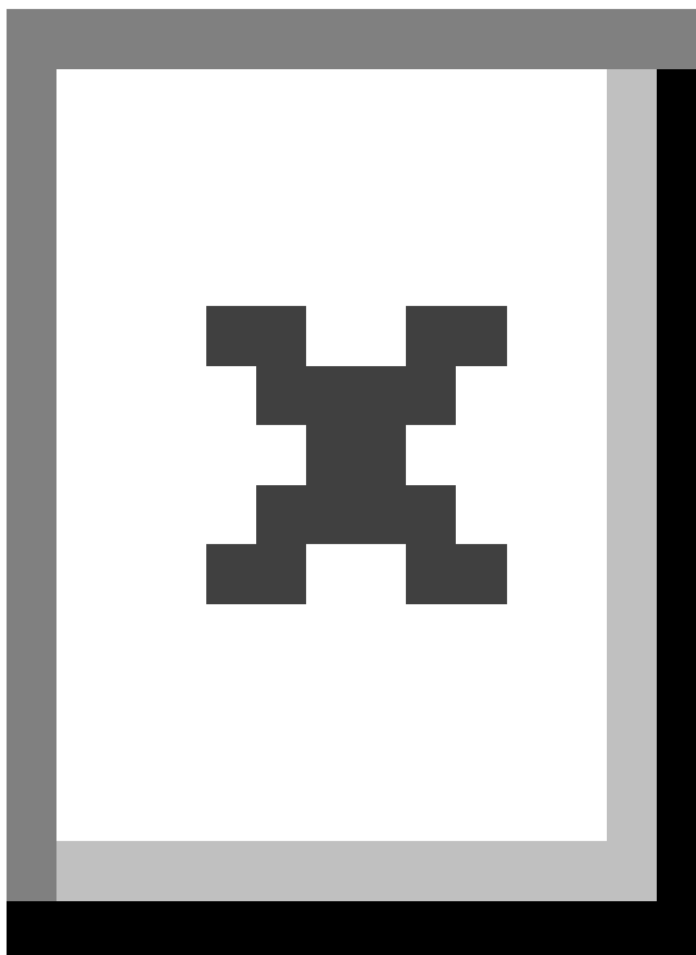
# Pandemics: spend on surveillance, not prediction

Trust is undermined when scientists make overblown promises about disease prevention, warn Edward C. Holmes, Andrew Rambaut and Kristian G. Andersen.

The resurgence of Ebola virus in the Democratic Republic of the Congo this May is a stark reminder that no amount of DNA sequencing can tell us when or where the next virus outbreak will appear. More genome sequence data were obtained for the 2013–16 Ebola epidemic than for any other single disease outbreak. Still, health workers in Mbandaka, the country's northwestern provincial capital, are scrambling to contain a growing number of cases.

Over the past 15 years or so, outbreaks caused by viruses such as Ebola, SARS and Zika have cost governments billions of US dollars. Combined with a perception among scientists, health workers and citizens that responses to outbreaks have been inadequate, this has fuelled what seems like a compelling idea. Namely, that if researchers can identify the next pandemic virus before the first case appears, communities could drastically improve strategies for control, and even stop a virus from taking hold<sup>1,2</sup>. Indeed, since 2009, the US Agency for International Development has spent US\$170 million on evaluating the “feasibility of preemptively mitigating pandemic threats”<sup>1</sup>.

Various experts have flagged up problems with this approach (including the three of us)<sup>3,4</sup>. Nonetheless, an ambitious biodiversity-based approach to outbreak prediction — the Global Virome Project — was announced in February this year, with its proponents soliciting \$1.2 billion in funding from around the world (see ‘High stakes’). They estimate that other mammals and birds contain 1.67 million unknown viruses from the families of viruses that are most likely to jump to humans, and will use the funding to conduct a genomic survey of these unknown viruses, with the aim of predicting which might infect people<sup>1</sup>.



Sources: NIH; Global Virome Project

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Broad genomic surveys of animal viruses will almost certainly advance our understanding of virus diversity and evolution. **In our view, they will be of little practical value when it comes to understanding and mitigating the emergence of disease.**

We urge those working on infectious disease to focus funds and efforts on a much simpler and more cost-effective way to mitigate outbreaks — proactive, real-time surveillance of human populations.

The public has increasingly questioned the scientific credibility of researchers working on outbreaks. In the 2013–16 Ebola epidemic, for instance, the international response was repeatedly criticized for being too slow. And during the 2009 H1N1 influenza epidemic, people asked whether the severity of the virus had been overblown, and if the stockpiling of pharmaceuticals was even necessary<sup>5</sup>. Making promises about disease prevention and control that cannot be kept will only further undermine trust.

### **Forecasting fallacy**

Supporters of outbreak prediction maintain that if biologists genetically characterize all of the viruses circulating in animal populations (especially in groups such as bats and rodents that have previously acted as reservoirs for emerging viruses), they can determine which ones are likely to emerge next, and ultimately prevent them from doing so. With enough data, coupled with artificial intelligence and machine learning, they argue, the process could be similar to predicting the weather<sup>6</sup>.

Reams of data are available to train models to predict the weather. By contrast, it is exceedingly rare for viruses to emerge and cause outbreaks. Around 250 human viruses have been described, and only a small subset of these have caused major epidemics this century.

Advocates of prediction also argue that it will be possible to anticipate how likely a virus is to emerge in people on the basis of its sequence, and by using knowledge of how it interacts with cells (obtained, for instance, by studying the virus in human cell cultures).

This is misguided. Determining which of more than 1.6 million animal viruses are capable of replicating in humans and transmitting between them would require many decades' worth of laboratory work in cell cultures and animals. Even if researchers

managed to link each virus genome sequence to substantial experimental data, all sorts of other factors determine whether a virus jumps species and emerges in a human population, such as the distribution and density of animal hosts. Influenza viruses have circulated in horses since the 1950s and in dogs since the early 2000s, for instance<sup>7</sup>. These viruses have not emerged in human populations, and perhaps never will — for unknown reasons.

In short, there aren't enough data on virus outbreaks for researchers to be able to accurately predict the next outbreak strain. Nor is there a good enough understanding of what drives viruses to jump hosts, making it difficult to construct predictive models.

Biodiversity-based prediction also ignores the fact that viruses are not fixed entities. New variants of RNA viruses appear every day. This speedy evolution means that surveys would need to be done continuously to be informative. The cost would dwarf the proposed \$1.2-billion budget for one-time sequencing.

Even if it were possible to identify which viruses are likely to emerge in humans, thousands of candidates could end up being identified, each with a low probability of causing an outbreak. What should be done in that case? Costs would skyrocket if vaccines and therapeutics were proposed for even a handful of these.

### **Screen and sequence**

Currently, the most effective and realistic way to fight outbreaks is to monitor human populations in the countries and locations that are most vulnerable to infectious disease. This can be done by local clinicians, health workers in non-governmental organizations such as Médecins Sans Frontières (MSF; also known as Doctors Without Borders), and global institutions such as the World Health Organization (WHO).

We advocate the detailed screening of people who are exhibiting symptoms that cannot easily be diagnosed. Such tests should use the latest sequencing technologies to characterize all the pathogens that have infected an individual — the human 'infectome'<sup>8</sup>. To track previous infections, investigators should also assess each person's immune response, by analysing components of their blood using broad-scale serology<sup>9</sup>.

Emerging diseases are commonly associated with population expansions — when people encroach on habitats occupied by animals — as well as with environmental disturbances and climate change. Deforestation, for instance, can promote human interactions with animals that carry new threats, and can increase encounters with new vector species such as ticks and mosquitoes<sup>10</sup>. Animal die-offs, for example that of bar-headed geese (*Anser*

*indicus*) at Lake Qinghai in China in 2005 (which was caused by the H5N1 influenza virus), can also flag problem regions or emerging pathogens. Surveillance efforts should therefore focus on communities that live and work in such environments.

Identifying which pathogen is causing an outbreak is no longer the bottleneck it once was. It took researchers two years to determine HIV as the cause of AIDS in the early 1980s using microscopy and other techniques. By contrast, in 2012 it took only weeks for investigators using genomic technologies to discover the coronavirus that caused Middle East respiratory syndrome (MERS).

Rapid identification of viruses can be achieved only if such technologies — and the people trained to use them — are globally available, including in resource-limited regions where the risk of outbreaks might be higher. Thankfully, relevant capacity-building programmes are now beginning to be established, such as the Human Heredity and Health in Africa (H3Africa) Initiative, run by the UK Wellcome Trust and the US National Institutes of Health<sup>11</sup>.

Once an emerging outbreak virus has been identified, it needs to be analysed quickly to establish what type it is; which molecular mechanisms (such as receptor type) enable it to jump between individuals; how it spreads through human populations; and how it affects those infected. In other words, at least four kinds of analysis are needed: genomic, virological, epidemiological and clinical. And the data must be passed to key stakeholders, from researchers and health workers on the ground to international agencies such as the WHO and the MSF. Data must be kept as free of restrictions as possible, within the constraints of protections of patient privacy and other ethical issues.

This will best be achieved through an established global network of highly trained local researchers, such as the WHO Global Outbreak Alert and Response Network (GOARN). Real-time tools for reconstructing and tracking outbreaks at the genomic level, such as portable sequencing devices, are improving fast<sup>8</sup>. Information gathered during recent outbreaks has quickly had tangible impacts on public-health decisions, largely owing to data generation and analysis by many research teams within days of people being infected<sup>12</sup>.

For instance, in the 2013–16 Ebola epidemic, genome sequencing of the virus proved that a person could sexually transmit the disease more than a year after becoming infected. This prompted the WHO to increase its recommended number of tests for persistent infection in survivors of the disease.



Ultimately, the challenge is to link genomic, clinical and epidemiological data within days of an outbreak being detected, including information about how people in an affected community are interacting. Such an open, collaborative approach to tackling the emergence of infectious disease is now possible. This is partly thanks to technology, but is mainly due to a shift in perception about the importance of this approach. At least in genomic epidemiology, there is a growing move towards real-time, open-access data and analysis, aided by the use of preprint servers and wikis such as Virological (<http://virological.org>). This type of collaborative effort can complement the work of agencies including the WHO and the MSF, which focus predominantly on providing information, isolating those who have been infected, and so on.

So far, researchers have sampled little of the viral universe. Surveys of animals will undoubtedly result in the discovery of many thousands of new viruses. These data will benefit studies of diversity and evolution, and could tell us whether and why some pathogens might jump species boundaries more frequently than others. But, given the rarity of outbreaks and the complexity of host–pathogen interactions, it is arrogant to imagine that we could use such surveys to predict and mitigate the emergence of disease.

New viruses will continue to emerge unexpectedly. There is a lot we can and must do to be better prepared.

*Nature***558**, 180-182 (2018)

*doi:*<https://doi.org/10.1038/d41586-018-05373-w>

**From:** Steven Quay (b)(6)  
**Sent:** Thursday, November 26, 2020 4:03 AM  
**To:** (b)(6)@state.gov>  
**Subject:** Re: Fw: RaTG13 (shared in confidence)

(b)(6)

Tank you for your kind words. We will be camping in the mountains of Taiwan until Saturday and I'm not sure of Internet access but please feel free to send me things. I hope you can have a happy Thanksgiving in some fashion this year.

Regards, Steve

On Wed, Nov 25, 2020, 11:31 PM (b)(6)@state.gov> wrote:  
Steve,

Very helpful! Thank you.

(b)(5) DPP

You are superb scientific detective and scientific researcher. A rare combination!

We are indebted for your insight and assistance,

(b)(6)

**From:** Steven Quay (b)(6)

**Sent:** Wednesday, November 25, 2020 9:15 AM

**To:** (b)(6)@state.gov>

**Cc:** (b)(6)

**Subject:** Re: Fw: RaTG13 (shared in confidence)

(b)(6)

See answers attached. Regards, Steve

On Wed, 25 Nov 2020 at 14:56, (b)(6)@state.gov> wrote:  
Steve,

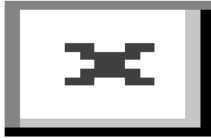
(b)(5) DPP

Thanks.

(b)(6)

<https://www.newsweek.com/controversial-wuhan-lab-experiments-that-may-have-started-coronavirus-pandemic-1500503>

Why The Wuhan Lab Remains A  
Suspect In the Coronavirus  
Investigation



After reporting that Covid-19 occurred naturally, U.S. intelligence modified its stance to say it might have leaked from a lab.

[www.newsweek.com](http://www.newsweek.com)

**From:** Feith, David (b)(6)@state.gov>

**Sent:** Tuesday, November 24, 2020 7:29 PM

**To:** (b)(6)@state.gov>; (b)(6)@state.gov>; Switzer, Bryan R (Rick)

(b)(6)@state.gov>

**Subject:** RE: RaTG13

With Q&A attached...

~~SENSITIVE BUT UNCLASSIFIED~~

**From:** Feith, David

**Sent:** Tuesday, November 24, 2020 7:25 PM

**To:** (b)(6)@state.gov>; (b)(6)@state.gov>; Switzer, Bryan R (Rick)

(b)(6)@state.gov>

**Subject:** RaTG13

(b)(5) DPP

WIV said that RaTG13 was found in the Yunnan cave in 2013, (b)(5) DPP

(b)(5) DPP

It seems that WIV's original Nature article of Feb. 3, 2020 didn't include this history:

<https://www.nature.com/articles/s41586-020-2012-7>. After public challenges, WIV published an addendum just last week, on Nov. 17 2020: <https://www.nature.com/articles/s41586-020-2951-z>. Shi Zhengli also gave an interview to Science published July 31

(<https://science.sciencemag.org/content/369/6503/487?rss=1>); the full Q&A attached includes her statement that WIV "didn't isolate this virus" (page 5).

(b)(5) DPP

(b)(5) DPP

Appreciate any thoughts. Thanks.

--

David Feith

Deputy Assistant Secretary

Bureau of East Asian and Pacific Affairs (EAP)  
U.S. Department of State

(b)(6)

(b)(6)@state.gov

~~SENSITIVE BUT UNCLASSIFIED~~

~~SENSITIVE BUT UNCLASSIFIED~~

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Steven C Quay, MD, PhD, FCAP

T: (b)(6)

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Dr. Quay Official Website

STAY SAFE: #1 Best Seller Amazon Medical eBooks

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